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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

#### NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

#### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

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The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, butilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compound that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

#### 4. DETAILED DESCRIPTION OF THE INVENTION

#### 4.1 DEFINITIONS

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

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The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "delctions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in it's natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

#### 4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

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In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

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Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

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In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1351-2700.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

WO 01/57188

A variety of \_\_\_\_\_ PCT/US01/03800

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed therapeutic compounds and in immunological processes for the development of antibodies.

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The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and process is a full length or mature form of the protein.

In an alternative method, the polypeptide or readily follow known naturally produce the polypeptide or protein, in order to obtain one of the isolated methods for isolating polypeptides and ention. These include, but are not limited to, polypeptides or proteins of the execulusion chromatography, ion-exchange chromatography, immunochromatography receiptions. See, e.g., Scopes, Protein Purification: Principles and Practice, Sprir 4., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

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The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

#### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

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For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) Current Protocols in Molecular Biology, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

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In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

# 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

# 4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells 20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology, J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse 25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology, J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology, J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patcnt No. 5,690,926).

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Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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# 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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#### 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

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The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β<sub>2</sub> microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

# 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

### 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissuc Culture Collection catalogs.

# 4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

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#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

# 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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#### 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

# 4.10.16 LEUKEMIAS

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Leukemias and related disorders may be treated or prevented by administration of a
therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see
Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis:
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

# 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

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The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

# 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

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The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### **4.11.1 EXAMPLE**

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

# 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

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As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

### 4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

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comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, tale, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

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Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

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The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials 5 are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above 10 mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter porc size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. 15 In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

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The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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## 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the  $\mathrm{ED}_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu$ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu$ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

## 4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

## 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}$  and  $F_{(ab)/2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as  $IgG_1$ ,  $IgG_2$ , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

#### 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

#### 5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

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The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

### 5.13.2 Humanized Antibodies

10 The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human 15 immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some 20 instances. Fy framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human 25 immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 30 2:593-596 (1992)).

## 5.13.3 Human Antibodies

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Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

# 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)/2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)/2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_{v}$  fragments.

#### 5.13.5 Bispecific Antibodies

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

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Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., <u>J. Exp. Med.</u> 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

# 5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HTV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

## 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

# 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>I, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

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A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

## 4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem.

56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

## 4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

# 4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

#### 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

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For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

## 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

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Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these arc duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

# 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

# 4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

#### 5.0 EXAMPLES

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#### 5.1 EXAMPLE 1

# Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

#### 5.2 EXAMPLE 2

# **Novel Contigs**

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

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TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
			976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151
	)		217 225 238 271 317 404 446 469 503
	1		513-514 535 550 564 573 666-669 798
	[		898 910 927 976 1067 1083 1085 1178
			1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121
			1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145
	1	•	147 188 197 208 225 227-239 250 300-
	Ì		303 312 316 328-331 340 357-362 374
	<u> </u>	•	380 384-391 408 414 446 448 464-467
			483 488 495-496 505 512 521 535 550
	Ì		566 571 577 585 590 594 598 634 641
	1	•	658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887-
	1		923 927 934 943 950-951 963 976 995
			1000-1001 1006 1026 1034 1048 1057- 1067 1086 1088 1090 1118 1120 1122-
	j		1128 1142 1162 1181-1192 1199 1204
			1218-1219 1225 1232 1253 1267 1271-
	[		1306 1342 1347 1349-1350
adult brain	Clontech	ABR011	49 238 1219
adult brain	BioChain	ABR012	74 238
adult brain	Invitrogen	ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535
dun orum	I III I I I I I I I I I I I I I I I I	1121001	566 596 663 670 746 798 816-819 876
	]	1	892 898 922 943 963 1034-1036 1121
cultured	Strategene	ADP001	41 74 101 138 211 238 304 537 582
preadipocytes	J G		740 798 883 943 976 1067
adrenal gland	Clontech	ADR002	49 74 101 111 120 127 151 215 238
		1	240-247 316 330 363-364 404 414 534-
		ì	535 833 924-940 950 963 976 1001
			1003 1067-1070 1118 1156 1193-1200
		<u> </u>	1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111
			118 129 132 138 151 158-163 182 195-
		İ	203 215 217 238 264 269 353 384 398
		1	408 434-439 446 504 512-513 519 537
		1	562-573 577 611-614 616-619 658 661
		1	671-672 722 734 757-773 815 828-835
		ľ	874 891 898 919 926-927 976 988
	ļ	1	1021 1037 1041 1062 1067 1071 1080
	į	1	1083 1093 1122 1131 1185 1201 1254
adult kidney	GIBCO	AKD001	1308 1331 1335 41 49 51 71-74 78-85 94 100-101 103-
adult Kidney	GIBCO	AVINOI	107 111 119-120 138 151 157 215 217-
			218 238 250 264 294 304 384 404 440
	1	1	446 454 477 504-505 509 514 518-519
		1	535 537 564 574-583 620-627 639 653
			673-675 705 753 789 831 844 851 859
			877 909 918 927 956 963 976 1067
			1074 1083 1095 1178 1302 1331 1335
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316
		,,	446 487 564 575 844 868 910 927 976
			1116
adult lung	GIBCO	ALG001	8 101 111 151 187 402 446 490 514
			1

Tissue Origin	RNA Source	Hyseq Library N	ame SEQ ID NOS:
			518 537 545 549 580 582 592 594 634
			640 651-652 676-678 725 851 873 918
			952 976 1042 1067 1076 1083 1152
lymph node	Clontech	ALN001	8 111 121 151 180-182 188 215 537
			545 549 651 679-682 789 804-810 868
			873 927 952 976 1042 1059 1335
young liver	GIBCO	ALV001	8 64 79 111 186 215-216 238 446 514
	}	1	519 537 564 653 683-684 698 753 798
			813 833 840 858 927 976 1038-1039
			1051 1085 1224 1245 1256
adult liver	Invitrogen	ALV002	40 71 292-293 305 384 468-469 496
			505 657 675 714 753 832 844 941-942
			976 1040 1076 1256 1293
adult liver	Clontech	ALV003	976
adult ovary	Invitrogen	AOV001	8 32 36 38 41 49 51 71 74 79-80 101
	ĺ		104 111 120 122-125 138 140 143-149
	j		151 188-190 207-212 215-217 238 264
			316 384 409 440 445-446 496 504 512
			514 518-519 535 537 549-550 564 566
	[		571 580 582 600 618 638 657 667 681 685-697 699 705 722 735-744 761 771
			815 833 842-865 868 875-876 918 926-
			927 950 952 963 976 1023 1042 1048
			1051 1059 1072 1076 1083 1117 1120
			1124 1131 1144 1174 1224 1268 1331
			1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238
addit spicon	GIBCO	7153 001	294 414 446 477 504 514 534 545 549
			592 722 873 883 952 976 1041-1042
			1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215
	İ		238 446 497 537 642 701-706 811 877
			927 962 976 1083 1117 1131
adult bladder	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545
			592 607 706 873 952 1178 1329-1335
bone marrow	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137
			147 151 164-174 213-215 238 305-307
			374 404 446 460 466 516 519 534 538-
	1		541 544-546 549-554 566 584 586 592
			596 607 610 628-629 643-645 652 707-
	1		708 774-789 844 866-871 873 919 927
			952 963 976 998 1034 1042 1064 1083
			1085 1120 1132 1152 1225 1229 1268
			1307 1310
bone marrow	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132 210 317 510-511 545 549 581 598 628
			638 724 766 789 844 860 868 873 919
			927 952 963 968 976 1042 1111 1141
			1160-1161 1229 1266 1346
hone marrow	Clontech	BMD004	111 238 282 549 1083
bone marrow adult colon	Invitrogen	CLN001	52 260 264 299 494 536 545 564 592
acuit COIOII	HIAITIOREII	CLIVOI	844 873 877 952 976 1042 1152 1268
			1336-1337
adult cervix	BioChain	CVX001	49 51 129 132 151 205 207 238 332-
adust cetaix	BioChain	CANODI	335 365-367 392-401 440 466 470-471
			518 537 597 629 832 877 927 976 1006
		İ	1085 1117 1129-1134 1192 1202-1205
			1219 1309-1328
diaphragm	BioChain	DIA002	74 976 1083
arahin agui	Diconani	1221002	

Tissuc Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
endothelial cells	Strategene	EDT001	32 40-41 49 74 79 101 111 120 132
			138 151 204-206 215-217 238 269 316
	)	!	414 433 505 510 513 550 555 580 582
i		(	596 675 722 745 798 814 836-841 851
}	}		918 976 1041 1043 1073 1083 1131
			1331
Genomic clones	Genomic DNA	EPM001	525-532 927
from the short arm	from Genetic	ļ	j
of chromosome 8	Research		<u> </u>
Genomic clones	Genomic DNA	EPM003	47 525
from the short arm	from Genetic		Į
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM004	525 927
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM005	531
from the short arm	from Genetic		
of chromosome 8	Research	70000	74 100 000
esophagus	BioChain	ESO002	74 138 238
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
fetal brain	Clontech	FBR006	48 61 101 120 132 138 140 147 208 225 271 317 319 336 359 368 405-414
			1
			519 550 571 594 686 715 722 764 824
		ĺ	829 836 859 909 927 943 947 963 1057 1067-1068 1104 1135-1140 1162 1206-
		)	1207 1235 1268 1288 1307-1308 1319
		ĺ	1338-1350
fetal brain	Clontech	FBRs03	111 446
fetal brain	Invitrogen	FBT002	41 51 120 151 192-194 264 504 512
	invinogen	11002	535 683 761 798 820-827 844 876 909
			963 976 1026 1048 1083 1144 1302
fetal heart	Invitrogen	FHR001	446 566 761
fetal kidney	Clontech	FKD001	51 74 111 127 140 151 184 294 537
1010.1110)	) Cloude	, , , , , , , , , , , , , , , , , , , ,	550 630-631 1319
fetal kidney	Clontech	FKD002	111 976 1083
fetal kidney	Invitrogen	FKD007	238 974
fetal lung	Clontech	FLG001	463 566 976 1074 1083 1093
fetal lung	Invitrogen	FLG003	41 238 330 407 415-416 537 573 844
[ 			859 1048 1083 1116 1192
fetal liver-spleen	Columbia	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-64
(	University	1	69-71 74 77 79 87-90 101 107 110-111
			114 120 128-131 138 140 147 150-155
			197 210 215 217 225 238 312 367 384
į	1		414 440 446 460 468 483 496 504-507
			511-515 518-519 523 533-535 537 541 544-545 547-550 555-560 564 566 571
ĺ	1	Í	,
	1		577 582 585-586 598 636 646-647 649 652 664 698 709-710 714 722-723 731
}			735-736 746-753 761 784 798 823 829
}	1		832 844 851 858-859 868 873 876 898
		,	927 943 949 952 963 976 984 1002
ļ			1021 1023 1040 1042 1044 1050 1083
}		}	1093 1116 1120 1129 1131 1144 1174
			1217 1251 1254 1256 1302 1308 1311
			1319
fetal liver-spleen	Columbia	FLS002	8 36-37 41-46 49 54 64 71 74 79 101
,	University		111 120 129 147 207 210 215-216 238
1			250 330 353 359 366 383-384 414 478
			505 508-509 511 515-524 534-535 537
			544-545 564 566 571 577 591 598 638

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			663 671 698 714 722 725 727 751 798
	1	- (	851 859 873 876 909 927 949 952 983-
	ľ	İ	984 1002 1023 1042-1044 1085 1095
	- {	- {	1131 1144 1178 1199 1233 1240-1270
		1	1331 1340
fetal liver-spleen	Columbia University	FLS003	64 535 976 1256
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566
iciai iivci	mvidogen	1 E V OOT	580 722 730 749 844 918 943 976 1051
	i		1256 1331
fetal liver	Clontech	FLV004	537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421
		1	425 535 537 577 598 614 836 857 1141
	1		1208 1268
fetal muscle	Invitrogen	FMS002	537
fetal skin	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151
			225 264 316 405 422-429 488-494 496
	}	<u> </u>	519 534-535 537 566 675 732 859 876-
			877 898 947 949-950 963 976 1001
		İ	1062 1076 1083 1117 1144 1165 1268
	1	1	1281
fetal skin	Invitrogen	FSK002	537 812
fetal spleen	BioChain	FSP001	87 549
umbilical cord	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301
		1	316 446 495-503 519 521 534-535 537
		}	582 634 691 877 883 927 944-950 963
			976 1001 1075 1142-1143 1171 1218
	_		1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135
	1		138 145 151 188 197 207 215 238 264
		1	271 294 316 367 414 440 446 466 504
			513-514 535 542-543 550 564 571 596
		1	635 648-654 675 711-715 722-723 798 832 872 876 883 927 976 1095 1144
			1168 1171 1178 1211 1335
macrophage	Invitrogen	HMP001	238
infant brain	Columbia	IB2002	49-50 77 81 89 105 111 136-138 140
miani Oranj	University	152002	151 161 175-179 185 216-217 264 295
	Oliversity		299 308-310 371-373 462 476 504 511-
			513 533 537 564 566 571 655-657 662
	1		683 716-720 723 752 790-803 829 832
			858-859 876 898 909 949 976 1045-
			1047 1076-1087 1090 1093 1116 1122
	1		1144 1209-1213 1225 1233 1256 1319
			1341
infant brain	Columbia	IB2003	41 50 77 104 132 215 238 508 512-513
	University	ļ	519 566 655 714 794 918 943 976 1067
			1092-1093 1233
infant brain	Columbia	IBM002	311 472-473 753 1214
	University		
infant brain	Columbia	IBS001	51 111 376 474 790 876 949 1144 1204
	University		1221
lung, fibroblast	Strategene	LFB001	151 316 462 514 534 582 675 939 1131
lung tumor	Invitrogen	LGT002	1-7 41 74 79 94 115 120 138-139 156
		<b> </b>	215 217 269 280 296 337 374-375 384
	}		404 446 454 475-480 498 514 518-519
			522 537 545 564 577 597 653 658 705
	)		721-724 754-756 779 859 868 872-874
	1		876-877 919 927 949 951-952 959 976
	1	1	
			1002 1042 1048-1053 1076 1083 1088- 1089 1131 1144-1147 1216-1218 1229

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1293 1311
lymphocytes	ATCC	LPC001	41 74 111 132 151 253 316 446 550
L			634 844 927 976 1085 1268
leukocyte	GIBCO	LUC001	8 11 41 74 86 91-98 101 109 111 120
			147 151 212 215 218 238 252 288 312-
	ļ	}	314.316.338.359.408.427.443-447.505
			510 512 514 518 534 545 549-550 561
		1	564 566 571 577 580 582 587-609 615
			632-638 658-659 698 714 725-728 832
		]	836 841 859 866 873-874 882-883 918-
			919 927 943 952 963 976 1042 1076
			1083 1090 1148 1152 1168 1195 1219-
			1220 1224
leukocyte	Clontech	LUC003	74 100 215 232 238 339-341 446 545
		1	657 660 729 873 883 927 952 963 1008
			1042 1116 1120 1149-1150 1215 1222
Melanoma from cell	Clontech	MEL004	210 215 238 342 534 545 592 722 873
line ATCC #CRL		1	919 929 939 952 976 1071 1118 1218
1424			1235 1245
mammary gland	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147
			217 250-256 264 297-299 305 377-378
	}		398 446 481-486 505 512 537 545 549
†	[		571 592 725 730-733 816 829 836 844
İ		ţ	868 873 876-877 898 926 943 951-960
1	ł	1	963 976 995 1034 1042 1048 1054-
	1	1	1055 1076 1083 1091 1093 1116-1117
			1124 1152 1302
induced neuron cells	Strategene	NTD001	39 101 111 138 238 361 1225 1251
*			1319
retinoid acid induced	Strategene	NTR001	74 225 976
neuronal cells			
neuronal cells	Strategene	NTU001	129 225 238 304 313 361 657 976
pituitary gland	Clontech	PIT004	976
placenta	Clontech	PLA003	38 976
prostate	Clontech	PRT001	111 188 238 257-258 564 724 961-966
ļ	<del> </del>	DECOME.	1067 1095
rectum	Invitrogen	REC001	238 430-431 841 859 868 963 1001
<del></del>	<del></del>	0.17.001	1116
salivary gland	Clontech	SAL001	8 151 402 432-433 446 496 868 952
17.	Olember 1	GDY001	976 1083 1120 1151 1184 8 101 147 215 259-266 446 462 505
small intestine	Clontech	SIN001	
[			545 592 660 789 836 866 873 927 952
,	1		963 967-978 1042 1120 1152 1223-
alcalatal mass 1-	Classach	CVMOOT	238 302 927 943 992 1031
skeletni muscle	Clontech	SKM001	
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267-
	j		270 343-344 353 379 516 537 566 740 828 927 976 979-994 1092 1153-1159
	Clastast	CD7 +01	1225 1250 698 859 1042
adult spieen	Clontech	SPLc01	210 238 271-272 537 580 705 918 952
stomach	Clontech	STO001	
thalanus	Clambach	THAOD	995 1171
thalamus	Clontech	THA002	
thronio	Clonetoch	TUMOOI	963 996-1007 1059 1093 1160-1162 8 120 151 208 221 316-317 353 639
thymus	Clonetech	THM001	
			750 867 874 878-881 927 963 1023 1083 1094-1096 1124
<b>ab.</b>	Clamah	77104-02	8 61 114 129 132 210 225 231 306
thymus	Clontech	THIMc02	•
	Ì		317-319 336 340 359 380 398 446 448-
I	1	1	463 512 519 545 554 587 598 698 724-
1		}	725 789 812 836 868 873 927 947 952

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			976 1007 1042 1083 1085 1097-1116
			1122 1147 1177 1226-1229 1234 1311
l			1313
thyroid gland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
		į.	210 217 222 253 264 271 277-286 294
			320-326 345-352 361 381-382 446 467
			483 514 534 549-550 564 578 602 649
			844 882-883 927 950 956 976 1008-
]		}	1028 1076 1083 1117-1120 1142 1163-
			1175 1230-1238 1308
trachea	Clontech	TRC001	223-225 238 287 353-354 514
,			545 592 611 873 883-884 927
	į	Ì	952 1029-1031 1042 1151-1152
	1		1170 1176-1177 1239
uterus	Clontech	UTR001	151 226 288-290 355 537 877
			885-886 976 1001 1032-1033
			1232

# TABLE 2

SEQ	Accession	Species	Description	Smith-	%
ID NO:	No.		TF.	Waterman Score	Identity
1	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
2	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	111	51
3	R26173	Homo sapiens	Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY2.	293	76
4	L29536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	65
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	50
6	M11507	Homo sapiens	transferrin receptor	120	95
7	AF099100	Homo sapiens	WD-repeat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-45.	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
10	AJ133798	Homo sapiens	copine VII protein	1127	68
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
12	X98330	Homo sapiens	ryanodine receptor 2	282	78
13	AL024498	Homo sapiens	dI417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase))	293	100
14	AF045577	Pan troglodytes	olfactory receptor OR93Ch	191	36
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	93	39
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor	569	89
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	99	44
18	Y36203	Homo sapiens	Human secreted protein #75.	165	75
19	U15647	Mus musculus	reverse transcriptase	106	40
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	380	96
23	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	123	50
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor, second form	284	90
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	96	32
26	S80119	Rattus sp.	reverse transcriptase homolog	100	34
27	U83303	Homo sapiens	line-1 reverse transcriptase	101	35
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	135	45

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman Score	Identity
NO:	004067	TT	II	Score 83	42
29	G04067 G02872	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 8148. Human secreted protein, SEQ ID NO: 6953.	116	72
30 31	G02872 G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	96	67
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7432.	58	32
33	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	2457	98
34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID	348	95
5.	10,0,7	Tiomo supresa	NO:110.		
35	U15131	Homo sapiens	p126	182	48
36	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein	982	90
		<u> </u>	sequence SEQ ID NO:150.		<u> </u>
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain,	687	99
		1	immunoglobulin domain (Ig), transmembrane	ł	
		<del> </del>	domain (TM) and short cytoplasmic domain))	386	66
38	AC067969	amino acids 3338-4088	Homo sapiens ryanodine receptor 1 (skeletal)	380	00
39	AL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN,	493	76
37	AL031300	Homo sapiens	FGENES and GENEWISE)	1 "	'
40	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	110	51
41	AF132969	Homo sapiens	CGI-35 protein	228	68
42	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	220	88
43	X61048	Hydra sp.	mini-collagen	105	35
44	M76546	Helianthus	hydroxyproline-rich protein	110	31
		annuus			<u> </u>
45	U82288	Caenorhabditi	Rac-like GTPase	139	70
15	000455	s elegans	Human secreted protein, SEQ ID NO: 7558.	118	58
46	G03477	Homo sapiens	PRO0657	113	63
47 48	AF090942 G03564	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	90	59
49	AJ005560	Mus	SPR2B protein	72	56
77	73003300	musculus	SI K2D protein	1.5	
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	98
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by	973	94
		•	gene 60 SEQ ID NO:322.		
52	U93563	Homo sapiens	putative p150	105	38
53	Y55927	Homo sapiens	Human STLK2 protein.	699	85
54	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	145	56
55	AB008175	Mus	hepatic nuclear factor 1-beta short form	356	74
56	M68941	Homo sapiens	protein-tyrosine phophatase	165	41
57	AL031600	Homo sapiens	c390E6.1 (chloride channel 7)	338	76
58	AE011417	Mus	putative pheromone receptor	143	55
20	7011417	musculus	parativo prioromono recepto.	1	
59	AF167320	Mus	zinc finger protein ZFP113	558	68
		musculus			L
60	U73036	Homo sapiens	interferon regultory factor 7	263	96
61	X07984	Mus	protein-tyrosine kinase	297	69
	<del>                                      </del>	musculus		1701	100
62	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	791 485	65
63	U35376 AF265555	Homo sapiens Homo sapiens	repressor transcriptional factor ubiquitin-conjugating BIR-domain enzyme	785	74
64	AF 203333	riomo sapiens	APOLLON	, , , ,	'*
65	G03883	Homo sapiens	Human secreted protein, SEQ ID NO: 7964.	88	95
66	AF177390	Manduca	antennal specific membrane protein AMP	274	54
		sexta			
67	AB040800	Homo sapiens	SREB2	614	100
68	AF030027	Equine	24	213	26
		herpesvirus 4			L
69	G02965	Homo sapiens	Human secreted protein, SEQ ID NO: 7046.	261	95
70	W75770	Homo sapiens	Human oxidoreductase YTFO3.	1144	98
71	AB011135	Homo sapiens	KIAA0563 protein	239	76
72	AB014885	Halocynthia	HrPOPK-1	813	78
-77	41:045454	roretzi	ahomholimosa D	955	73
73	AF045454	Cavia porcellus	phospholipase B	933	'3
74	J02870	Mus	laminin receptor ·	308	61

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
140.	<del> </del>	musculus		Beete	<del> </del>
75	Y00826	Rattus	gp210 (AA I-1886)	413	84
76	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	351	54
77	Y38422	Homo sapiens	Human secreted protein.	468	76
78	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha- 1-I (hCavT3).	1357	99
79	Y14591	Human papillomaviru s type 68	APM-1 protein	767	100
80	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	71	34
81	AP000383	Arabidopsis thaliana	protein arginine N-methyltransferase-like protein	359	65
82	L46815	Mus musculus	DNA binding protein Rc	895	75
83	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
84	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	538	71
85	AB029002	Homo sapiens	KIAA1079 protein	134	42
86	Y28678	Homo sapiens	Human cw272_7 secreted protein.	325	62
87	Y99368	Homo sapiens	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.	156	48
88	AJ225124	Mus musculus	hyperpolarization-activated cation channel, HAC3	487	95
89	AF177203	Homo sapiens	cerebral cell adhesion molecule Human G-protein coupled receptor GRIR-2.	290 326	56 79
90 91	Y28280 L39891	Homo sapiens	polycystic kidney disease-associated protein	1751	95
92	AF064876	Homo sapiens	ion channel BCNG-1	953	99
93	AF170723	Homo sapiens	protein kinase STK10	401	53
94 .	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)	151	37
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	661	99
96	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)	1775	92
97	AF134213	Homo sapiens	ubiquitin-specific protease	1995	99
98	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	213	38
99	AF021935	Rattus norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase	675	48
100	AF279265	Homo sapiens	putative anion transporter 1	867 160	98 60
101	AC007878	Homo sapiens	match to nuclear protein, NP220; note: sequence difference at residue 58		
102	U22829	Mus musculus	P2Y purinoceptor	264	42
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	99
104	Y94990 Y87342	Homo sapiens Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20. Human signal peptide containing protein HSPP- 119 SEQ ID NO:119.	787 343	98 57
106	AF169312	Homo sapiens	hepatic angiopoietin-related protein	212	67
107	AF116657	Homo sapiens	PRO1310	74	52
108	AE000401	Escherichia coli	sialic acid transporter	587	96
109	Y38395	Homo sapiens	Human secreted protein encoded by gene No. 10.	693	100
110	Y78801	Homo sapiens	Hydrophobic domain containing protein clone HP00631 amino acid sequence.	182	94
111	Z25535	Homo sapiens	nuclear pore complex protein hnup 153	464	85
112	Y94939	Homo sapiens	Human secreted protein clone ye90_1 protein sequence SEQ ID NO:84.	274	51
113	AF016365	Homo sapiens	hexokinase 1 isoform td	301	71
114	AC007956	Homo sapiens	unknown	520	75
115 116	M83738 AL157952	Homo sapiens Homo sapiens	protein-tyrosine phosphatase dJ875K15.1.1 (ets homologous factor (ets-	251 484	92
110	ML13/932	Homo sapiens	domain transcription factor ESE-3A, isoform 1))	707	* '

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SEQ	Accession	Species	Description	Waterman	Identity
ID	No.			Score	Identity
NO:		<del></del>			1.0
118	L41816	Homo sapiens	cam kinase I	407	62
119	AJ006710	Rattus	phosphatidylinositol 3-kinase	627	93
	<u> </u>	norvegicus	<u></u>		<del> </del>
120	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory	1646	94
	1		subunit precursor, PDPr		1
121	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC	373	68
			3.1.3.48}	<u> </u>	
122	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	262	88
123	Y44403	Homo sapiens	Human truncated tankyrase-1.	111	35
124	U88167	Caenorhabditi	contains similarity to C2 domains	219	29
		s elegans		L	<u> </u>
125	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit	693	90
			4		<u> </u>
126	AB021861	Mus	apoptosis signal-regulating kinase 2	153	65
		musculus			
127	AF305210	Homo sapiens	concentrative Na+-nucleoside cotransporter	807	97
	I	İ	hCNT3		
128	M90360	Homo sapiens	protein kinase	220	73
129	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	86
130	AF208043	Homo sapiens	IFI16b	496	67
131	AF201734	Mus	testis specific serine kinase-3	800	87
	1	musculus			1
132	AF112886	Bos taurus	differentiation enhancing factor 1	159	74
133	AJ278314	Homo sapiens	phospholipase C-beta-1 b	554	85
134	W74802	Homo sapiens	Human secreted protein encoded by gene 73	1157	87
		·	clone HSQEL25.		
135	AB020335	Homo sapiens	Pancreas-specific gene	668	96
136	W80408	Homo sapiens	A secreted protein encoded by clone dt674 2.	866	98
137	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95%	5041	99
			similarity to P49205 (PID:g1345860)		1
138	Y96736	Homo sapiens	PRO3434, a novel secreted protein.	891	100
139	AB024034	Arabidopsis	DNA-damage inducible protein DDI1-like	147	55
		thaliana			
140	W97809	Homo sapiens	Human GTPase regulator GRAF.	248	56
141	Y51557	Homo sapiens	Human PLA2 protein.	125	46
142	AF090113	Rattus	AMPA receptor binding protein	623	93
		norvegicus			
143	W26642	Homo sapiens	Human RECK cancer-inhibiting protein.	641	82
144	U87306	Rattus	transmembrane receptor UNC5H2	578	84
		norvegicus			
145	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein	727	92
		-	M160 precursor	_	<u> </u>
146	W63683	Homo sapiens	Human secreted protein 3.	140	40
147	M96264	Homo sapiens	galactose-1-phosphate uridyl transferase	513	81
148	D64014	Escherichia	HrsA	818	90
		coli			
149	M83316	Escherichia	pppGpp phosphohydrolase	915	95
		COL		j	}
		COII		1261	99
150	AL163279		homolog to cAMP response element binding and	1201	1 //
150	AL163279	Homo sapiens	homolog to cAMP response element binding and beta transducin family proteins	1201	''
150	AL163279 AF179867		beta transducin family proteins STE20-like kinase	940	99
151		Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase		L
	AF179867	Homo sapiens	beta transducin family proteins	940	99
151	AF179867	Homo sapiens Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain	940	99
151 152	AF179867 R95332	Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1	940 392	99
151 152 153	AF179867 R95332 AF151859	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1	940 392 370	99 61 92
151 152 153 154 155	AF179867 R95332 AF151859 X66957 Y16355	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form	940 392 370 489	99 61 92 81
151 152 153 154 155 156	AF179867 R95332 AF151859 X66957 Y16355 G00857	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938.	940 392 370 489 432	99 61 92 81 92
151 152 153 154 155	AF179867 R95332 AF151859 X66957 Y16355	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form	940 392 370 489 432 349	99 61 92 81 92 78
151 152 153 154 155 156 157	AF179867 R95332 AF151859 X66957 Y16355 G00857 AF159455	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus Mus musculus	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938. zinc finger protein	940 392 370 489 432 349	99 61 92 81 92 78
151 152 153 154 155 156 157	AF179867 R95332 AF151859 X66957 Y16355 G00857 AF159455	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938. zinc finger protein interleukin-1 receptor-associated kinase	940 392 370 489 432 349 352	99 61 92 81 92 78 74
151 152 153 154 155 156 157	AF179867 R95332 AF151859 X66957 Y16355 G00857 AF159455	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus Mus musculus	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938. zinc finger protein interleukin-1 receptor-associated kinase putative gene, ankirin like, possible dual	940 392 370 489 432 349 352	99 61 92 81 92 78 74
151 152 153 154 155 156 157 158 159	AF179867 R95332 AF151859 X66957 Y16355 G00857 AF159455 L76191 AP001743	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus Mus Homo sapiens Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938. zinc finger protein interleukin-1 receptor-associated kinase putative gene, ankirin like, possible dual specifity Ser/Thr/Tyr kinase domain	940 392 370 489 432 349 352 537 670	99 61 92 81 92 78 74 76 98
151 152 153 154 155 156 157	AF179867 R95332 AF151859 X66957 Y16355 G00857 AF159455	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens	beta transducin family proteins STE20-like kinase Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). CGI-101 protein hexokinase type 1 alternatively spliced form Human secreted protein, SEQ ID NO: 4938. zinc finger protein interleukin-1 receptor-associated kinase putative gene, ankirin like, possible dual	940 392 370 489 432 349 352	99 61 92 81 92 78 74

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:				Score	1.00
162	Z22968	Homo sapiens	M130 antigen	610	100
163	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1	336	92
164	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	94
165	AF160798	Rattus norvegicus	calcium transporter CaT1	700	96
166	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	327	45
167	Y48607	Homo sapiens	Human breast tumour-associated protein 68.	1072	99
168	AB020741	Mus musculus	NIK-related kinase	197	43
169	AF252293	Homo sapiens	PAR3	596	44
170	U59429	Cricetinae gen. sp.	diacylglycerol kinase eta	481	82
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	42
172	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	507	82
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	653	99
174	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
175	U36488	Mus musculus	embryonic stem cell phosphatase	168	55
176	W95629	Homo sapiens	Homo sapiens secreted protein gene clone gm196_4.	1022	100
177	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	255	93
178	X04936	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in codon)	710	99
179	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP exchange factor	175	80
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	517	94
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	671	96
182	AF110640	Homo sapiens	orphan seven-transmembrane receptor	862	100
183	AB020854	Bos taurus	orphan transporter short splicing variant	766	84
184	AF169691	Homo sapiens	cadherin-like protein VR8	375	38
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	985	99
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	301	98
189	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100
190	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	73
191	U36771	Rattus norvegicus	sn-glycerol 3-phosphate acyltransferase	707	92
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
193	M92084	Theileria parva	cascin kinase II alpha subunit	364	50
194	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	448	90
195	W95631	Homo sapiens	Homo sapiens secreted protein gene clone hj968_2.	382	49
196	AF255614	Rattus norvegicus	scaffolding protein SLIPR	680	99
197	AC021640	Arabidopsis thaliana	putative phosphatidate phosphohydrolase	300	41
198	AF073967	Mus musculus domesticus	olfactory receptor	316	43
199	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	617	98
200	AF117948	Homo sapiens	pancreas-enriched phospholipase C	625	89
201	AF128625	Homo sapiens	CDC42-binding protein kinase beta	636	94
202	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	1303	100
203	Y53021	Homo sapiens	Human secreted protein clone qc646_1 protein sequence SEQ ID NO:48.	701	99
204	AF227968	Homo sapiens	SH2-B beta signaling protein	182	79
			DPH2L=candidate tumor suppressor gene	375	100

SEQ	Accession	Species	Description	Smith-	%
ID	No.		·	Waterman	Identity
NO:				Score	i
		† <del></del>	{ovarian cancer critical region of deletion}		<u> </u>
206	U18315	Sus scrofa	parathyroid receptor	122	60
207	AF255342	Homo sapiens	putative pheromone receptor VIRLI long form	170	96
208	S52051	Rattus sp.	neurotransmitter transporter	715	94
209	W63683	Homo sapiens	Human secreted protein 3.	840	99
210	D79992	Homo sapiens	similar to Drosophila photoreceptor cell-specific	541	82
210	D/9992	Homo sapiens	protein, calphotin.	341	02
	15115010	<del>  ,                                   </del>		1348	99
211	AF117948	Homo sapiens	pancreas-enriched phospholipase C	47L	69
212	U81035	Rattus	ankyrin binding cell adhesion molecule	4/1	99
	1	norvegicus	neurofascin	700	1
213	AF154846	Homo sapiens	zinc finger protein	798	56
214	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	933	93
	<u> </u>	musculus			
215	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	89
216	U26595	Rattus	prostaglandin F2a receptor regulatory protein	563	78
		norvegicus	precursor		
217	G04095	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
218	X75756	Homo sapiens	protein kinase C mu	314	81
219	Y66723	Homo sapiens	Membrane-bound protein PRO1100.	770	98
220	D88577	Mus	Kupffer cell receptor	567	40
- •		musculus		<b>!</b>	1
221	AF258465	Homo sapiens	OTRPC4	853	100
222	AF021935	Rattus	mytonic dystrophy kinase-related Cdc42-binding	636	96
	1.1.021,000	norvegicus	kinase		
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein	693	100
223	AD130327	110mo sapiens	11)	0,3	100
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	690	99
225	AF030430	Mus	semaphorin VIa	703	68
223	Ar030430	musculus	Schiaphorni Via	,03	1 00
226	AE000218	Escherichia	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
220	AE000218	coli	published diffydroxyacetoffe killase (EC 2.7.1.2)	291	"
207	A 5202160	1	The Later with 2 shows his discount in 2	2080	100
227	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	265	88
228	AB024573	Mus	GTP-binding like protein 2	263	88
	1	musculus	71-1-1-1-1-1-1	316	40
229	AF122924	Xenopus	Wnt inhibitory factor-1	316	40
556	1	laevis	GEO 10 NO. 7004	220	100
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.	229	92
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	1
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	95
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific	290	100
	<u> </u>	ļ. <u>.</u>	phospholipase-D.		
234	W69431	Homo sapiens	Human secreted protein cw1233_3.	235	97
235	Y08686	Homo sapiens	serine palmitoyltransferase, subunit II	859	81
236	AF118275	Homo sapiens	atrophin-related protein ARP	117	37
237	X81466	Mus	Embryo Brain Kinase	460	62
	}	musculus	_		
238	U64857	Caenorhabditi	similar to the BPTI/Kunitz family of inhibitors;	284	33
		s elegans	most similar to tissue factor pathway inhibitor		Ì
	1	_	precursor (TFPI)	)	
239	AJ250840	Mus	serine/threonine protein kinase	739	63
		musculus	•		
240	AJ223472	Mus	transcription elongation factor TFIIS.h	222	38
	1.65223	musculus	<b>8</b>	1	1
241	Y94906	Homo sapiens	Human secreted protein clone rb649 3 protein	353	52
241	1 54500	1101110 Sapions	sequence SEQ ID NO:18.	1 333	1
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1	591	99
242		Rattus	orphan transporter v7-3	667	93
243	L22022	norvegicus	Orphan dansporter v /-3	307	1
244	AFOICIO	<del></del>	iiiiiiii	1042	98
244	AF016191	Rattus	potassium channel	1043	75
		norvegicus			1
245	AF097366	Homo sapiens	cone sodium-calcium potassium exchanger	645	98
246	Y29868	Homo sapiens	Human secreted protein clone pp325_9.	497	98
247	AF180475	Homo sapiens	Not4-Np	188	83
		I I I ama seminas	Human secreted protein (clone yal-1).	690	99
248	Y17227 AF250910	Homo sapiens	death-associated small cytoplasmic leucine-rich	0.0	31

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:	140.			Score	Identity
		sexta	protein SCLP		
250	AF192756	Kaposi's sarcoma-	Orf73	134	34
		associated		1	
	İ	herpesvirus	_	1	
251	AB022694	Homo sapiens	MOK protein kinase	209	83
252	W55045	Homo sapiens	Neural adhesion molecule (ethb0018f2 product).	469	100
253	L46815	Mus musculus	DNA binding protein Rc	251	67
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus	Citron-K kinase	1201	98
		musculus		<u> </u>	<u> </u>
256 257	G02491 Z12841	Homo sapiens Oryctolagus	Human secreted protein, SEQ ID NO: 6572.  Phospholipase	460 368	100 80
237	212041	cuniculus	Filosphotipase	300	1 00
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
259	AJ222968	Mus	L-periaxin	430	72
		musculus		1	100
260 261	AJ250839 AJ249977	Homo sapiens	serine/threonine protein kinase AMP-activated protein kinase gamma 3 subunit	861 758	100 98
262	AF141386	Rattus	SLIT-2	198	40
	1.2.1.1.2.2	norvegicus		1	
263	AF022859	Homo sapiens	neuropilin-2(a0)	335	62
264	AF160477	Homo sapiens	Ig superfamily receptor LNIR precursor	387	91
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor (GPCR).	636	99
266	U27269	Mus musculus	sodium glucose cotransporter	204	56
267	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	159	75
268	AF127389	Rattus norvegicus	putative taste receptor TR1	209	39
269	X98296	Homo sapiens	ubiquitin hydrolase	215	95
270	X78482	Streptococcus pyogenes	Fc-gamma receptor	129	26
271	AB009883	Nicotiana tabacum	KED	109	26
272	AF137367	Mus	VPS10 domain receptor protein SORCS	899	97
273	L34938	Rattus	ionotropic glutamate receptor	460	86
		norvegicus		1400	L _
274	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	188	74
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	173	94
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	56
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis thaliana	Contains PF 00069 Eukaryotic protein kinase domain.	157	43
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	73
281	AK024397	Homo sapiens	unnamed protein product	439	91
282	AF141326 AF156530	Homo sapiens	RNA helicase HDB/DICE1	497	76
		Mus musculus	ETS-domain transcriptional repressor PE1	605	
284	Y29336	Homo sapiens	Human secreted protein clone cs756_2 alternate reading frame protein.	647	100
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein sequence SEQ ID NO:26.	300	90
286	AF016411	Homo sapiens	KCNA3.1B	137	100
287	W89253	Homo sapiens	Human ALP.	688	97
288	AF112886	Bos taurus	differentiation enhancing factor 1	750	96
289 290	AF113131 U52111	Homo sapiens Homo sapiens	host cell factor homolog LCP plexin-related protein	367 698	100
291	AF026504	Rattus	SPA-1 like protein p1294	603	89

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
		norvegicus			
292	AF102854	Rattus norvegicus	membrane-associated guanylate kinase- interacting protein 2 Maguin-2	124	53
293	X99211	Drosophila melanogaster	ubiquitin-specific protease	143	38
294	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	185	94
295	Y94890	Homo sapiens	Human protein clone HP02798.	108	59
296	AF019767	Homo sapiens	zinc finger protein	154	96
297	Y28568	Homo sapiens	Secreted peptide clone bd577_1.	568	84
298	Y94943	Homo sapiens	Human secreted protein clone yt14 1 protein sequence SEQ ID NO:92.	182	97
299	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	605	69
300	R58890	Homo sapiens	Human-32 cadherin-related molecule.	212	97
301	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
302	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
303	Y44297	Homo sapiens	Human receptor tyrosine kinase.	228	97
304	D32050	Homo sapiens	alanyl-tRNA synthetase	192	80
305	U43586	Homo sapiens	protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	428	72
306	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	280	95
307	D78572	Mus musculus	membrane glycoprotein	199	41
308	AF255614	Rattus norvegicus	scaffolding protein SLIPR	639	88
309	S79463	Mus sp.	semaphorin homolog=M-Sema F	162	89
310	AF178941	Homo sapiens	ATP-binding cassette sub-family A member 2	736	100
311	U03413	Dictyostelium discoideum	calcium binding protein	151	36
312	Y87347	Homo sapiens	Human signal peptide containing protein HSPP- 124 SEQ ID NO:124.	744	100
313	Z97055	Homo sapiens	dJ388M5.4 (putative GS2 like protein)	789	99
314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	197	38
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and GENEWISE)	278	38
316	U70209	Mus musculus	polycystic kidney disease l protein	165	38
317	AF109643	Rattus norvegicus	coxsackie-adenovirus-receptor homolog	223	38
318	AF104923	Homo sapiens	putative transcription factor	138	84
319	AF100287	Trypanosoma vivax	activated protein kinase C receptor homolog	141	38
320	G00588_	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	125	51
321	Y21591	Homo sapiens	Human secreted protein (clone CC332-33).	459	97
322	D26070	Homo sapiens	human type 1 inositol 1,4,5-trisphosphate receptor	232	97
323	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	306	88
324	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	70
325	M19650	Homo sapiens	2',3'-cyclic-nucleotide 3'-phosphodiesterase (EC 3.1.4.37)	214	97
326	W80396	Homo sapiens	A secreted protein encoded by clone bp646_10.	140	70
327	X75756	Homo sapiens	protein kinase C mu	540	78
328	G02292	Homo sapiens	Human secreted protein, SEQ ID NO: 6373.	721	99
329	AF168990	Homo sapiens	putative GTP-binding protein	877	99
330	S67984	Homo sapiens	anti-HIV gp120 antibody heavy chain variable region	581	80
331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	2823	98
332	Y87330	Homo sapiens	Human signal peptide containing protein HSPP- 107 SEQ ID NO:107.	1127	100
333	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	320	98
334	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95%	327	93

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	ļ	<del> </del>	similarity to P49205 (PID:g1345860)	Score	<del> </del>
335	Y87347	Homo sapiens	Human signal peptide containing protein HSPP- 124 SEQ ID NO:124.	1111	67
336	AF006466	Mus musculus	lymphocyte specific formin related protein	193	75
337	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	632	97
338	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2.	516	100
339	Y07637	Homo sapiens	putative GABA-gated chloride channel	189	100
340	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia coli	L-idonate transcriptional regulator	928	98
342	D90855	Escherichia coli	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	769	99
343	D85613	Escherichia coli	membrane component	399	100
344	M93239	Escherichia coli	transmembrane protein	232	100
345	M60177	Escherichia coli	enterobactin	759	99
346	D90699	Escherichia coli	Sensor protein copS (EC 2.7.3).	638	97
347	D90843	Escherichia coli	CapB protein.	552	100
348	M13422	Escherichia coli	49 kd protein	1193	96
349	L10328	Escherichia coli	similar to drug resistance translocases	340	90
350	X69942	Mus musculus	enhancer-trap-locus-i	560	82
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+- activated potassium channel	463	80
352	D90777	Escherichia coli	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (b- hydroxybutyryl-CoA dehydrogenase) (BhbD).	577	100
353	D90863	Escherichia coli	similar to	311	98
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	58
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-7).	482	55
356	Y58637	Homo sapiens	Protein regulating gene expression PRGE-30.	119	51
357	AF119226	Homo sapiens	dual-specificity tyrosine phosphatase YVH1	1788	100
358	Y87219	Homo sapiens	Human secreted protein sequence SEQ ID NO:258.	165	100
359	J00132	Homo sapiens	beta-fibrinogen	233	93
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
361 362	R28916 U16655	Homo sapiens Rattus norvegicus	Type III procollagen (prior art). phospholipase C delta-4	108 649	65
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	42
364	U47276	Gallus gallus	chicken brain factor-2	104	34
365	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	118	46
367	X98258	Homo sapiens	M-phase phosphoprotein 9	564	75
368	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3387	99
369	U70932	Peromyscus leucopus	reverse transcriptase	92	59
370	X86400	Homo sapiens	gamma subunit of sodium potassium ATPase	242	73
371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56
372	U49974 X13916	Homo sapiens	mariner transposase	257 21193	55 99
373 374	AF234765	Homo sapiens Rattus	LDL-receptor related precursor (AA -19 to 4525) serine-arginine-rich splicing regulatory protein	1182	78
375	U49974	norvegicus Homo sapiens	SRRP86 mariner transposase	172	55
3/3	U477/4	Homo sapiens	mariter dansposase	1/2	<u> </u>

SEQ	Accession	Species	Description	Smith-	1%
ID	No.	Species	Description	Waterman	Identity
NO:	140.	•		Score	Identity
	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	221	67
376	·				1
377	G00669	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	600	100
378	X52574	Mus	GTP binding protein	1456	91
	<u></u>	musculus			
379	R69095	Homo sapiens	Anti-HIV Fab tat3 I light chain.	68	37
380	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
381	AB002405	Homo sapiens	LAK-4p	530	43
382	U64830	Dictyostelium	protein tyrosine kinase	115	44
	•	discoideum			
383	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	618	98
384	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	617	93
385	AJ245822	Homo sapiens	type I transmembrane receptor	4560	100
386	D86974	Homo sapiens	KIAA0220	2148	98
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	50
388	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	59
389	M12140		envelope protein	197	51
390		Homo sapiens		461	77
	AJ293309	Homo sapiens	NHP2 protein		1
391	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	94
392	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	241	66
393	Y14442	Homo sapiens	olfactory receptor protein	339	54
394	W85607	Homo sapiens	Secreted protein clone da228_6.	957	100
395	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	171	34
396	G03930	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	250	100
397	AB032904	Hylobates	dopamine receptor D4	105	35
391	AB032704	syndactylus	dopainme receptor 154	103	33
398	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	861	85
				1047	92
399	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.		
400	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	162	37
401	D87002	Homo sapiens	similar to rat integral membrane glycoprotein; accession number Z21513.	527	78
402	AF100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
403	X74904	Gallus gallus	alpha-2-macroglobulin receptor	258	60
404	AF075462	Mus	ADP-ribosylation factor-directed GTPase	545	89
707	71 075702	musculus	activating protein isoform b	373	07
405	X92887	Human	pol/env	162	30
705	7.72007	endogenous	posare	102	30
	ļ	retrovirus K		}	
406	Y30162	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
407	AK022626			2833	99
	L13802	Homo sapiens	unnamed protein product		92
408		Homo sapiens	ribosmal protein small subunit	264	
409	Y91600	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEO ID NO:273.	1788	89
410	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone	2004	99
410	W 00 /43	Troing Sapiens	HTSEV09.	2004	1
411	AB043953	Mus	Chat-H	2628	82
411	ABU43933		Chai-H	2020	02
410	340.6222	musculus	T	1014	100
412	Y86233	Homo sapiens	Human secreted protein HNTMX29, SEQ ID	1014	92
	ļ	ļ <u> </u>	NO:148.	ļ	<u> </u>
413	U10542	Pan	MHC class I A	265	71
	<u> </u>	troglodytes			<u> </u>
414	AF155097	Homo sapiens	NY-REN-7 antigen	850	95
415	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	88	48
416	Y57911	Homo sapiens	Human transmembrane protein HTMPN-35.	266	89
417	W27651	Homo sapiens	Secreted protein AT205.	481	60
418	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	3077	87
419	AF255559	Notothenia	alpha tubulin	289	68
		coriiceps			
420	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	209	74
421	AL 109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar	1446	96
741	/TL 10302/	Troute sabicits	to rat sperm antigen 4 (SPAG4)))	'0	1
422	AC008075	Arabidopsis	F2415.4	112	35
144	12000013	thaliana	E 4712,7	112	33
	1	i initiana	l	1 1	

SEO	Accession	Species	Description	Smith-	%
ID	No.	1	· ·	Waterman	Identity
NO:			·	Score	_
423	AF231705	Homo sapiens	Alu co-repressor 1	1090	100
424	AF234887	Homo sapiens	FLAMINGO I	6268	97
425	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 191.	1961	99
426	AB009288	Homo sapiens	N-copine	635	98
427	L12392	Homo sapiens	Huntington's Disease protein	16080	99
428	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
429	AJ293573	Homo sapiens	zinc finger protein Cezanne	542	87
430	Y84441	Homo sapiens	Amino acid sequence of a human RNA- associated protein.	2074	100
431	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
432	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	73	42
433	AF159296	Lycopersicon esculentum	extensin-like protein	613	48
434	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	44
435	X73874	Homo sapiens	phosphorylase kinase	3442	97
436	AF161426	Homo sapiens	HSPC308	268	74
437	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
438	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator 1	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	54
443	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
445	X98330	Homo sapiens	ryanodine receptor 2	9356	99
446	AF116712	Homo sapiens	PRO2738	227	49
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	576	99
448	AF133086	Homo sapiens	membrane-type serine protease 1	2630	94
449	U87305	Rattus norvegicus	transmembrane receptor UNC5H1	817	93
450	AF081249	Homo sapiens	JAW1-related protein MRVIIA long isoform	4568	99
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapiens	granule membrane protein-140	464	73
453	AB036706	Homo sapiens	intelectin	730	88
454	G00918	Homo sapiens	Human secreted protein, SEQ ID NO: 4999.	263	81
455	Y22634	Homo sapiens	Human cytokine inducible regulatory protein-1 (CIRP-1).	192	67
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	106	40
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
458	M19155	Plasmodium falciparum	S-antigen precursor	110	36
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	149	43
461	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	184	54
462	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	135	47
463	X84960	Triticum aestivum	low molecular weight glutenin	109	33
464	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	1781	85
465	AF189764	Mus musculus	alpha/beta hydrolase-1	502	59
466	U93569	Homo sapiens	p40	101	30
467	Y41528	Homo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	99
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	149	52
469	AJ000008	Homo sapiens	PI3-kinase	5832	97
470	X70922	Mus musculus	neurotoxin homologue	118	47
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75
472	Y36705	Homo sapiens	Fragment of human secreted protein encoded by	72	57

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
			gene 62.	i	
473	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
474	Y07007	Homo sapiens	Breast cancer associated antigen precursor sequence.	1013	97
475	W93254	Homo sapiens	Human ESRP1 protein.	943	80
476	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
477	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	202	60
478	G01870	Homo sapiens	Human secreted protein, SEQ ID NO: 5951.	267	100
479	AF102777	Mus musculus	FYVE finger-containing phosphoinositide kinase	3427	92
480	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
481	W87701	Homo sapiens	A human membrane fusion protein designated SYTAX1.	221	77
482	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
483	AF210651	Homo sapiens	NAG18	124	59
484	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
485	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
486	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	149	73
487	Y76167	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
488	AJ275213	Homo sapiens	stabilin-l	1244	91
489	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
490	L12392	Homo sapiens	Huntington's Disease protein	16081	100
491	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
492	J03799	Homo sapiens	laminin-binding protein	228	70
493	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	128	41
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	197	67
495	AC005175	Homo sapiens	R31449_3	889	94
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	229	61
497	AB030237	Canis familiaris	D4 dopamine receptor	90	48
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
499	U70935	Peromyscus maniculatus	reverse transcriptase	213	52
500	U48508	Homo sapiens	skeletal muscle ryanodine receptor	26406	99
501	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
502	AF119851	Homo sapiens	PRO1722	156	62
503	AF113685	Homo sapiens	PRO0974	116	50
504	U79458	Homo sapiens	WW domain binding protein-2	322	59
505	W29651	Homo sapiens	Human secreted protein CD124_3.	608	55
506 507	W85459 Y86265	Homo sapiens Homo sapiens	Secreted protein encoded by clone dh1135_9.  Human secreted protein HUSXE77, SEQ ID	986 115	70 33
508	AL160175	Homo sapiens	NO:180. bA243116.3 (similar to MYLK (myosin, light	184	92
			polypeptide kinase))		
509	U43360	Peromyseus maniculatus	reverse transcriptase	97	62
510	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	63
511	W79092	Homo sapiens	Human secreted protein dn740_3.	1058	100
512	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	205	64
513 514	AJ133439	Homo sapiens Drosophila	GRIP1 protein	2151	100
	AE003456	melanogaster	CG6393 gene product	259	42
515	Z17206	Xenopus laevis	p46X1Eg22	128	40
516	AF104413	Homo sapiens	large tumor suppressor 1	1766	94
517	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	40
518	AF151083	Homo sapiens	HSPC249	444	98
519	S80864	Homo sapiens	cytochrome c-like polypeptide	318	50
520	X92485	Plasmodium vivax	pval	170	61

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:	000000	<del>                                      </del>	11	Score	50
521	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	59
522	AF121857	Homo sapiens	sorting nexin 7	259	40
523	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	82	37
524	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	253	73
525	AF119851	Homo sapiens	PRO1722	162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein, SEQ ID NO: 6788.	70	45
528	U47924	Homo sapiens	C8	1112	86
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	45
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	60
531	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	92	65
532	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
533	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484 206	75 53
537 538	AF219232 AF135022	Gallus gallus Homo sapiens	gin-induced kinase mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141	59
540	AF016430	Caenorhabditi	contains similarity to a BR-C/TTK domain	853	39
		s elegans			1
541	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	408	66
542	M29487	Homo sapiens	integrin alpha subunit precursor	517	81
543	AF102530	Mus musculus	olfactory receptor F3	327	73
544	Y73431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	100
545	AE004833	Pseudomonas aeruginosa	probable TonB-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264	53
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein B receptor protein.	1772	67
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:166.	176	100
549	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1	1953	88
551	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein sequence.	1224	94
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus musculus	granuphilin-a	501	41
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	183	32
559	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	68
560	D86214	Mus musculus	Ca2+ dependent activator protein for secretion	1010	93
561	AF187325	Canis familiaris	melanoma antigen	287	55
562	AJ001981	Homo sapiens	OXAIL	2512	99
563	Z17238	Rattus norvegicus	glutamate receptor subtype delta-1	338	66
564	W30638	Homo sapiens	Partial human 7-transmembrane receptor HAPO167 protein.	371	100
565	AC005620	Homo sapiens	R33590 1	467	97
566	Y99358	Homo sapiens	Human PRO1772 (UNQ834) amino acid	1138	78
	AL031177	Homo sapiens	sequence SEQ ID NO:63. dJ889M15.3 (novel protein)	1002	58
567					

OFO	Accession	Cassian	Description	Smith-	%
SEQ	No.	Species	Description	Waterman	Identity
ID	No.	j			lachuty
NO:		ļ <u>.</u>		Score	
569	AF097518	Homo sapiens	liver-specific transporter	231	100
570	AB035698	Homo sapiens	Misshapen/NIK-related kinase MINK-1	1532	100
571	Y07096	Homo sapiens	Colon cancer associated antigen precursor	1064	100
			sequence.		-
572	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	735	55
573	Y66639	Homo sapiens	Membrane-bound protein PRO290.	254	45
574	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
575	D43949	Homo sapiens	This gene is novel.	836	100
576	1 - 102 1-	Homo sapiens	Human breast tumour-associated protein 57.	108	50
	Y48596		Human breast rumour-associated protein 57.		
577	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	141	75
578	R95913	Homo sapiens	Neural thread protein.	140	65
579	AK025116	Homo sapiens	unnamed protein product	201	70
580	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ	77	70
			ID NO:388.		
581	AF196779	Homo sapiens	JM10 protein	450	100
582	AF188706	Homo sapiens	g20 protein	330	98
583	AB030234	Canis	D4 dopamine receptor	64	56
		familiaris		L	<del> </del>
584	G02621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
585	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	268	85
			Antigen)	1	ĺ
586	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	235	35
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	56
588	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	79
589	AF235017	Mus	2P1 protein	764	80
309	AT 255017	musculus	Zr i protein	1 704	30
600	11/00/20		Secreted protein encoded by gene 94 clone	300	<del>  01</del>
590	W88627	Homo sapiens	, , ,	329	81
			HPMBQ32.		
591	Y30709	Homo sapiens	Amino acid sequence of a human secreted	110	43
			protein.	İ	
592	Y53875	Homo sapiens	A human seven transmembrane signal transducer	1369	92
	1	1	polypeptide.	İ	}
593	Y53051	Homo sapiens	Human secreted protein clone dd119_4 protein	1112	97
			sequence SEQ ID NO:108.		
594	Y27658	Homo sapiens	Human secreted protein encoded by gene No. 92.	763	79
595	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	156	58
			CODE		95
596	AF151110	Mus	COPI protein	2215	95
		musculus	 		
597	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	157	65
598	AF192499	Mus	putative secreted protein ZSIG37	143	40
	ſ	musculus			
599	AF119855	Homo sapiens	PRO1847	236	76
600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	73
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	567	88
602	AF 184971	Homo sapiens	class II cytokine receptor ZCYTOR7	2015	74
603	AF061936	Homo sapiens	diacylglycerol kinase iota	773	96
		1			96
604	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	1333	<sup>93</sup>
			Antigen)		
605	AB033106	Homo sapiens	KIAA1280 protein	3915	100
606	X75756	Homo sapiens	protein kinase C mu	3916	99
607	D86983	Homo sapiens	similar to D.melanogaster peroxidasin(U11052)	5758	99
608	W69341	Homo sapiens	Secreted protein of clone CG279 1.	1377	99
609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	339	82
407	1100021	ATOMIC Supicits	HPMBQ32.	1337	
610	V27020	Homo sapiens		114	63
610	Y27868	nomo sapiens	Human secreted protein encoded by gene No.	116	62
	L	<del> </del>	107.		<b>L</b>
611	AF202636	Homo sapiens	angiopoietin-like protein PP1158	2164	100
612	AF090944	Homo sapiens	PRO0663	218	82
613	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	195	59
		,	clone HTDAD22.		
614	M87053	Rattus	lens membrane protein	450	84
		norvegicus		1	1
615	AC004232	Homo sapiens	FPM315	163	37
616	G01984				79
OID	1 001784	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	205	1 /7

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
617	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74 SEQ ID NO:197.	821	99
618	AJ245621	Homo sapiens	CTL2 protein	2258	99
619	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	108	64
620	AF067864	Homo sapiens	transferrin receptor 2 alpha	3922	94
621	D90721	Escherichia	Transmembrane protein dppC	573	90
622	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	730	100
623	Y94982	Homo sapiens	Human secreted protein vb12 1, SEQ ID NO:4.	733	100
	AF034745			637	83
624	AF034743	Mus musculus	LNXp80	637	83
625	U42580	Paramecium bursaria Chlorella	Pro-rich, IPPPNMSLPLS (3x)	94	46
		virus 1		•	
626	U79260	Homo sapiens	unknown	194	70
627	R95913	Homo sapiens	Neural thread protein.	99	50
628	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
629	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	100
630	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	165	76
631	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	268	96
632	U16996	Homo sapiens	protein tyrosine posphatase	351	80
633	AF121857	Homo sapiens	sorting nexin 7	2019	100
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10	340	77
			encoded by GenBank Accession Number L25899		
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAQBK61.	615	62
643	AB015982	Homo sapiens	serine/threonine kinase	485	98
644	Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	46
645	AF122904	Homo sapiens	membrane protein DAP10	474	100
646	AF233323	Homo sapiens	Fas-associated phosphatase-1	200	38
647	W48804	Homo sapiens	Homo sapiens clone BK158_1 protein.	1203	99
648	AF257330	Homo sapiens	COBW-like protein	1440	98
549	Y36203	Homo sapiens	Human secreted protein #75.	233	73
650	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	173	78
651	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
652	AB032909	Hylobates agilis	dopamine receptor D4	122	32
653	AK021848	Homo sapiens	unnamed protein product	186	69
554	W73411	Homo sapiens	Human secreted protein encoded by Gene No. 15.	57	37
655	L22455	Rattus	mu opioid receptor	116	34
656	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	110	45
657	G02345	Homo sapiens	Human secreted protein, SEQ ID NO: 6426.	459	97
658	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	291	75
			HPMBQ32.		<u> </u>
659	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	65
660	Y91423	Homo sapiens	Human secreted protein sequence encoded by gene 11 SEQ ID NO:144.	333	96

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:				Score	<del> </del>
661	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	168	68
662	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	375	43
663	W75771	Homo sapiens	Human GTP binding protein APD08.	629	100
664	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	480	55
665	AB037734	Homo sapiens	KIAA1313 protein	978	96
666	W82841	Homo sapiens	Human cerebral protein-1.	192	84
667	W82841	Homo sapiens	Human cerebral protein-1.	182	87
668	AB030184	Mus musculus	contains transmembrane (TM) region and ATP binding region	757	68
669	AB032919	Hylobates muelleri	dopamine receptor D4	85	37
670	AF107295	Rattus norvegicus	outer membrane protein	746	81
671	Z33642	Homo sapiens	leukocyte surface protein	394	93
672	W85608	Homo sapiens	Secreted protein clone du410_5.	261	91
673	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
674	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	2388	99
675	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	1134	53
676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	74
677	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr	1013	95
678	L11625	Mus musculus	receptor protein-tyrosine kinase	545	96
679	AL031427	Homo sapiens	dJ167A19.3 (novel protein)	745	100
680	AJ133430	Mus musculus	olfactory receptor	528	77
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	70
682	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	336	76
683	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	118	100
684	U43360	Peromyscus maniculatus	reverse transcriptase	100	37
685	G00885	Homo sapiens	Human secreted protein, SEQ ID NO: 4966.	162	60
686	AK001518	Homo sapiens	unnamed protein product	590	100
687	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
688	Y92241	Homo sapiens	Human cancer associated antigen precursor (MO-REN-46).	2405	99
689	AC024792	Caenorhabditi s elegans	contains similarity to TR:P78316	423	36
690	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	183	81
691	Y56514	Homo sapiens	Human Jurkat cell clone P2-15 AIM10 longest ORF protein sequence.	180	88
692	Y27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	1539	99
693	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	428	98
694	U12465	Homo sapiens	ribosomal protein L35	308	89
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1517	99
696	AF191838	Homo sapiens	TANK binding kinase TBK1	1242	98
697	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	275	75
698	Y87280	Homo sapiens	Human signal peptide containing protein HSPP- .57 SEQ ID NO:57.	576	90
699	Y97999	Homo sapiens	Human SCAD family molecule HSFM-1, SEQ ID NO:1.	729	99
700	AJ006701	Homo sapiens	putative serine/threonine protein kinase	610	79
701	AF209198	Homo sapiens	zinc finger protein 277	2357	100
702	AJ298841	Mus musculus	torsinA protein	709	45
703	AK021729	Homo sapiens	unnamed protein product	622	98
704	Z46787	Caenorhabditi s elegans	similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	920	51
705	G02882	Homo sapiens	Human secreted protein, SEQ ID NO: 6963.	589	98

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
706	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	125	58
707	R95326	Homo sapiens	Tumor necrosis factor receptor I death domain ligand (clone 2DD).	121	95
708	G03002	Homo sapiens	Human secreted protein, SEQ ID NO: 7083.	125	39
709	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	98
710	M63577	Saccharomyc es cerevisiae	SFP1	131	59
711	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	467	85
712	D21211	Homo sapiens	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
713	AF044033	Marmota marmota	olfactory receptor	615	83
714	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.	251	100
715	AB033062	Homo sapiens	KIAA1236 protein	1380	100
716	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	73
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	835	99
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	234	100
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid receptor beta4 subunit	578	99
720	AB020598	Homo sapiens	peptide transporter 3	1096	100
721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	570	74
722	J05046	Homo sapiens	insulin receptor-related receptor	6787	100
723	AF001958	Ambystoma tigrinum	electrogenic Na+ bicarbonate cotransporter, NBC	111	41
724	AF127084	Mus musculus	semaphorin cytoplasmic domain-associated protein 3A	5253	94
725	X54673	Homo sapiens	GABA transporter	3114	99
726	AF016191	Rattus norvegicus	potassium channel	370	100
727	AB029559	Rattus norvegicus	BATI	139	35
728	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	97
729	AJ011415	Homo sapiens	plexin-B1/SEP receptor	729	56
730	Z93096	Homo sapiens	bK390B3.1 (manic fringe (Drosophila) homolog)	142	68
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor homologue Vanilrep1.	675	99
732	AF161382	Homo sapiens	HSPC264	492	94
733	AB029033	Homo sapiens	KIAA1110 protein	3826	99
734	AE000493	Escherichia coli	putative transport protein	592	97
735	AL033379	Homo sapiens	dJ417O22.2 (novel 7 transmembrane receptor (rhodopsin family) protein similar to high- affinity lysophosphatidic acid receptor homolog)	2173	99
736	AF132599	Homo sapiens	RANTES factor of late activated T lymphocytes-	245	56
737	X55019	Homo sapiens	acetylcholine receptor delta subunit	883	99
738	X91906	Homo sapiens	voltage-gated chloride ion channel	1978	100
739	AB026116	Homo sapiens	organic anion transporter 4	1444	98
740	D00570	Mus musculus	open reading frame (196 AA)	83	24
741	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	118	40
742	U66059	Homo sapiens	V_segment translation product	614	100
743	AF119815	Homo sapiens	G-protein-coupled receptor	2751	99
744	X16663	Homo sapiens	haematopoietic lineage cell protein (AA 1-486)	148	93
745	W67838	Homo sapiens	Human secreted protein encoded by gene 32 clone HLTCJ63.	448	95
746	W57260	Homo sapiens	Human semaphorin Y.	2414 .	100
747	W21578	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS2232.	968	65
748	Y94935	Homo sapiens	Human secreted protein clone yd218_1 protein sequence SEQ ID NO:76.	622	100
749	AL022238	Homo sapiens	dJ1042K10.5 (novel protein)	314	85
750	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	391	87

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
751	AB025258	Mus musculus	granuphilin-a	773	41
752	Y52386	Homo sapiens	Human transmembrane protein HP02000.	900	99
753	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	2527	99
754	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	694	100
755 755	M85183	Rattus	vasopressin receptor	979	68
		norvegicus	·		
7 <del>5</del> 6	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
758	Z22535	Homo sapiens	ALK-3	439	98
759	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175 clone HE8BI92.	1217	99
761	G03706	Homo sapiens	Human secreted protein, SEQ ID NO: 7787.	223	88
762	AB020676	Homo sapiens	KIAA0869 protein	4433	99
763	AK026992	Homo sapiens	unnamed protein product	2285	99
			glucocorticoid receptor AF-1 coactivator-1	573	100
764	AF173358	Homo sapiens	<del>                                    </del>		89
765	AF268066	Mus musculus	netrin 4	2019	-
766	Y48585	Homo sapiens	Human breast tumour-associated protein 46.	1169	89
767	AF230378	Mus musculus	interleukin-1 delta	309	45
768	AF121975	Mus musculus	odorant receptor S18	268	62
769	AB008515	Homo sapiens	RanBPM	611	57
770	Y09945	Rattus norvegicus	putative integral membrane transport protein	458	50
771	AF226731	Homo sapiens	AD026	688	99
772	Y27132	Homo sapions	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
773	X87832	Homo sapiens	NOV/plexin-Al protein	1821	98
774	AB025258	Mus musculus	granuphilin-a	500	41
775	AF125101	Homo sapiens	HSPC040 protein	232	93
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	314	95
		Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
777	G02493		Sequence of pre-human atrial natriuretic peptide.	213	45
778	R03301	Homo sapiens			1
779 780	AL357374 AF100346	Homo sapiens Homo sapiens	bA353C18.2 (novel protein) neuronal voltage gated calcium channel gamma- 3 subunit	232 1434	100 89
781	Y19566	Homo sapiens	Amino acid sequence of a human secreted protein.	103	52
782	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	1098	93
783	AF084464	Rattus	GTP-binding protein REM2	141	30
784	W49042	Homo sapiens	Human low density lipoprotein binding protein LBP-3.	2693	99
785	AF238381	Homo sapiens	PTOVI	1904	91
786	Y91870	Homo sapiens	Human apoptosis related protein.	547	100
787			Human membrane transport protein, MTRP-7.	1062	94
	Y71062	Homo sapiens			98
788	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	8684	<u>L</u>
789	AL049569	Homo sapiens	dJ37C10.3 (novel ATPase)	2848	96
790	AF151848	Homo sapiens	CGI-90 protein	745	96
791	Y08639	Homo sapiens	nuclear orphan receptor ROR-beta	1421	95
792	Y41706	Homo sapiens	Human PRO381 protein sequence.	644	99
793	AF121228	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP95	1037	100
794	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	62
795	Y69384	Homo sapiens	Amino acid sequence of a 14274 receptor	119	100
193	1		protein.		1

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:				Score	
797	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
798	AF159615	Homo sapiens	FGF receptor activating protein 1	461	98
799	Y59863	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
800	W70459	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
801	L00073	Homo sapiens	renin	1913	93
802	P92219	Homo sapiens	CR1 protein.	11963	97
		(human)		ì	1
803	X15357	Homo sapiens	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
805	AJ243874	Homo sapiens	oligophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
807	Z24680	Homo sapiens	garp	1562	83
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter LAT2	1364	90
809	W70321	Homo sapiens	Secreted protein CC198 1.	1154	96
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115	855	99
	1		clone HOVBA03.	1	
811	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
812	AF092135	Homo sapiens	PTD014	862	100
813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone	358	100
817	G01082		gn114_1.  Human secreted protein, SEQ ID NO: 5163.	549	100
		Homo sapiens		1	
818	AF151800	Homo sapiens	CGI-41 protein	1106	95
819	L00352	Homo sapiens	low density lipoprotein receptor	3980	100
820	X04434	Homo sapiens	IGF-I receptor	5832	99
821	G03844	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
822	AF212220	Homo sapiens	TERA	396	48
823	Y50125	Homo sapiens	Human glycophosphatidylinositol-anchored protein GPI-122.	4897	99
824	AF156778	Homo sapiens	ASB-3 protein	2675	98
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma- 2 subunit	1105	100
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	100
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by gene 24 SEQ ID NO:147.	541	98
830	X54232	Homo sapiens	glypican	1625	87
831	X14830	Homo sapiens	acetylcholine receptor beta-subunit preprotein	2540	100
832	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
833	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	638	96
834	AC003030	Homo sapiens	R29828_1	1389	93
835	Y38422	Homo sapiens	Human secreted protein.	964	87
836	U41557	Caenorhabditi s elegans	glycine-rich	85	36
837	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	998	75
838	AJ011415	Homo sapiens	plexin-B1/SEP receptor	1580	60
839	W80398	Homo sapiens	A secreted protein encoded by clone cw1543_3.	1105	67
840	G00862	Homo sapiens	Human secreted protein, SEQ ID NO: 4943.	255	92
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
842	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	99
843	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein sequence SEO ID NO:114.	1089	100
844	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	357	69
845	AF151810	Homo sapiens	CGI-52 protein	1443	88
	X83378	Homo sapiens	putative chloride channel	1620	99
846					

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:		<u> </u>	4 F00 00 00 00 00 00 00 00 00 00 00 00 00	Score	ļ
040	VADDOG	17	to AF038969 (PID:g2827207)	170	7.
848	X99886 AC005587	Homo sapiens	monocyte chemotactic protein-2 similar to mouse olfactory receptor 13; similar to	160 963	76
849			P34984 (PID:g464305)		
850	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
851	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
852	Y86217	Homo sapiens	Human secreted protein HWHGU54, SEQ ID NO:132.	1189	99
853	AF224741	Homo sapiens	chloride channel protein 7	3748	99
854	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapiens	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HLDRM43.	824	100
862	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkephalin (	1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	96
876	M15530	Homo sapiens	B-cell growth factor	171	56
877 878	W63681 L27867	Homo sapiens Rattus	Human secreted protein 1.	1652 1448	99
		norvegicus	neurexophilin		
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted protein.	321	100
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528	100
883 884	Y18462 Y94950	Homo sapiens Homo sapiens	cathepsin L Human secreted protein clone dh1073_12 protein	209 348	72 100
		·	sequence SEQ ID NO:106.		<u>.</u>
885	AF070661	Homo sapiens	HSPC005	404	100
886 887	Y04315 X92744	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 23.	385	100
888	Y22496	Homo sapiens	hBD-1  Human secreted protein sequence clone	375 994	94
889	Y41293	Homo sapiens	cn621_8.  Human soluble protein ZTMPO-1.	4595	99
890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	63
891	AF208856	Homo sapiens	BM-014	1012	99
892	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	Clone HNFGW06 of EGFR receptor family.	326	63
896	M24110	Homo sapiens	G0S19-2 peptide precursor	481	100
897	Z68747	Homo sapiens	imogen 38	2018	99
898	AF186112	Homo sapiens	neurokinin B-like protein ZNEUROKI	619	100
899	AF225420	Homo sapiens	AD025	734	100

CEO.	T A	I Cassino	Description	Smith-	1%
SEQ ID	Accession No.	Species	Description	Waterman	Identity
NO:	10.			Score	lacinity
900	P60657	Homo sapiens	Sequence of human lipocortin.	1835	100
901	M27288	Homo sapiens	oncostatin M	1297	99
902	W85737	Homo sapiens	Polypeptide with transmembrane domain.	749	100
903	G01349	Homo sapiens	Human secreted protein, SEQ ID NO: 5430.	650	99
904	Y00261	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
904	AF039688	Homo sapiens	antigen NY-CO-3	771	99
906	AB007836	Homo sapiens	Hic-5	2544	100
907	AB007836 AB017507	Homo sapiens	Apg12	224	100
908	AK000056	Homo sapiens	unnamed protein product	1537	98
909	Y86299	Homo sapiens	Human secreted protein HFOXB55, SEQ ID	427	100
909	1 80299	Hoino Sapiens	NO:214.	421	100
910	AF231023	Homo sapiens	protocadherin Flamingo 1	7393	99
911	Y14134	Homo sapiens	Vascular endothelial cell growth inhibitor beta	1319	100
911	114134	rionio sapiens	protein sequence.	1317	1 100
912	290420	Homo sapiens	Human GDF-3 (hGDF-3) polypeptide encoding	1950	100
712	230420	Homo sapicus	cDNA.	1750	1 100
913	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	1361	100
914	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	48
915	U14971	Homo sapiens	ribosomal protein S9	886	90
916	AF172854	Homo sapiens	cardiotrophin-like cytokine CLC	1204	99
917	AC005525	Homo sapiens	F22162 1	1963	100
918	AF166350	Homo sapiens	ST7 protein	4711	99
919	Y87285	Homo sapiens	Human signal peptide containing protein HSPP-	430	100
717	187283	Homo Sapiciis	62 SEQ ID NO:62.	450	100
920	Y36131	Homo sapiens	Human secreted protein #3.	465	88
921	AF193766	Homo sapiens	cytokine-like protein CI7	724	100
922	Y95013	Homo sapiens	Human secreted protein vc48 1, SEQ ID NO:66.	357	100
923	X75208	Homo sapiens	protein tyrosine kinase-receptor	5256	100
924	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	813	98
925	AB039886	Homo sapiens	down-regulated in gastric cancer	785	78
926	G03368	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	55	50
927	Y48606	Homo sapiens	Human breast tumour-associated protein 67.	539	100
927	Y36151	Homo sapiens	Human secreted protein #23.	668	100
929	AF110399	Homo sapiens	elongation factor Ts	1666	100
930	AF210317	Homo sapiens	facilitative glucose transporter family member	2763	99
930	AF210317	rioino sapiens	GLUT9	2703	"
931	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
932	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
933	U47924	Homo sapiens	B-cell receptor associated protein	1469	100
934	G03827	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	529	93
935	AB039371	Homo sapiens	mitochondrial ABC transporter 3	196	63
936	X56385	Canis	rab8	1064	100
730	730363	familiaris	1400	1007	1 ***
937	B08906	Homo sapiens	Human secreted protein sequence encoded by	117	44
751	500,00	Tionno Sabiens	gene 16 SEQ ID NO:63.	111	"
938	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein	515	42
,,,,	133000	1 Joino Sapicits	designated HSCOP-6.	7.5	**
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor	1904	99
770	110030	1 Torne Saprens	(PAR).	1,504	~
941	AC005102	Homo sapiens	small inducible cytokine subfamily A member	627	99
J (1	110000102	1 2010 Suprens	24	1	
942	M12886	Homo sapiens	T-cell receptor beta chain	1289	81
943	AF226046	Homo sapiens	GK003	1049	98
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ	667	100
277	130076	110mo sapiois	ID NO. 463.	1 30.	
	+	Homo sapiens	cytochrome c	565	100
945	1 8/1/2/2007/7				93
945	M22877		Human secreted protein encoded by gene 62	1 551	
945 946	W67869	Homo sapiens	Human secreted protein encoded by gene 63	551	93
946	W67869	Homo sapiens	clone HHGDB72.		
	<del></del>		clone HHGDB72.  Human secreted protein encoded by gene 53	283	100
946 947	W67869 W67859	Homo sapiens Homo sapiens	clone HHGDB72.  Human secreted protein encoded by gene 53 clone HBMCL41.	283	100
946 947 948	W67869 W67859 W85726	Homo sapiens Homo sapiens	clone HHGDB72.  Human secreted protein encoded by gene 53 clone HBMCL41.  Novel protein (Clone BG33_7).	283	100
946 947	W67869 W67859	Homo sapiens Homo sapiens	clone HHGDB72.  Human secreted protein encoded by gene 53 clone HBMCL41.	283	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO: 951	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	1314	100
952	Y36111	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 496.	402	70
953	AB012109	Homo sapiens	APC10	990	100
954	AF246221	Homo sapiens	transmembrane protein BRI	1405	100
955	AF054986	Homo sapiens	putative transmembrane GTPase	1883	100
956	W74726	Homo sapiens	Human secreted protein fg949_3.	1879	100
957	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
958	AJ222967	Homo sapiens	cystinosin	1920	100
959	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	587	100
960	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	283	100
961	AF151855	Homo sapiens	CG1-97 protein	1214	96
962	U26592	Homo sapiens	diabetes mellitus type I autoantigen	250	65
963	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	3796	100
964	AF078859	Homo sapiens	PTD004	2089	100
965	AB020315	Homo sapiens	homologue of mouse dkk-1 gene: Ace# AF030433	1466	100
966	X04571	Homo sapiens	precursor polypeptide (AA -22 to 1185)	6580	99
967	AF146019	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
968	AF071002	Homo sapiens	minK-related peptide 1; MiRP1	632	100
969	AB021227	Homo sapiens	membrane-type-5 matrix metalloproteinase	3545	100
970	AF180920	Homo sapiens	cyclin L ania-6a	1579	100
971	AF105365	Homo sapiens	K-Cl cotransporter KCC4	5621	99
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	739	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4	6295	100
974	W61619	Homo sapiens	Clone HTPEF86 of TM4SF superfamily.	454	100
975	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
976	AF275948	Homo sapiens	ABCA1	11763	99
977 978	AB026891 AF117657	Homo sapiens Homo sapiens	cystine/glutamate transporter thyroid hormone receptor-associated protein	2552 3348	99
			complex component TRAP80		
979	AF044201	Rattus norvegicus	neural membrane protein 35; NMP35	1570	92
980	AF119297	Homo sapiens	neuroendocrine-specific protein-like protein I	1170	99
981	AF155652	Homo sapiens	potassium channel modulatory factor	1983	99
982	W88499	Homo sapiens	Human stomach carcinoma clone HP10412- encoded protein.	1553	99
983	Z56281	Homo sapiens	interferon regulatory factor 3	2012	98
984	AB026125	Homo sapiens	ART-4	2160	100
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	172	70
986	AB023888	Homo sapiens	b-chemokine receptor CCR4	1895	100
987	W27291	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
988	AF153450	Manduca sexta	juvenile hormone esterase binding protein	226	32
989	G03697	Homo sapiens	Human secreted protein, SEQ ID NO: 7778.	194	88
990	AF204159	Homo sapiens	potassium large conductance calcium-activated channel beta 3a subunit	1486	100
991	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
992	AL031266	Caenorhabditi s elegans	VM106R.1	327	40
993	Y66749	Homo sapiens	Membrane-bound protein PRO1124.	4730	99
994	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	77
995	AF133845	Homo sapiens	corin	5811	99
996	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	4999	100
997	W62066	Homo sapiens	Human stem cell antigen 2.	284	93
998	Y87173	Homo sapiens	Human secreted protein sequence SEQ ID NO:212.	725	100
	1772220	Homo sapiens	Amino acid sequence of protein PRO263.	1654	99
999	Y13379		Parmio acid sequence of pretein i Rozos.		
999 1000	Y95008 AF190167	Homo sapiens	Human secreted protein vf3_1, SEQ ID NO:56.  membrane associated protein SLP-2	676 1747	47 100

1002	SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
Homo sapiens   Human secreted protein encoded by Gene No.   2150   100		G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	398	96
1006   X33735   Homo sapiens   Rembrane protein   642   100   1006   X37345   Homo sapiens   Extended human secreted protein sequence, SEQ   824   99   1008   AB032918   Hylobates   moloch   1009   Y91680   Homo sapiens   Extended human secreted protein sequence encoded by   1372   99   1010   AL136125   Homo sapiens   Human secreted protein sequence encoded by   1372   99   1011   G03733   Homo sapiens   Human secreted protein   SEQ (ID NO: 353   379   98   1012   Y1731   Homo sapiens   Human secreted protein   SEQ (ID NO: 4805   462   100   1014   AP1283092   Nagleria   gruberi   Human secreted protein   SEQ (ID NO: 4805   462   100   1015   AB045292   Homo sapiens   Human secreted protein   SEQ (ID NO: 4805   462   100   1016   X15940   Homo sapiens   Human secreted protein   SEQ (ID NO: 4805   462   100   1017   Y94873   Homo sapiens   Human secreted protein   SEQ (ID NO: 4805   462   100   1018   AL024498   Homo sapiens   M83 protein   3867   99   1020   W03516   Homo sapiens   Human protein   Homo   Hylosophical   Human		W73420		Human secreted protein encoded by Gene No.	2150	100
1006	1004	X12791				100
1007   V35997   Homo sapiens   Extended human secreted protein sequence, SEQ   824   99   1008   AB032918   Hylobates   dopamine receptor D4   92   35   35   1009   V91680   Homo sapiens   Human secreted protein sequence encoded by   1372   99   1010   AL136125   Homo sapiens   Human secreted protein, SEQ ID NO: 7814   379   98   1011   G03733   Homo sapiens   Human secreted protein, SEQ ID NO: 7814   379   98   1013   G00724   Homo sapiens   Human secreted protein, SEQ ID NO: 7814   379   98   1014   AP288992   Nageleria gruberi   AB045292   Homo sapiens   Human secreted protein, SEQ ID NO: 4805   462   100   1014   AP288992   Nageleria gruberi   AB045292   Homo sapiens   Human secreted protein, SEQ ID NO: 4805   462   100   1017   Y94873   Homo sapiens   Homo sapiens   Human secreted protein, SEQ ID NO: 4805   462   100   1017   Y94873   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1017   Y94873   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   Y91689   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   Y91689   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   X600660   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   X600660   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   X600660   Homo sapiens   Human secreted protein   SEQ ID NO: 5041   398   100   1002   X600660   Homo sapiens   Human   TR-interacting protein   SI03a   1466   97   1002   X600660   Homo sapiens   Human   TR-interacting protein   SI03a   1466   97   1002   X600660   Homo sapiens   Human   TR-interacting protein   SI03a   1466   97   1003   X60682   Homo sapiens   Human   X600660   Homo sapiens   Human   X600660   X600660   Homo sapiens   X600660   Homo sapiens   Human   X600660   X600660   X600660   X600660   X600660   X600660   X600660   X600660   X600660	1005	M23323	Homo sapiens	membrane protein		
ID NO. 382.	1006	X63745	Homo sapiens	KDEL receptor	326	98
Mono Sapiens   Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.   99	1007	Y35997	Homo sapiens		824	99
			moloch	· ·		i
1011   G03733   Homo sapiens   Human secreted protein, SEQ ID NO: 7814.   379   98   98   1012   17531   Homo sapiens   Human secreted protein clone BL203 I by protein.   318   97   1013   G00724   Homo sapiens   Human secreted protein, SEQ ID NO: 4805.   462   100   1014   AF288092   Naegleria   haem lyuse   114   37   37   1015   AB045292   Homo sapiens   M83 protein   3867   99   1016   X15940   Homo sapiens   human protein clone HP02632.   1876   100   1017   Y94873   Homo sapiens   Human protein clone HP02632.   1876   100   1018   AL024498   Homo sapiens   Human protein clone HP02632.   1876   100   1018   AL024498   Homo sapiens   Human protein clone HP02632.   1876   100   1018   AL024498   Homo sapiens   Human protein clone HP02632.   1876   100   1019   X83425   Homo sapiens   Human secreted protein   3054   99   1020   W03516   Homo sapiens   Prostaglandin DP receptor.   1864   100   1021   G03960   Homo sapiens   Human secreted protein, SEQ ID NO: 8041   398   100   1022   Y91689   Homo sapiens   Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.   1023   AE000660   Homo sapiens   Human secreted protein sequence encoded by gene 93 SEQ ID NO:362   1024   AF132965   Homo sapiens   Human TR-interacting protein S103a   1466   97   1025   W92380   Homo sapiens   Human TR-interacting protein S103a   1466   97   1026   R66278   Homo sapiens   Human TR-interacting protein   1530   100   1028   Y41741   Homo sapiens   Human PRO704 protein sequence   1323   100   1028   Y41741   Homo sapiens   Human PRO704 protein sequence   1323   100   1024   AF03682   Homo sapiens   Human PRO704 protein sequence   1323   100   1024   AF036682   Homo sapiens   Human Secreted protein   1540   103   103   W65682   Homo sapiens   Human Secreted protein   1540   103   103   W65682   Homo sapiens   Human secreted protein   1047   W74809   Homo sapiens   Human secreted protein   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   1047   104				gene 81 SEQ ID NO:353.		
1013		1				
1013   G00724   Homo sapiens   Human secreted protein, SEQ ID NO: 4805.   462   100	1011	G03733				
1014	1012	Y17531	Homo sapiens			
1015   AB045292   Homo sapiens   M83 protein   3867   99	1013	G00724		Human secreted protein, SEQ ID NO: 4805.		
1016	1014	AF288092	gruberi	haem lyase	114	37
1016			Homo sapiens	M83 protein	1	
1018	1016		Homo sapiens	ribosomal protein L31 (AA 1-125)	1 -	
1019   X83425   Home sapiens   Lutheran blood group glycoprotein   3054   99   1020   W03516   Home sapiens   Prostaglandin DP receptor   1864   100   1021   G03960   Home sapiens   Human secreted protein   SEQ ID NO: 8041   398   100   1022   Y91689   Home sapiens   Human secreted protein   SEQ ID NO: 8041   398   100   1023   AE000660   Home sapiens   Human secreted protein   SEQ ID NO: 362   100   1024   AF132965   Home sapiens   CGI-31 protein   1550   100   1025   W92380   Home sapiens   Human TR-interacting protein   S103a   1466   97   1026   R66278   Home sapiens   Human TR-interacting protein   S103a   1466   97   1027   X65614   Home sapiens   S100P calcium-binding protein   476   100   1028   Y41741   Home sapiens   Human PRO704 protein sequence   1323   100   1029   AJ001014   Home sapiens   Human PRO704 protein   S406   100   1030   W63682   Home sapiens   Human Secreted protein   2.   1354   99   1031   AK023007   Home sapiens   Human Secreted protein   2.   1354   99   1032   W97900   Home sapiens   Human SR-BI class B scavenger   2672   99   1033   Y82453   Home sapiens   Human TGC-440 secretory protein SEQ ID   639   99   1034   Y73473   Home sapiens   Human TGC-440 secretory protein   752   93   1035   Y86468   Home sapiens   Human Secreted protein clone yd178_1 protein   752   93   1036   U09813   Home sapiens   Human Secreted protein fragment, SEQ   90   1037   AJ242832   Home sapiens   calpain   Sequence SEQ ID NO:168   100   1039   AJ242730   Home sapiens   calpain   Sequence   SEQ ID NO: 4449   75   50   1040   AF169968   Mus   muscultus   Permability increasing protein   SEQ ID NO: 6613   60   53   1041   X52563   Bos taurus   permability increasing protein   SEQ ID NO: 6613   60   53   1044   AF125101   Home sapiens   Human secreted protein, SEQ ID NO: 6613   60   53   1046   AF125101   Home sapiens   Human secreted protein encoded by gene 81   176   100   1046   AF125101   Home sapiens   Human secreted protein encoded by gene 81   176   100   1049   W88667   Home sapiens   Gerted pro				Human protein clone HP02632.		
1019   X83425   Homo sapiens   Lutheran blood group glycoprotein   3054   99	1018	AL024498		dJ417M14.1 (novel protein)	1	
1020   W03516   Homo sapiens   Prostaglandin DP receptor.   1864   100   1021   G03960   Homo sapiens   Human secreted protein, SEQ ID NO: 8041.   398   100   1022   Y91689   Homo sapiens   Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.   573   100   1024   AF132965   Homo sapiens   CGI-31 protein   1550   100   1025   W92380   Homo sapiens   Therapeutic polypeptide from glioblastoma cell   1850   100   1026   R66278   Homo sapiens   Therapeutic polypeptide from glioblastoma cell   1830   100   1028   Y41741   Homo sapiens   Human PRO:704 protein sequence.   1323   100   1029   AJ001014   Homo sapiens   Human PRO:704 protein sequence.   1323   100   1029   AJ001014   Homo sapiens   Human PRO:704 protein sequence.   1354   99   1031   AK023007   Homo sapiens   Human secreted protein 2.   1354   99   1031   AK023007   Homo sapiens   Human SR-BI class B scavenger.   2672   99   NO:11   1034   Y73473   Homo sapiens   Human SR-BI class B scavenger.   2672   99   NO:13   Y82453   Homo sapiens   Human secreted protein clone yd178_1 protein   752   93   1036   U09813   Homo sapiens   Human secreted protein fragment, SEQ   90   NO:18   Human secreted protein fragment, SEQ   90   1037   AJ242832   Homo sapiens   mitochondrial ATP synthase subunit 9 precursor   698   100   1037   AJ242730   Homo sapiens   nitochondrial ATP synthase subunit CHRNE   2574   100   1039   AJ242730   Homo sapiens   Human secreted protein, SEQ ID NO: 6613   60   63   60   63   60   63   60   60			Homo sapiens	Lutheran blood group glycoprotein	3054	99
1022   Y91689	1020	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	
1023	1021	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1024 AF132965 Homo sapiens   CGI-31 protein   1550   100   1025 W92380 Homo sapiens   Human TR-interacting protein S103a   1466   97   1026 R66278 Homo sapiens   Human TR-interacting protein S103a   1466   97   1027 X65614 Homo sapiens   S100P calcium-binding protein   476   100   1028 Y41741 Homo sapiens   S100P calcium-binding protein   476   100   1029 AJ001014 Homo sapiens   RAMP1   806   100   1030 W63682 Homo sapiens   Human PRC704 protein sequence   1323   100   1031 AK023007 Homo sapiens   Human secreted protein 2   1354   99   1032 W97900 Homo sapiens   Human SR-BI class B scavenger   2672   99   1033 Y82453 Homo sapiens   Human SR-BI class B scavenger   2672   99   1034 Y73473 Homo sapiens   Human secreted protein clone yd178_1 protein   752   93   1035 Y86468 Homo sapiens   Human secreted protein fragment, SEQ   90   1037 AJ242832 Homo sapiens   mitochondrial ATP synthase subunit 9 precursor   698   100   1039 AJ242730 Homo sapiens   calpain   catefylcholine receptor epsilon subunit CHRNE   2574   100   1039 AJ242730 Homo sapiens   polyhomeotic 2   1310   100   1040 AF169968 Mus   musculus   DNA binding protein DESRT   1453   80   1041 X52563 Bos taurus   permability increasing protein   1850   100   1042 G00368 Homo sapiens   Human secreted protein, SEQ ID NO: 6613   60   53   1044 M94582 Homo sapiens   Human secreted protein, SEQ ID NO: 6613   60   53   1044 M94582 Homo sapiens   Human secreted protein, SEQ ID NO: 6613   60   53   1046 AF125101 Homo sapiens   Himan secreted protein, SEQ ID NO: 6613   60   53   1047 W74809 Homo sapiens   HSPC040 protein   S80   100   1048 AL02238 Homo sapiens   Himan secreted protein encoded by gene 81   176   100   1049 W88667 Homo sapiens   Secreted protein encoded by gene 134 clone   1559   99	1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by	768	100
1024	1023	AE000660	Homo sapiens	hADV36S1	573	100
1026   R66278	1024	AF 132965		CGI-31 protein	1550	100
1026   R66278   Homo sapiens   Therapeutic polypeptide from glioblastoma cell   100	1025	W92380	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1028	1026	R66278		Therapeutic polypeptide from glioblastoma cell	830	100
1028         Y41741         Homo sapiens         Human PRO704 protein sequence.         1323         100           1029         AJ001014         Homo sapiens         RAMP1         806         100           1030         W63682         Homo sapiens         Human secreted protein 2.         1354         99           1031         AK023007         Homo sapiens         human secreted protein product         766         100           1032         W97900         Homo sapiens         Human SR-BI class B scavenger.         2672         99           1033         Y82453         Homo sapiens         Human TGC-440 secretory protein SEQ ID         639         99           1034         Y73473         Homo sapiens         Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.         752         93           1035         Y86468         Homo sapiens         Mitchan gene 48-encoded protein fragment, SEQ plotter         96         90           1036         U09813         Homo sapiens         mitchchondrial ATP synthase subunit 9 precursor         698         100           1037         A1242832         Homo sapiens         mitchchondrial ATP synthase subunit Proteins         2574         100           1039         A12642832         Homo sapiens         polyhomeotic 2	1027	X65614	Homo sapiens	S100P calcium-binding protein	476	100
1029   AJ001014   Homo sapiens   RAMP1   806   100   1030   W63682   Homo sapiens   Human secreted protein 2.   1354   99   1031   AK023007   Homo sapiens   Human SR-BI class B scavenger.   2672   99   1032   W97900   Homo sapiens   Human SR-BI class B scavenger.   2672   99   1033   Y82453   Homo sapiens   Human TGC-440 secretory protein SEQ ID   639   99   NO:1.					1323	100
1031   AK023007   Homo sapiens   unnamed protein product   766   100	1029	AJ001014			806	100
1032   W97900   Homo sapiens   Human SR-BI class B scavenger.   2672   99     1033   Y82453   Homo sapiens   Human TGC-440 secretory protein SEQ ID   639   99     1034   Y73473   Homo sapiens   Human secreted protein clone yd178_1 protein   752   93     1035   Y86468   Homo sapiens   Human gene 48-encoded protein fragment, SEQ   96   90     1036   U09813   Homo sapiens   mitochondrial ATP synthase subunit 9 precursor   698   100     1037   AJ242832   Homo sapiens   calpain   3699   99     1038   X66403   Homo sapiens   polyhomeotic 2   1310   100     1040   AF169968   Mus   DNA binding protein DESRT   1453   80     1041   X52563   Bos taurus   permability increasing protein   383   29     1042   G00368   Homo sapiens   Human secreted protein, SEQ ID NO: 4449   75   50     1043   G02532   Homo sapiens   Human secreted protein, SEQ ID NO: 6613   60   53     1044   M94582   Homo sapiens   bG256022.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))   1046   AF125101   Homo sapiens   Human secreted protein encoded by gene 81   176   100     1049   W88667   Homo sapiens   Secreted protein encoded by gene 134 clone   1559   99     HAIBP89   HAIBP89	1030	W63682	Homo sapiens	Human secreted protein 2.	1354	99
1032   W97900   Homo sapiens   Human SR-BI class B scavenger.   2672   99     1033   Y82453   Homo sapiens   Human TGC-440 secretory protein SEQ ID   639   99     1034   Y73473   Homo sapiens   Human secreted protein clone yd178_1 protein   752   93     1035   Y86468   Homo sapiens   Human secreted protein fragment, SEQ   96   90     1036   U09813   Homo sapiens   mitochondrial ATP synthase subunit 9 precursor   698   100     1037   AJ242832   Homo sapiens   calpain   3699   99     1038   X66403   Homo sapiens   acetylcholine receptor epsilon subunit CHRNE   2574   100     1039   AJ242730   Homo sapiens   polyhomeotic 2   1310   100     1040   AF169968   Mus   DNA binding protein DESRT   1453   80     1041   X52563   Bos taurus   permability increasing protein   383   29     1042   G00368   Homo sapiens   Human secreted protein, SEQ ID NO: 4449.   75   50     1043   G02532   Homo sapiens   Human secreted protein, SEQ ID NO: 6613.   60   53     1044   M94582   Homo sapiens   human secreted protein, SEQ ID NO: 6613.   60   53     1045   AL080239   Homo sapiens   bG256022.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))     1046   AF125101   Homo sapiens   Human secreted protein, acid labile subunit))     1047   W74809   Homo sapiens   Human secreted protein encoded by gene 81   176   100     1049   W88667   Homo sapiens   Secreted protein encoded by gene 134 clone   1559   99     HAIBP89.   HAIBP89.	1031	AK023007	Homo sapiens	unnamed protein product	766	100
1033   Y82453   Homo sapiens   Human TGC-440 secretory protein SEQ ID   NO:1.	1032	W97900	Homo sapiens	Human SR-BI class B scavenger.	2672	99
Sequence SEQ ID NO:168.	1033	Y82453		Human TGC-440 secretory protein SEQ ID	639	99
ID NO:383.	1034			sequence SEQ ID NO:168.	752	93
1037   AJ242832   Homo sapiens   calpain   3699   99     1038   X66403   Homo sapiens   acetylcholine receptor epsilon subunit CHRNE   2574   100     1039   AJ242730   Homo sapiens   polyhomeotic 2   1310   100     1040   AF169968   Mus	1035	Y86468	Homo sapiens	ID NO:383.	96	90
1038   X66403   Homo sapiens   acetylcholine receptor epsilon subunit CHRNE   2574   100				mitochondrial ATP synthase subunit 9 precursor		
1039   AJ242730   Homo sapiens   polyhomeotic 2   1310   100		AJ242832				1
1040	1038	X66403	Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
musculus   musculus	1039	AJ242730	Homo sapiens	polyhomeotic 2		
1042         G00368         Homo sapiens         Human secreted protein, SEQ ID NO: 4449.         75         50           1043         G02532         Homo sapiens         Human secreted protein, SEQ ID NO: 6613.         60         53           1044         M94582         Homo sapiens         interleukin 8 receptor B         1850         100           1045         AL 080239         Homo sapiens         bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))         1704         50           1046         AP125101         Homo sapiens         HSPC040 protein         580         100           1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone         1559         99	1040 -	AF169968		DNA binding protein DESRT	1453	80
1043         G02532         Homo sapiens         Human secreted protein, SEQ ID NO: 6613.         60         53           1044         M94582         Homo sapiens         interleukin 8 receptor B         1850         100           1045         AL 080239         Homo sapiens         bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))         1704         50           1046         AP125101         Homo sapiens         HSPC040 protein         580         100           1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone         1559         99	1041	X52563	Bos taurus		383	29
1043         G02532         Homo sapiens         Human secreted protein, SEQ ID NO: 6613.         60         53           1044         M94582         Homo sapiens         interleukin 8 receptor B         1850         100           1045         AL 080239         Homo sapiens         bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))         1704         50           1046         AP125101         Homo sapiens         HSPC040 protein         580         100           1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone         1559         99	1042	G00368	Homo sapiens		75	50
1044         M94582         Homo sapiens         interleukin 8 receptor B         1850         100           1045         AL080239         Homo sapiens         bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))         1704         50           1046         AF125101         Homo sapiens         HSPC040 protein         580         100           1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81 clone HMWDN32.         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone HAIBP89.         1559         99	1043			Human secreted protein, SEQ ID NO: 6613.	60	53
1045	1044	M94582				
1046         AF125101         Homo sapiens         HSPC040 protein         580         100           1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81 clone HMWDN32.         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone HAIBP89.         1559         99				bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile	1704	50
1047         W74809         Homo sapiens         Human secreted protein encoded by gene 81 clone HMWDN32.         176         100           1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone HAIBP89.         1559         99	1046	AP125101	Homo saniens		580	100
1048         AL022238         Homo sapiens         dJ1042K10.4 (novel protein)         2201         100           1049         W88667         Homo sapiens         Secreted protein encoded by gene 134 clone         1559         99           HAIBP89.         HAIBP89.         1559         1559         1559         1559				Human secreted protein encoded by gene 81		
1049 W88667 Homo sapiens Secreted protein encoded by gene 134 clone 1559 99 HAIBP89.	1048	AL022238	Homo saniens	dJ1042K10.4 (novel protein)	2201	100
				Secreted protein encoded by gene 134 clone		
1050 AF097518 Homo sapiens liver-specific transporter 2820 100	1050	AF097518	Homo sapiens	liver-specific transporter	2820	100

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
1051	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1052	Y21851	Homo sapiens	Human signal peptide-contianing protein (SIGP) (clone ID 2328134).	1643	95
1053	AL163815	Arabidopsis thaliana	putative protein	661	62
1054	Y76200	Horno sapiens	Human secreted protein encoded by gene 77.	262	100
1055	AJ276567	Homo sapiens	TC10-like Rho GTPase	1160	100
1056	Y27620	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1057	D14530	Homo sapiens	ribosomal protein	745	100
1058	AF132000	Homo sapiens	TADA1 protein	1132	100
1059	AL031778	Homo sapiens	dJ34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, lsoquinoline-binding protein)) LlKE protein)	920	100
1060	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
061	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1062	Z11697	Homo sapiens	HB15	1088	100
1063	AF123757	Homo sapiens	putative transmembrane protein	819	100
1064	AF155135	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
065	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
1066	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575	100
1067	Y36087	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 472.	770	85
1068	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	100
1069	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	100
1070	W64535	Homo sapiens	Human leukocyte ceil clone HP00804 protein.	2014	99
1071	X03145	Homo sapiens	pot. ORF III	148	50
1072	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	821	91
1073	X82200	Homo sapiens	gpStaf50	249 99	62
1074	G03213	Homo sapiens	Human secreted protein, SEQ ID NO: 7294.	506	47
1075 1076	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	424	55 98
1077	G03187 L25899	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7268. ribosomal protein L10	332	76
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by	898	97
		<u> </u>	gene 48 SEQ ID NO:168.		
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	290	89
1080	AB039723	Homo sapiens	WNT receptor frizzled-3	1376	92
1081	AB020527	Homo sapiens	Na/PO4 cotransporter homolog	269	100
1082	L13802	Homo sapiens	ribosmal protein small subunit	499	80
1083	W75098	Homo sapiens	Human secreted protein encoded by gene 42 clone HSXB125.	143	81
1084	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	83	51
1085 1086	G04063 AF090942	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88 124	64
1086	G00517	Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598.	124	41
1087	G04091	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4398.  Human secreted protein, SEQ ID NO: 8172.	126	
1089	AF140631	Homo sapiens	G-protein coupled receptor 14	364	36 82
1090	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	114	32
1090	S72304	Mus sp.	LMW G-protein	146	83
1092	W88708	Homo sapiens	Secreted protein encoded by gene 175 clone HEMAM41.	405	100
1093	W85612	Homo sapiens	Secreted protein clone fh123 5.	4358	97
094	Y53012	Homo sapiens	Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30.	1013	99
1095	Y92345	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-62.	409	100
096	AF090942	Homo sapiens	PRO0657	147	60
097	L24521	Homo sapiens	transformation-related protein	166	58
098	X56932	Homo sapiens	23 kD highly basic protein	490	70
1099	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	35
1100	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	149	59

SEQ	Accession	Species	Description	Smith-	%
ID `	No.			Waterman	Identity
NO:				Score	
1101	AF119851	Homo sapiens	PRO1722	183	72
1102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8167.	207	62
1103	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	91	52
1104	X74856	Mus	ribosomal protein L28	128	69
		musculus			1
1105	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	130	62
1106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
1107	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	69	43
1108	AF039942	Homo sapiens	HCF-binding transcription factor Zhangfei	744	99
1109	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor	738	94
	1	,	beta subunit		1
1110	AF111108	Mus	transient receptor potential 2	223	79
		musculus			
1111	AF119900	Homo sapiens	PRO2822	144	59
1112	Y16589	Homo sapiens	A protein that interacts with presentlins.	265	39
1113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	178	67
1114	Y02999	Horno sapiens	Fragment of human secreted protein encoded by	164	63
	[		gene 121.		
1115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	1217	99
1116	X51394	Xenopus	APEG precursor protein	130	40
		laevis			
1117	M27826	Homo sapiens	neutral protease large subunit	442	65
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	72	60
1119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	491	97
1120	Y35906	Homo sapiens	Extended human secreted protein sequence, SEQ	244	97
			ID NO. 155.		i
1121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1122	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88
1125	W64469	Homo sapiens	Human secreted protein from clone CW795 2.	191	53
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1127	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1128	Y84320	Homo sapiens	Human cardiovascular system associated protein kinase-1.	815	99
1129	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	88	73
1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone	700	100
1150	132323	Homo sapiciis	HP01512.	700	100
1131	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	260	91
1132	Y91644	Homo sapiens	Human secreted protein sequence encoded by	525	96
1152	1310	Tionio sapiens	gene 43 SEQ ID NO:317.	323	1 -0
1133	Y91449	<del></del>			
1133		Homo saniens	Human secreted protein sequence encoded by	542	100
	131447	Homo sapiens	Human secreted protein sequence encoded by	542	100
1134			gene 49 SEQ ID NO:170.		
1134	AB017908	Homo sapiens	gene 49 SEQ ID NO:170. 4F2 light chain	2399	93
1135	AB017908 X51760	Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170. 4F2 light chain zine finger protein (583 AA)	2399 312	93
	AB017908	Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain zinc finger protein (583 AA) Human PRO1604 (UNQ785) amino acid	2399	93
1135 1136	AB017908 X51760 Y99426	Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain zinc finger protein (583 AA) Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	2399 312 917	93 55 72
1135 1136	AB017908 X51760 Y99426 G03790	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.	2399 312 917	93   55   72   50
1135 1136 1137 1138	AB017908 X51760 Y99426 G03790 AF155106	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen	2399 312 917 102 768	93   55   72   50   91
1135 1136 1137 1138	AB017908 X51760 Y99426 G03790	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane	2399 312 917	93   55   72   50
1135 1136 1137 1138 1139	AB017908 X51760 Y99426 G03790 AF155106 AL031055	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen d128H20.1 (novel protein similar to membrane transport proteins)	2399 312 917 102 768 117	93 55 72 50 91 30
1135 1136 1137 1138 1139	AB017908 X51760 Y99426 G03790 AF155106 AL031055	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Bos taurus	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen d128H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7	2399 312 917 102 768 117	93   55   72   50   91   50   96
1135 1136 1137 1138 1139	AB017908 X51760 Y99426 G03790 AF155106 AL031055	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen dJ28H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7  Human Protease and associated protein-12	2399 312 917 102 768 117	93 55 72 50 91 30
1135 1136 1137 1138 1139 1140 1141	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen dJ28H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).	2399 312 917 102 768 117 138 623	93 55 72 50 91 50 96 100
1135 1136 1137 1138 1139 1140 1141	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zine finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane transport proteins)  regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.	2399 312 917 102 768 117 138 623	93 55 72 50 91 50 96 100
1135 1136 1137 1138 1139 1140 1141	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen dJ28H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).	2399 312 917 102 768 117 138 623	93 55 72 50 91 50 96 100
1135 1136 1137 1138 1139 1140 1141 1142 1143	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018 G04091 AB030235	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Canis familiaris	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane transport proteins)  regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor	2399 312 917 102 768 117 138 623 113	93 55 72 50 91 50 96 100
1135 1136 1137 1138 1139 1140 1141	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane transport proteins)  regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor  Human secreted protein clone pv6_1 protein	2399 312 917 102 768 117 138 623	93 55 72 50 91 50 96 100
1135 1136 1137 1138 1139 1140 1141 1142 1143	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018 G04091 AB030235	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Canis familiaris Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane transport proteins)  regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor  Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	2399 312 917 102 768 117 138 623 113 89	93 55 72 50 91 50 96 100 38 48
1135 1136 1137 1138 1139 1140 1141 1142 1143	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018 G04091 AB030235 Y94922	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Canis familiaris Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  d128H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor  Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50. rab-related GTP-binding protein	2399 312 917 102 768 117 138 623 113 89 539	93 55 72 50 91 30 96 100 38 48 88
1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018 G04091 AB030235 Y94922 X99962 G03807	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Canis familiaris Homo sapiens Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  dJ28H20.1 (novel protein similar to membrane transport proteins)  regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRO-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor  Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.  rab-related GTP-binding protein Human secreted protein, SEQ ID NO: 7888.	2399 312 917 102 768 117 138 623 113 89 539 398 168	93 55 72 50 91 50 96 100 38 48 88
1135 1136 1137 1138 1139 1140 1141 1142 1143 1144	AB017908 X51760 Y99426 G03790 AF155106 AL031055 AF011359 Y70018 G04091 AB030235 Y94922	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Canis familiaris Homo sapiens	gene 49 SEQ ID NO:170.  4F2 light chain  zinc finger protein (583 AA)  Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.  Human secreted protein, SEQ ID NO: 7871.  NY-REN-36 antigen  d128H20.1 (novel protein similar to membrane transport proteins) regulator of G-protein signaling 7  Human Protease and associated protein-12 (PPRG-12).  Human secreted protein, SEQ ID NO: 8172.  D4 dopamine receptor  Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50. rab-related GTP-binding protein	2399 312 917 102 768 117 138 623 113 89 539	93 55 72 50 91 30 96 100 38 48 88

SEQ	Accession	Species	Description	Smith-	%
ID	No.	1		Waterman	Identity
NO:	·			Score	
		s elegans	cerevisiae zinc resistance protein		
150	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	117	62
151	G01003	Homo sapiens	Human secreted protein, SEQ ID NO: 5084.	181,	80
152	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	198	63
1153	X88799	Oryza sativa	DNA binding protein	95	41
1154	D85245	Homo sapiens	TR3beta	155	96
1155	R74272	Homo sapiens	Turnour suppressor protein, p53.	341	87
1156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID	99	41
			NO:180.		
157	G02577	Homo sapiens	Human secreted protein, SEQ ID NO: 6658.	263	98
158	AF104334	Homo sapiens	putative organic anion transporter	185	42
159	G01393	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
160	W75771	Homo sapiens	Human GTP binding protein APD08.	224	81
161	AF216833	Homo sapiens	M-ABC2 protein	410	83
162	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
163	AF119851	Homo sapiens	PRO1722	230	70
164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP-	113	31
172	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	<del>                                     </del>	29 SEQ ID NO:29.	1339	1-02
165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	82
166	AF269286	Homo sapiens	HC6	134	64
167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	51
168	D90789	Escherichia coli	Dipeptide transport system permease protein DppC.	411	90
1169	R63783	Homo sapiens	TG0847 protein.	344	90
170	Y45274	Homo sapiens	Human secreted protein encoded from gene 18.	478	98
171	D64154	Homo sapiens	Mr 110,000 antigen	347	96
172	AB026256	Homo sapiens	organic anion transporter OATP-B	311	67
			Human secreted protein, SEQ ID NO: 4438.	60	52
173	G00357	Homo sapiens		178	59
174	D87717	Homo sapiens	similar to human GTPase-activating protein(A49869)	L	
175	M64716	Homo sapiens	ribosomal protein	391	78
176	R08330	Homo sapiens	Human IL-7 receptor clone H6.	285	67
177	L06505	Homo sapiens	ribosomal protein L12	242	72
178	AJ251885	Homo sapiens	organic cation transporter (OCT2)	276	88
179	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	155	71
180	G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	282	90
181	AF181856	Rattus	tRNA selenocysteine associated protein	249	62
101	71 101050	norvegicus	de 171 Seletion y Steine autociated proton	1	] ""
182	AF161524	Homo sapiens	HSPC176	138	90
183	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	282	66
				107	71
184	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	/1
185	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	88	69
186	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	118	46
187	AB032905	Hylobates concolor	dopamine receptor D4	96	37
188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 5037.	292	78
189	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	178	79
190	G03238	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	324	76
				187	70
191	AF117755	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP230		<u> </u>
192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-5).	202	67
193	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	99	42
194	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	192	76
195	W29661	Homo sapiens	Homo sapiens CI542 2 clone secreted protein.	2001	98
196	Y14104	Homo sapiens	Human GABAB receptor 1d protein sequence.	239	69
197	X61972	Homo sapiens	macropain subunit iota	149	90
				145	51
198	G00534	Homo sapiens	Human secreted protein, SEQ ID NO: 4615.  Human secreted protein HELHN47, SEQ ID	1089	89
1199	Y86260	Homo sapiens	NO:175.	154	
1200	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.		57

Description   Description		TA-TOURIS -	1.6		Smith-	T%
NO:	SEQ	Accession	Species	Description		
1902   1902		No.				Identity
1202   M27826			<u> </u>			<u> </u>
1203   Y73424   Homo sapiess   Human secreted protein clone yi4   protein   Secure Seq Did No? 10.	1201	L				
Sequence SEQ ID NO:70.	1202	M27826	Homo sapiens		202	49
Sequence SEQ ID NO:70.	1203	Y73424	Homo sapiens	Human secreted protein clone vi4 1 protein	265	61
AF264014	1230					1
M160   precursor	1704	A E264014	Home coniens		625	100
1206 U78111 Gallas gallus   AO   205   57   1207 AF095448 Homo sapiens   PRO8259   127   75   1208 AF16/715 Homo sapiens   PRO8259   127   75   1210 AF205718 Homo sapiens   PRO8259   127   75   1210 AF205718 Homo sapiens   PRO8259   127   75   1210 AF205718 Homo sapiens   PRO8259   127   75   1210 AF205718 Homo sapiens   PRO8259   127   75   1211 Y27868 Homo sapiens   PRO8259   PRO8259   127   75   1212 G00719 Homo sapiens   Human secreted protein encoded by gene No.   224   70   1213 G01009 Homo sapiens   Human secreted protein, SEQ ID NO: 4800   117   44   1213 G01009 Homo sapiens   PRO8259   Human secreted protein, SEQ ID NO: 5090   351   73   1214 AF20504 Homo sapiens   PRO8259   Human secreted protein encoded by gene 17   124   70   1215 Y14427 Ilomo sapiens   PRO8259   Human secreted protein encoded by gene 17   124   70   1216 G03905 Homo sapiens   PRO8259   Human secreted protein encoded by gene 17   124   70   1217 Y37897 Homo sapiens   Human secreted protein encoded by gene 17   124   70   1218 J00194 Homo sapiens   Human secreted protein encoded by gene 17   124   70   1219 V39709 Homo sapiens   Secreted protein follows   173   173   174   1220 W81576 Homo sapiens   Secreted protein follows   174   175   175   1221 W96745 Homo sapiens   Secreted protein follows   174   175   175   1222 Y35911 Homo sapiens   Secreted protein follows   174   175   175   1223 Y00278 Homo sapiens   Human secreted protein sequence, SEQ   135   31   1224 Y47070 Homo sapiens   Human secreted protein encoded by gene 21   260   95   1225 U4970 Homo sapiens   Human secreted protein sequence, SEQ   135   31   1226 G01733 Homo sapiens   Human secreted protein sequence, SEQ   135   31   1227 AF09973 Musculus   175   175   175   175   175   175   1231 X98333 Homo sapiens   Human secreted protein, SEQ ID NO: 5814   610   110   1232 W76960 Homo sapiens   Human secreted protein encoded by gene 77   121   131   1233 Y4940 Homo sapiens   Human secreted protein encoded by gene 77   121   131   1234 W86833 Homo sapiens   Human secreted	1204	AC 204014	Homo Sapiens		023	1 20
1206			<u> </u>		-	1
1206						
1208   AF116715   Homo sapiens   PRO2839   127   75	1206	[ U78111			1	57
1210	1207	AF095448	Homo sapiens	putative G protein-coupled receptor	416	76
1210	1208	AF116715	Homo sapiens	PRO2829	127	75
1210   AF205718   Homo sapiens suppressor   Homo sapiens suppressor   Homo sapiens suppressor   Homo sapiens   EBV-induced G-protein coupled receptor (EBI- 220   Polypeptide.   Homo sapiens   Homo sa					475	95
Suppressor   Human secreted protein encoded by gene No.   224   70   107   1		1				
1211   V27868	1210	AI 203/16	Figure Sapicits		423	''
107.   107.		ļ	<u> </u>			<del> </del>
1212   G00719   Homo sapiens   Human secreted protein, SEQ ID NO: 4800.   117   31   31   301009   Homo sapiens   Human secreted protein, SEQ ID NO: 5090.   351   73   73   73   74427   110mo sapiens   Tluman secreted protein, SEQ ID NO: 5090.   124   70   70   71   70   71   70   71   71	1211	Y27868	Homo sapiens		224	70
1213   G01009   Homo sapiens   Human secreted protein, SEQ ID NO: 5090.   351   73   70   1214   70   1215   Y14427   Homo sapiens   Human secreted protein encoded by gene 17   99   77   1216   G03905   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   57   1217   Y57897   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   57   1217   Y57897   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   100   1218   100194   Homo sapiens   Human secreted protein   454   78   1219   Y59709   Homo sapiens   Secreted protein for-28-3-A12-FL1.   470   92   1220   W81576   Homo sapiens   Secreted protein for-28-3-A12-FL1.   470   92   1221   W96745   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-2) polypeptide.   High affinity immunoglobulin E receptor-like   650   98   1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   11   1233   Y00278   Homo sapiens   Human secreted protein sequence, SEQ   135   11   1224   AF 161422   Homo sapiens   Human secreted protein encoded by gene 21.   260   95   1226   G01733   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100   1227   AF099973   Mus			I			_[
1213   G01009   Homo sapiens   Human secreted protein, SEQ ID NO: 5090.   351   73   70   1214   70   1215   Y14427   Homo sapiens   Human secreted protein encoded by gene 17   99   77   1216   G03905   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   57   1217   Y57897   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   57   1217   Y57897   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   100   1218   100194   Homo sapiens   Human secreted protein   454   78   1219   Y59709   Homo sapiens   Secreted protein for-28-3-A12-FL1.   470   92   1220   W81576   Homo sapiens   Secreted protein for-28-3-A12-FL1.   470   92   1221   W96745   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-2) polypeptide.   High affinity immunoglobulin E receptor-like   650   98   1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   11   1233   Y00278   Homo sapiens   Human secreted protein sequence, SEQ   135   11   1224   AF 161422   Homo sapiens   Human secreted protein encoded by gene 21.   260   95   1226   G01733   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100   1227   AF099973   Mus	1212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 4800.	117	44
1214   AF000042   Homo sapiens   PRO057   1215   Y14427   Homo sapiens   Human secreted protein encoded by gene 17   99   77   1216   G03905   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   57   1217   Y37897   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   100   1218   J00194   Homo sapiens   Human transmembrane protein HTMPN-21.   1173   100   1218   J00194   Homo sapiens   Secreted protein for 28-3-A12-Ft.1.   470   92   1220   W81576   Homo sapiens   Secreted protein for 28-3-A12-Ft.1.   470   92   1220   W81576   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-2) polypeptide.   1221   W96745   Homo sapiens   High affinity immunoglobulin E receptor-like   650   98   1222   V35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   31   1223   Y00278   Homo sapiens   Human secreted protein encoded by gene 21   266   95   1204   AF161422   Homo sapiens   Human secreted protein sequence, SEQ   35   1225   U14970   Homo sapiens   Human secreted protein S5   202   95   1226   G01733   Homo sapiens   Human secreted protein, SEQ ID NO: 5814   610   100   1227   AF099973   Mus   schiafen2   333   56   56   301   323   401   324   32	1213	G01009	Homo sapiens	Human secreted protein, SEO ID NO: 5090.	351	73
1215						70
Colone HSIEA/14.     Colone HSIEA/14.     Colone HSIEA/14.     Tys7897						1
1216   G03905   Homo sapiens   Human secreted protein, SEQ ID NO: 7986.   173   173   174   175897   Homo sapiens   Human transmembrane protein HTMPN-21.   1173   100   1218   100194   Homo sapiens   Ha-dr antigen alpha chain   454   78   1219   759709   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-220   W81576   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-224   2) polypeptide.   1221   W96745   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-224   2) polypeptide.   1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   31   1224   AF161422   Homo sapiens	1215	X 14427	110mo sapiens		99	''
1217					<u> </u>	<b></b> _
1218   J00194   Homo sapiens   Ala-dr antigen alpha chain   454   78		1				
1219   Y59709   Homo sapiens   Secreted protein 76-28-3-A12-FL1   470   92	1217	Y57897	Homo sapiens	Human transmembrane protein HTMPN-21.	1173	100
1219	1218	J00194	Homo sapiens	hla-dr antigen alpha chain	454	78
1220   W81576   Homo sapiens   EBV-induced G-protein coupled receptor (EBI-2) polypeptide.   2) polypeptide.   2) polypeptide.   3   20   20   20   20   3   3   3   3   3   3   3   3   3					470	92
1221   W96745   Homo sapiens   High affinity immunoglobulin E receptor-like protein (IGERB).   1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   31   123   Y00278   Homo sapiens   Human secreted protein encoded by gene 21.   260   95   1224   AF161422   Homo sapiens   HSPC304   568   90   1225   U14970   Homo sapiens   HSPC304   568   90   1225   U14970   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100   100   1227   AF099973   Mus musculus   Schlafen2   333   56   1228   G01218   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100   102						
1221   W96745   Homo sapiens   High affinity immunoglobulin E receptor-like   650   98     1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   31     1223   Y00278   Homo sapiens   Human secreted protein encoded by gene 21.   260   95     1224   AF161422   Homo sapiens   HSPC304   568   90     1225   U14970   Homo sapiens   High secreted protein encoded by gene 21.   260   95     1226   G01733   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100     1227   AF099973   Mus   schlafen2   333   56     1228   G01218   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   610   100     1229   AF217188   Mus   YIP1B   801   63     1230   AF176813   Homo sapiens   organic cation transporter   1704   100     1231   X98333   Homo sapiens   Human secreted protein encoded by gene 77   212   53     1233   Y94940   Homo sapiens   Human secreted protein encoded by gene 77   212   53     1234   U76618   Mus   N-RAP   482   82     1235   AF044924   Homo sapiens   Human secreted protein clone yi62_1 protein   526   100     1236   G01459   Homo sapiens   Human secreted protein   164   84     1238   W88633   Homo sapiens   Human secreted protein   164   84     1239   W29660   Homo sapiens   Human secreted protein   164   84     1239   W29660   Homo sapiens   Human secreted protein   164   84     1239   W29600   Homo sapiens   Human secreted protein   164   84     1239   W29600   Homo sapiens   Human secreted protein   164   84     1240   Y95002   Homo sapiens   Human membrane-associated protein   159     1241   Y92710   Homo sapiens   Human membrane-associated protein   151   97     1242   Y95002   Homo sapiens   Human membrane-associated protein   511   97     1244   AF284422   Homo sapiens   Human potassium channel molecule   ERG-LP2   325   100     1244   AF284422   Homo sapiens   Human secreted protein designated   1888   93     1246   AB039371   Homo sapiens   mitochondrial ABC transporter   3 89   97	1220	W81370	riomo sapicus		1 123	100
Protein (IGERB).			<u> </u>	2) polypeptide.		<u> </u>
1222   Y35911   Homo sapiens   Extended human secreted protein sequence, SEQ   135   31   1223   Y00278   Homo sapiens   Human secreted protein encoded by gene 21   260   95   1224   AF161422   Homo sapiens   HSPC304   568   90   1225   U14970   Homo sapiens   HSPC304   568   90   1225   U14970   Homo sapiens   Himan secreted protein, SEQ ID NO: 5814   610   100   100   1227   AF099973   Mus musculus   Schlafen2   333   56   56   100   100   1228   G01218   Homo sapiens   Human secreted protein, SEQ ID NO: 5299   155   81   1229   AF217188   Mus musculus   Y1P1B   801   63   63   1231   X98333   Homo sapiens   Soluble adenylyl cyclase   275   100   100   1232   W74955   Homo sapiens   organic cation transporter   1704   100   100   1232   W74954   Homo sapiens   Human secreted protein encoded by gene 77   212   53   2134   U76618   Mus musculus   N-RAP   482   82   1235   AF044924   Homo sapiens   hook2 protein   1236   G01459   Homo sapiens   hook2 protein   1238   W88633   Homo sapiens   Human secreted protein, SEQ ID NO: 5540   417   100   1237   AF000018   Homo sapiens   Adapter protein encoded by gene 100 clone   482   492   1238   W88633   Homo sapiens   Human secreted protein encoded by gene 100 clone   482   492   1239   W29660   Homo sapiens   Human secreted protein encoded by gene 100 clone   482   492   1240   AF004161   Oryctolagus   cuniculus   Oryctolagus   cuniculus   Homo sapiens   Human membrane-associated protein   256   90   1240   AF004161   Oryctolagus   cuniculus   Human secreted protein encoded by gene 100 clone   482   1241   Y92710   Homo sapiens   Human membrane-associated protein   256   90   1240   AF004161   Oryctolagus   Cuniculus   Human secreted protein encoded by gene 100 clone   483   1243   Y44905   Homo sapiens   Human secreted protein encoded by gene 100 clone   488   1243   Y44905   Homo sapiens   Human petreted protein encoded by gene 100 clone   154   52   154   154   154   154   154   154   154   154   154   154   154   154   154   154   154   154   154   154   154   1	1221	W96745	Homo sapiens		650	98
ID NO. 160		ł		protein (IGERB).		<u> </u>
ID NO. 160	1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	135	31
1224	j			ID NO. 160.		
1224	1223	Y00278	Homo saniens	Human secreted protein encoded by gene 21.	260	95
1225   U14970						
1226   G01733   Homo sapiens   Human secreted protein, SEQ ID NO: 5814.   G10   100						
1227				Thosomal protein 55	1	
1228   G01218   Homo sapiens   Human secreted protein, SEQ ID NO: 5299.   155   81						
1228   G01218   Homo saplens   Human secreted protein, SEQ ID NO: 5299.   155   81	1227	AF099973		schlafen2	333	56
1229		<u> </u>				
1230   AF176813   Homo sapiens   Soluble adenylyl cyclase   275   100     1231   X98333   Homo sapiens   Organic cation transporter   1704   100     1232   W74955   Homo sapiens   Human secreted protein encoded by gene 77   212   53     1233   Y94940   Homo sapiens   Human secreted protein clone yi62_1 protein   526   100     1234   U76618   Mus   M-RAP   482   82     1235   AF044924   Homo sapiens   hook2 protein   380   97     1236   G01459   Homo sapiens   Human secreted protein, SEQ ID NO: 5540.   417   100     1237   AF000018   Homo sapiens   Adapter protein   164   84     1238   W88633   Homo sapiens   Secreted protein encoded by gene 100 clone   488EU04.     1239   W29660   Homo sapiens   Homo sapiens CH27_1 clone secreted protein.   697   98     1240   AF004161   Oryctolagus   peroxisomal Ca-dependent solute carrier   154   52     1241   Y92710   Homo sapiens   Human membrane-associated protein Zsig24.   709   97     1242   Y95002   Homo sapiens   Human secreted protein vc34_1, SEQ ID NO: 44.   908   88     1243   Y44905   Homo sapiens   Human potassium channel molecule ERG-LP2   325   100     1244   AF284422   Homo sapiens   Human potassium channel molecule ERG-LP2   325   100     1245   Y53629   Homo sapiens   A bone marrow secreted protein designated   1888   93     1246   AB039371   Homo sapiens   mitochondrial ABC transporter   389   97	1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.		81
1230   AF176813   Homo sapiens   Soluble adenylyl cyclase   275   100     1231   X98333   Homo sapiens   Organic cation transporter   1704   100     1232   W74955   Homo sapiens   Human secreted protein encoded by gene 77   212   53     1233   Y94940   Homo sapiens   Human secreted protein clone yi62_1 protein   526   100     1234   U76618   Mus	1229	AF217188	Mus	YIP1B	801	63
1230   AF176813   Homo sapiens   Soluble adenylyl cyclase   275   100     1231   X98333   Homo sapiens   Organic cation transporter   1704   100     1232   W74955   Homo sapiens   Human secreted protein encoded by gene 77   212   53     1233   Y94940   Homo sapiens   Human secreted protein clone yi62_1 protein   526   100     1234   U76618   Mus			musculus		[	1
1231   X98333	1230	AF176813		soluble adentityl cyclase	275	100
1232   W74955   Homo sapiens   Human secreted protein encoded by gene 77   212   53						
Clone HOEAS24.						
1233   Y94940   Homo sapiens   Human secreted protein clone yi62_1 protein sequence SEQ ID NO:86.   100	1232	W /4955	Homo sapiens		212	33
Sequence SEQ ID NO:86.		L	L			
1234   U76618   Mus musculus   N-RAP   1482   82     1235	1233	Y94940	Homo sapiens		526	100
1235   AF044924   Homo sapiens   hook2 protein   380   97     1236   G01459   Homo sapiens   Human secreted protein, SEQ ID NO: 5540.   417   100     1237   AF000018   Homo sapiens   adapter protein   164   84     1238   W88633   Homo sapiens   Secreted protein encoded by gene 100 clone   250   90     1239   W29660   Homo sapiens   Homo sapiens CH27_1 clone secreted protein.   697   98     1240   AF004161   Oryctolagus cuniculus   peroxisomal Ca-dependent solute carrier   154   52     1241   Y92710   Homo sapiens   Human membrane-associated protein Zsig24.   709   97     1242   Y95002   Homo sapiens   Human secreted protein vc34_1, SEQ ID NO:44.   908   88     1243   Y44905   Homo sapiens   Human potassium channel molecule ERG-LP2   325   100     1244   AF284422   Homo sapiens   cation-chloride cotransporter-interacting protein   511   97     1245   Y53629   Homo sapiens   mitochondrial ABC transporter 3   389   97				sequence SEQ ID NO:86.		1 _
1235	1234	U76618	Mus	N-RAP	482	82
1235						
1236         G01459         Homo sapiens         Human secreted protein, SEQ ID NO: 5540.         417         100           1237         AF000018         Homo sapiens         adapter protein         164         84           1238         W88633         Homo sapiens         Secreted protein encoded by gene 100 clone         250         90           1239         W29660         Homo sapiens         Homo sapiens CH27_1 clone secreted protein.         697         98           1240         AF004161         Oryctolagus cuniculus         peroxisomal Ca-dependent solute carrier         154         52           1241         Y92710         Homo sapiens         Human membrane-associated protein Zsig24.         709         97           1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated         1888         93           1246         AB039371         Homo sapiens	1235	AF044024	<del></del>	hook2 protein	380	97
1237         AF000018         Homo sapiens         adapter protein         164         84           1238         W88633         Homo sapiens         Secreted protein encoded by gene 100 clone         250         90           1239         W29660         Homo sapiens         Homo sapiens CH27_1 clone secreted protein.         697         98           1240         AF004161         Oryctolagus cuniculus         peroxisomal Ca-dependent solute carrier         154         52           1241         Y92710         Homo sapiens         Human membrane-associated protein Zsig24.         709         97           1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2 partial protein.         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97						
1238         W88633         Homo sapiens         Secreted protein encoded by gene 100 clone HE8EU04.         250         90           1239         W29660         Homo sapiens         Homo sapiens CH27_1 clone secreted protein.         697         98           1240         AF004161         Oryctolagus cuniculus         peroxisomal Ca-dependent solute carrier         154         52           1241         Y92710         Homo sapiens         Human membrane-associated protein Zsig24.         709         97           1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2 partial protein.         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated BMS115.         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97						
HE8EU04.						
HE8EU04.	1238	W88633	Homo sapiens	Secreted protein encoded by gene 100 clone	250	J 90
1239         W29660         Homo sapiens         Homo sapiens CH27_1 clone secreted protein.         697         98           1240         AF004161         Oryctolagus cuniculus         peroxisomal Ca-dependent solute carrier         154         52           1241         Y92710         Homo sapiens         Human membrane-associated protein Zsig24.         709         97           1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2 partial protein.         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated BMS115.         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97				HE8EU04.		1.
1240 AF004161 Oryctolagus cuniculus  1241 Y92710 Homo sapiens Human membrane-associated protein Zsig24. 709 97  1242 Y95002 Homo sapiens Human secreted protein vc34_1, SEQ ID NO:44. 908 88  1243 Y44905 Homo sapiens Human potassium channel molecule ERG-LP2 325 100  1244 AF284422 Homo sapiens cation-chloride cotransporter-interacting protein 511 97  1245 Y53629 Homo sapiens A bone marrow secreted protein designated BMS115.  1246 AB039371 Homo sapiens mitochondrial ABC transporter 3 389 97	1239	W29660	Homo saniens		697	98
1241   Y92710   Homo sapiens   Human membrane-associated protein Zsig24   709   97     1242   Y95002   Homo sapiens   Human secreted protein vc34_1, SEQ ID NO:44   908   88     1243   Y44905   Homo sapiens   Human potassium channel molecule ERG-LP2   325   100     1244   AF284422   Homo sapiens   cation-chloride cotransporter-interacting protein   511   97     1245   Y53629   Homo sapiens   A bone marrow secreted protein designated   1888   93     BMS115   BMS115   1246   AB039371   Homo sapiens   mitochondrial ABC transporter 3   389   97						<del></del>
1241         Y92710         Homo sapiens         Human membrane-associated protein Zsig24.         709         97           1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2 partial protein.         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated BMS115.         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97	12-70	2004101		paromisonar Caracpondont soute carror	157	1
1242         Y95002         Homo sapiens         Human secreted protein vc34_1, SEQ ID NO:44.         908         88           1243         Y44905         Homo sapiens         Human potassium channel molecule ERG-LP2 partial protein.         325         100           1244         AF284422         Homo sapiens         cation-chloride cotransporter-interacting protein         511         97           1245         Y53629         Homo sapiens         A bone marrow secreted protein designated BMS115.         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97	1071	1/00710		11	700	107
1243     Y44905     Homo sapiens     Human potassium channel molecule ERG-LP2 partial protein.     325     100       1244     AF284422     Homo sapiens     cation-chloride cotransporter-interacting protein     511     97       1245     Y53629     Homo sapiens     A bone marrow secreted protein designated BMS115.     1888     93       1246     AB039371     Homo sapiens     mitochondrial ABC transporter 3     389     97						
partial protein.						
partial protein.	1243	Y44905	Homo sapiens	Human potassium channel molecule ERG-LP2	325	100
1244     AF284422     Homo sapiens     cation-chloride cotransporter-interacting protein     511     97       1245     Y53629     Homo sapiens     A bone marrow secreted protein designated BMS115.     1888     93       1246     AB039371     Homo sapiens     mitochondrial ABC transporter 3     389     97				partial protein.		1
1245         Y53629         Homo sapiens         A bone marrow secreted protein designated BMS115.         1888         93           1246         AB039371         Homo sapiens         mitochondrial ABC transporter 3         389         97	1244	AF284422	Homo seniens		511	97
BMS115.						
1246 AB039371 Homo sapiens mitochondrial ABC transporter 3 389 97	1243	133047	Troute sabicits		1000	"
	1045	ADDOOR	·		380	102
1247 Y35911 Homo sapiens   Extended human secreted protein sequence, SEQ   168   39						
	1247	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	168	39

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
			ID NO. 160.		
1248	AF072509	Rattus norvegicus	glutamate receptor interacting protein 2	559	90
1249	AF247042	Homo sapiens	tandem pore domain potassium channel TRAAK	661	98
1250	B08974	Homo sapiens	Human secreted protein sequence encoded by gene 27 SEQ ID NO:131.	1087	97
1251	L15313	Caenorhabditi s clegans	putative	858	59
1252	Y29338	Homo sapiens	Human secreted protein clone it217_2 alternate reading frame protein.	278	75
1253	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	211	92
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	294	83
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1256	AF286368	Homo sapiens	eppin-l	222	54
1257	AF220264	Homo sapiens	MOST-1	87	93
1258	G02227	Homo sapiens	Human secreted protein, SEQ ID NO: 6308.	281	78
1259	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded from gene 26.	81	94
1260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	986	100
1261	AF140674	Homo sapiens	zinc metalloprotease ADAMTS6	172	36
1262	U28369	Homo sapiens	semaphorin V	237	67
1263	¥07049	Homo sapiens	Renal cancer associated antigen precursor sequence.	288	71
1264	Y36153	Homo sapiens	Human secreted protein #25.	187	80
1265	Y78114	Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ ID NO:2.	723	93
1266	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	191	100
1267	AF030558	Rattus norvegicus	phosphatidylinositol 5-phosphate 4-kinase gamma	859	95
1268	U73167	Homo sapiens	candidate tumor suppressor gene LUCA-1	159	96
1269	AF190664	Mus musculus	LMBR2	552	76
1270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP)	820	98
1271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	131	95
1272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	253	92
1273	AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthethase (acetate-coA ligase))	1280	100
1274	AF064748	Mus musculus	S3-12	3523	61
1275	D17554	Homo sapiens	TAXREB107	377	78
1276	Y30715	Homo sapiens	Amino acid sequence of a human secreted protein.	643	90
1277	AF146760	Homo sapiens	septin 2-like cell division control protein	707	100
1278	Y05069	Homo sapiens	Human PIGR-2 protein sequence.	281	46
1279	X59668	Oryctolagus cuniculus	aorta CNG channel (rACNG)	267	85
1280	G01051	Homo sapiens	Human secreted protein, SEQ ID NO: 5132.	489	98
1281	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	120	43
1282	AF055084	Homo sapiens	very large G-protein coupled receptor-1	1635	100
1283	AF117814	Mus musculus	odd-skipped related 1 protein	357	98
1284	U87318	Xenopus laevis	NaDC-2	535	60
1285	AF061346	Mus musculus	Edp1 protein	452	68
1286	AB030182	Mus musculus	contains transmembrane (TM) region	582	68
1287	A13595	synthetic construct	immunosuppresive protein PP15	185	97
1288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	100
1289	AF084205	Rattus norvegicus	serine/threonine protein kinase TAO1	319	98

SEQ	Accession	Species	Description	Smith-	%
ID NO:	No.	}		Waterman Score	Identity
1290	AF038563	Homo sapiens	membrane associated guanylate kinase 2	523	100
1291	AF034837	Homo sapiens	double-stranded RNA specific adenosine	468	100
		-l- <u>-</u>	deaminase		ļ
1292	M15888	Bos taurus	endozepine-related protein precursor	937	87
1293	AB010692	Arabidopsis thaliana	ATP-dependent RNA helicase-like protein	636	45
1294	AF209923	Homo sapiens	orphan G-protein coupled receptor	1570	100
1295	W67828	Homo sapiens	Human secreted protein encoded by gene 22 clone HFEAF41.	504	98
1296	AC004832	Homo sapiens	similar to 45 kDa secretory protein; similar to CAA10644.1 (PID:g4164418)	648	65
1297	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	575	70
1298	G02645	Homo sapiens	Human secreted protein, SEQ ID NO: 6726.	223	97
1299	Y59440	Homo sapiens	Human delta3 fragment #4.	122	32
1300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating type receptor protein JEG18.	459	81
1301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid sequence.	3916	99
1302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174	96
1303	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.	254	69
1304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	99
1305	AF148509	Homo sapiens	alpha 1,2-mannosidase	602	98
1306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.	333	98
1307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying protein SEQ ID NO:1.	332	98
1308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	348	52
1309	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	147	66
1310	AF063243	Bos taurus	ribosomal protein L30	296	90
1311	AF224494	Mus musculus	arsenite inducible RNA associated protein	688	70
1312	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	1154	100
1313	Y99419	Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	78
1314	AF116667	Homo sapiens	PRO1777	433	97
1315	W75100	Homo sapiens	Human secreted protein encoded by gene 44 clone HE8CJ26.	807	97
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	789	100
1317	AB041533	Homo sapiens	sperm antigen	2607	98
1318	U19617	Mus musculus	Elf-1	806	92
1319	U82598	Escherichia coli	ferric enterobactin transport protein	768	100
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2- DEHYDROGENASE (EC 1.1.1.140)	709	100
		con	(GLUCITOL-6- PHOSPHATE		
			DEHYDROGENASE) (KETOSEPHOSPHATE REDUCTASE).		
1321	W67847	Homo sapiens	Human secreted protein encoded by gene 41 clone HPBCJ74.	601	92
1322	AJ276101	Homo sapiens	GPRC5B protein	466	93
1323	AJ276101	Homo sapiens	GPRC5B protein	504	97
1324	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1584	100
1325	U91561	Rattus norvegicus	pyridoxine 5'-phosphate oxidase	1277	89
1326	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1606	100
1327	Y32206	Homo sapiens	Human receptor molecule (REC) encoded by	1531	90
1220	AE151040	Uarra ar	Incyte clone 2825826.	657	00
1328	AF151048	Homo sapiens	HSPC214	657	85
1329	Y10530	Homo sapiens	olfactory receptor	1645	100
1330	AF180681	Homo sapiens	guanine nucleotide exchange factor	4314	99
1331	AF111856	Homo sapiens	sodium dependent phosphate transporter isoform NaPi-3b	3591	99
1332 1333	Y13583	Homo sapiens	G-protein coupled receptor	2171	100
1277	AF078866	Homo sapiens	SURF-4	1395	100

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:				Score	
1334	Y25755	Homo sapiens	Human secreted protein encoded from gene 45.	1380	96
1335	AF152325	Homo sapiens	protocadherin gamma A5	4742	99
1336	X74070	Homo sapiens	transcription factor BTF3	639	81
1337	AF095927	Rattus norvegicus	protein phosphatase 2C	1931	95
1338	G03877	Homo sapiens	Human secreted protein, SEQ ID NO: 7958.	621	100
1339	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	626	100
1340	X61615	Homo sapiens	leukemia inhibitory factor receptor	5820	99
1341	Y01519	Homo sapiens	A carcinogenesis-inhibiting protein.	7528	97
1342	AF207600	Homo sapiens	ethanolamine kinase	2372	100
1343	U54807	Rattus norvegicus	GTP-binding protein	1167	97
1344	AC020579	Arabidopsis thaliana	putative phosphoribosylformylglycinamidine synthase; 25509-29950	3283	51
1345	Y28576	Homo sapiens	Secreted peptide clone pe503 1.	944	100
1346	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFHN61.	1171	100
1347	M55542	Homo sapiens	guanylate binding protein isoform I	2636	87
1348	AF183428	Homo sapiens	28.4 kDa protein	1329	100
1349	U70669	Homo sapiens	Fas-ligand associated factor 3	167	24
1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel modulatory subunit	562	99

## TABLE 3

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion
1	1351	A	2	337	1	TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA QPGPL*LLVPGSSGLPDPRDP
2	1352	A	27	100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETT\YHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK
3	1353	A	40	3	314	HASAHASVVLKDNSELEQQLGATGAYRARA LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R SCNYTLALILFL
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VI.PLP
5	1355	A .	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKEITLVVYIMDT GGAWWCYTFYLGTGDTCG*CFTTAG\TMGFF MTGYLPLGFEFAVEL\SYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN
6	1356	A	81	97	376	EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A YLRVPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CLFQEMGLSLQWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

SEQ ID NO: of NO: of nucleotide sequence   NO: of nucleotide sequence	ing nucleotide location corresponding to last amino pondi acid residue acid residue e of sequence with the corresponding to last amino pondi sirst acid residue of peptide sequence with the corresponding to last amino pondi residue of peptide sequence with the corresponding to the corresponding to last amino pondi residue of peptide sequence with the corresponding to the corresponding	acid sequence (A=Alanine C-Cysteine, partic Acid, E=Glutamic Acid, mylalanine, G=Glycine, H=Histidine, eucline, K=Lysine, L=Leucine, ethionine, N=Asparagine, P=Proline, atamine, R=Arginine, S=Serine, eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, iible nucleotide deletion, \=possible tide insertion GEILQAFRGHQGRGIRAIAAHERQAWVDBGIRLWHLVGRGYRGLG/DLGSLLQARYTQGCDSGWLLATAGSD*YRGPVSLQVLGAARG*TFPVLLPAGGSSWSRGLYGQWGRSCQGCPHQHSNCCCGPDPVSAQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKFELHLRGVSIYVLRHEAQIYGITPL\VCAL
nucle cotide sequence ue	tide location corresponding to last amino acid residue of peptide to fee of sequence with the condition of the condition of peptide to fee of sequence with the condition of the condition of peptide to fee of sequence with the condition of peptide to fee of sequence with the condition of peptide to fee of sequence with the condition of peptide to fee of peptide with the condition of peptide with the condition of peptide with the condition of the	nylalanine, G=Glycine, H=Histidine, eucine, K=Lysine, L=Leucine, ethionine, N=Asparagine, P=Proline, atamine, R=Arginine, S=Serine, eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \=possible etide insertion EGEILQAFRGHQGRGIRAIAAHERQAWVDDSGIRLWHLVGRGYRGLG/DLGSLLQARYTQGCDSGWLLATAGSD*YRGPVSLQVLGAAARG*TFPVLLPAGGSSWSRGLYGQWGRSCQGCPHQHSNCCCGPDPVSAQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKFELHLRGVSIYVLRHEAQIYGITPL\VCAL
Seq-   uence   USSN   location   109/496   1	ondi to last amino acid residue of peptide sequence wshe its its acid sequence wshe its its acid sequence wshe its its acid sequence wshe its its acid sequence wshe its acid sequence	eucine, K=Lysine, L=Leucine, ethionine, N=Asparagine, P=Proline, stamine, R=Arginine, S=Serine, eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \(\)-possible tide insertion  GEILQAFRGHQGRGIRAIAAHERQAWV  DDSGIRLWHLVGRGYRGLG/DLGSLLQ  ARYTQGCDSGWLLATAGSD*YRGPVSL  QVLGAAARG*TFPVLLPAGGSSWSRGL  YGQWGRSCQGCPHQHSNCCCGPDPVS  AQLELGPAWL  SGRISTLRDETGAILIDGDPAACAPIIKF  ELHLRGVSIYVLRHEAQIYGITPLVCAL
Sequence	bondi to last amino acid residue of peptide sequence wship ince with a sequence wship in	ethionine, N=Asparagine, P=Proline, atamine, R=Arginine, S=Serine, eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \=possible tide insertion  GEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPL\VCAL
914   ng to amino residu poptic seque:	irst acid residue q=Glu acid of peptide T=Thr y=Tyr /=poss nucleo WSHE ITGGI VP**/ *RRG RIVCY WEG/ 350 FSSLE LL/CR QCLG	atamine, R=Arginine, S=Serine, eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \=possible tide insertion GEEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPL\VCAL
8 1358 A 106 3  9 1359 A 115 49	acid of peptide T=Thr Y=Tyr /=poss nucleo WSHE ITGGI VP**4 *RRG-RIVC* WEGA 350 FSSLI LLTEL LJ/CR QCLG 186 QAWA	eonine, V=Valine, W=Tryptophan, rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \=possible tide insertion GEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
8 1358 A 106 3 9 1359 A 115 49	### sequence	rosine, X=Unknown, *=Stop codon, ible nucleotide deletion, \=possible tide insertion GEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPL\VCAL
8 1358 A 106 3 9 1359 A 115 49	/=poss   nucleo	ible nucleotide deletion, \possible nide insertion GEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPL\VCAL
8 1358 A 106 3 9 1359 A 115 49		aide insertion EGEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
8 1358 A 106 3 9 1359 A 115 49	WSHE ITGGI VP**/ *RRG- RIVCY WEGA 350 FSSLI LLTEI LI/CR QCLG	GEILQAFRGHQGRGIRAIAAHERQAWV DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	ITGGI VP**A *RRG- RIVCY WEGA 350 FSSLI LLTEI LL/CR QCLG	DDSGIRLWHLVGRGYRGLG/DLGSLLQ ARYTQGCDSGWLLATAGSD*YRGPVSL QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	VP**/ *RRG- RIVCY WEG/ 350 FSSLI LLTEI LL/CR QCLG 186 QAW/	ARYTQGCDSGWLLATAGSD*YRGPVSÌ QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	*RRG RIVCY WEGA 350 FSSLI LLTCR QCLG 186 QAWA	QVLGAAARG*TFPVLLPAGGSSWSRGL YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	RIVC   WEGA   350   FSSLI   LLTE    LVCR   QCLG   186   QAWA	YGQWGRSCQGCPHQHSNCCCGPDPVS AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	350 FSSLI LLTEJ LI/CR QCLG 186 QAW/	AQLELGPAWL SGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPLVCAL
9 1359 A 115 49	350 FSSLI LLTEJ LI/CR QCLG 186 QAW/	LSGRISTLRDETGAILIDGDPAACAPIIKF ELHLRGVSIYVLRHEAQIYGITPL\VCAL
9 1359 A 115 49	LLTEI LI/CR QCLG 186 QAW/	ELHLRGVSIYVLRHEAQIYGITPL\VCAL
	LI/CR QCLG 186 QAWA	
	QCLG   186   QAW	RL*SDSCMRAALNDRGLYQVLILDGLV
	186 QAWA	FVDSDSRKMVSTLT
		AIFKGKYKEGDTGGPAVWKTRLRCALN
10 1360 A 123 2		FNEGPERERMDV
1500 1 125 2		TOEKVORTEVIRTCINPVYSKLFTVDFY
		QRLRFEVHDISSNHNGLKEADFLGGME
		OIVSORKLSKSLLKHGNTAGKSSITVIA
		GNDDYVELAFNARKLDDKDFFSKSDPF
		MNDDATQQLVHRTEVVMNNLSPAWK
		SVNSLCSGDPDRRLKCIVWDWDSNGK
i		GEFTSTFKEMRGAMEGKQVQWECINPK
		KKNYKNSGTVILNLCKIHKMHSFLDYI
} } }		COLOFTVAIDFTASNGDPRNSCSLHYTHP
		EYLKALVAVGEICQDYDSDKMFPAFGF
		PPEYTDSHDFAINFNEDNPECAGIQGVV
		SCF\PKAPTFTGPTNICPHSSRKVAKFRR
		*HQGRAFAIIFILVDPGQVGVYSQDMGP
		GGHFV
11 1361 A 147 614	9 ACAR	KQLLGRTVFIWFVGQLLGGELKGYSKT
		SRPASSRG\TLSSSSSSSSSLTKDALPSSL
	,	TTITSGLVFPFRSLCVNPAKSSVSESVSSI
	1	SSSVKYLE*KRTSCCFPDSSESKLSQLSS
		SMGTSSRKPTNSSSSLGALKMSATS\*G
		SPTPFFLTGLQSPPSTRPREPGLTTARNS
	TTLT	•
12   1362   A   177   12		PALDSLVDPRVRSRKQPFVIYPVYDTAI
		HFSLLDGNVGEPDMSAGFCPNHKAAM
	VLFL	DRVYGIEVQDFLLHLLEGGFLPDLRAA
		T/AEIGAMDFLLS*LFTLCLMMFFFIYPFI
	NLLT	MNVY
13 1363 A 249 535		IRHLSPAPLIVCDQGTCVVSYYPQNIVQ
		QMEQGLN/HLFLDGNA*PHSVECYCPS
		likitsfylyfhryrapevllrssvysspi
	DVW	AVGSIMAELYMLRPLFPGTSEVDEIFKIC
	OVLG	TPKKVSTLVPKLL
14 1364 A 254 572		XIGNLMMLLVINADSCLRTXM*FFLGH
		DICYSSVTAQDAAEFPVS*KPILVWGYIT
		TIFSWGTNGCLLSAITYACYAAICHPLLS
		MNRPLCTATVNATNKMGFLNSQVN
15 1365 A 257 425		FLNKKFNIPKLVILPKLVYIVKAIPTKM
		LECDONIT/KLICENT*KNIAKNI*KRRV
		ET*HPVKQMIKWQ*LTAWLRNRGYKKI
		NSETAPSVCRNLVFDKCG
		TTEEDRGGDDCVVSVWTKQRNNSCVK
16 1366 A 263 INA		FSKPVNIFWALEESVLGVKAROPKPFFA
16 1366 A 263 104	I SKDV	TEMTCKVSSKNIKSPRYSVLIMAEKPV
16 1366 A 263 104		
16 1366 A 263 104	AGNT	—·
	AGNT GDLS	SPNETKYIISLDQDSVVKLENWTDASRV
16 1366 A 263 104 17 1367 A 298 68	AGNT GDLS 208 RKRT	SPNETKYIISLDQDSVVKLENWTDASRV NNPIKLDKKFEHFKNEDI*ITSKHTKMW
	AGNT GDLS 208 RKRT VSSL	SPNETKYIISLDQDSVVKLENWTDASRV

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- cotide	peptide seq-		in USSN	nucleotide location	location corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	,	İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	1	ł	peptide	Sequente	/-possible nucleotide deletion, \-possible
	ļ		<u> </u>	sequence		nucleotide insertion
						IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR WK*DY*C/LOEVTDPIMEKGKKKKRTASFFK
	ŀ	}		l		GQPHQSTNALLRRCVR*RYHLS\TVETAGLP*
		ł		ł		KNTGHIPGQPFLFKLVFKC*NVICI**QYKW*Q
	1					NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK   TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR
	l	ĺ				ISLMSSWDYRRPPQ
19	1369	A	302	3	445	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS
			Ì	1	Ì	WICRLRPLLWRAVREYLSKLKNAELSFDPGV
	ĺ		ĺ		1	SLLRIYAIDMPTSI*DEKEALLFAFLAFHE*HC KSRIWAVIQ/CIHLWDWLRKL*CFHRMKFYA
						AV*NKPRHLLSHIWKDVQNILLK
20	1370	A	304	1	1339	FFFCGKEVPLFEQNKHPGPRATTSPGA/HARA
	[	{		[		LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA
		ĺ		Ì		GGPCHQPGGSPGPWMHTTQAGHLWEGAYPG GSSTWHQVPGQLGGSWGPRERSLLGSFIKCSP
		Ì	Í	ļ	1	CPHPPGFRLWMSPNQKPPTENPGVMGRVWR
		[		1	ĺ	LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA
			1	l		PLHSSLGNTVKP*PKNQKPKQNRSRHGQ\GF
	ļ	i				MAGQGQSRPAAR*PPCPALTPASHSAGTWPP   RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWP
	1			1		DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR
	}		-	ļ	Į	CRALPGRLCSAPAAGLRRARPRLSESRRGNSP
	ļ			ĺ	ĺ	PASPAAASARCPSWGPSCPARPPSRPAAGTEP
			}			AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW
		]			ŀ	ALVRSRGG
21	1371	A	326	799	1587	GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC
						E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCLP HLSFSPRQGAAPDTEPSAWGPAPTGATGPGLP
		ĺ				LRHVRLFSAGAPRGAATPCPPALLHGPAWPP
	j		}	ļ		ARPMFRGHPPVRPLGPWGKVAAGPRALCLA
				Ì		GVPAVQGECATKPSG*GL*PAHLRGPPGPEVL
	J	j	j	ļ	j	QWHWQLSAGRDPVPAEDPPL*EGPLGPGGPA AAQAEPGADPEPEDKDQAAESRPAGAMSLSA
				)	ļ	QGSGPVGGQGLR
22	1372	Α	327	146	652	PHLENPHPEHSFPGAPLT*STLSWSILSPREPSP
}	1		}		)	GAPCYPGHPHLENPHLEHLLTWRTVTWSTLL
	Į.	1		ļ		PGAPCYPEHPHLEHPLTWSTPHLEHPSPGEPL SCRTPTRSILHRDHPLP*CLSTEESPI*GWGSLP
		ļ				APPSTPLVLDVAPPGPQPASSCPGRDSCYSVP
	\	L	<u> </u>			GTVVSP
23	1373	Α	348	397	2	CIVSSCOGTRKPCHLEDANKINKQSPTLEKIES LQESL*VKQ*LIVAEKYVQILHPRKKYFQRPL
						NNEKRKMKKRKEEKKKCRERMORRSKWRR
						EEKKE*RREE\EERKKEKEDRKERRKETSPRG
				 	' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	SRRLLRD
24	1374	Α	362	170	352	GRALDTAAGSPVQTAHGLPSDALAPLDDSMP
25	1375	A	384	373	128	WEGRTTAQWSLHRKRHLARTLLVSRVRGPQ YLITTILETGYLWKNRHSDO*KRTENPERDOH
	] .5/5	<b>``</b>	""	3.5		KYPKVDFCKSNSMKNRLCNKWHWTNWIFTD
	<u> </u>	L	<u> </u>		<u> </u>	KKINLNLKPHTKLTPNIKKN
26	1376	Α	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK
		1	}	l		*MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF
27	1377	A	406	103	380	KSKATGYMVNI*KLIV\FLYANDEQLEIEMNK
						IVP\FNGSKNKIAFTNLTKYQNIQNRHAENYKI
L	L	L	<u> </u>	L		LVNKIEDLNKWRNVLLSWIGRRNIINTMT

SEQ ID	SEQ ID	Met	TSEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	i	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
иепсе	ì	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	(	ĺ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	ł	i	1	peptide	ì	
		<u> </u>	100	sequence	427	nucleotide insertion TICTNKFNNLDEIK/FLERHKLSKLTQEEVENL
28	1378	A	408	14	427	ITLKTSRETELVINK*VIPHKEKPGPDSFTGEF
•		1	1		ĺ	YOTFKEEL/II/ILHKLFQTIKYGRILPNSVYETSI
	İ		:	1		TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
l	į	}	l	ł	ł	NRI**HIR
29	1379	A	434	395	128	IYSKMCMERORLNN*ILKKNKVRGIAVPDVK
~~	1 2017	]	1	1		VYYKPTVIK/TSWIL+KDSHIVEWNRLENLEID
	Į.			1		PN/IKRLILDKGAEATEWRKDSFFRQWQ
30	1380	A	455	2	228	FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
	1	1	1		ļ	SWDYRYAPPRP\ANF\*FLVETGFYYVAQAGL
		ĺ				KLLSPGDLPALAS
31	1381	A	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
		1		1	[	CRRMNLNPYLSRYIKINSR\KDLTVRPEPIKLV
		1	i	Į		EENTGKTIQDTGLGK*FIAKTSKAQSTKTNK*
ì	1	i	ľ		1	KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
	L	l				IFAN
32	1382	Λ	474	125	471	VKPYEIAVFLVKPIEYK*HLLSDPAIPLSGI*LK
ļ	]			İ		EIKAYT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
J	1		}		]	KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
		1.	100	1005	2	ILRETDRIHKTTYDVISLI
33	1383	A.	488	1825	2	KSACSFICSEEQPASPSPLKPGTYASET\RPRDP HAAGPRRDSSEAETRRPRGA/DGSGTVVKGT
}	1	1	1	1	}	PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR
!			1			APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP
	1		İ		<b>!</b>	STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
1		1	1			L/ASSPEPMGAALAEDGSGDSRGAGPRPQE*P
ł	1	İ		l	ļ	PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
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1		]	ļ		}	GGRSPAGTGHLGAQTVASPH*GHWPTALSCL WASASPPGPEAPPQTGACIGTNCRYRAASAR
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ļ		1			1	RLS\PPLASCGGRGPPGGAACATCAPPAGPAR
1	1	i	1		1	SSRCRRRSPPE*GPR*PSRPARPSPGSAASRRQ
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35	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
ļ		Į.			1	LTELVVAVTDENIVGLFAALLAERRVLLTAS
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	1	<u></u>	<u></u>		L	LLDYC*CPPLPRT
36	1386	A	512	3	1631	FFFSFVCHLYCVSPTPGPHGRLATWL/PGLLA
	J	}		1		FLGLAAGGQTLCPAGELPGHARAQASGAPGS
		l			1	VLIAVPGRRRVHTCGPGPAAPSTRGECPPPAL
ļ		1			1	GHTRPARPRPV\PFAPAVPQEPGGQGHGAA/P
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į		İ	1	1	1	PGQHLLDRPGAPPAQGSGPAPAPPRLAGPA
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NO. of   NO. of   NO. of   NO. of   NO. of   No. of   N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
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Sequence   Sequence		1	1				
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amino acid residue of sequence   residue	-						
Pepilide   Sequence		Ì	1			of peptide	
			i	]	residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
GRESOSO-PAGPPCMRGCCLRGW-PSSSGSD		l	)		peptide		/=possible nucleotide deletion, \=possible
		}	İ	į	sequence		
VSAAPQSPTTECPRGCAAAGICVILAAAGGA							GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD
HAGIGIEGYNYHTTÖRYHHITÖAG/GCOTTERRE   LRSLPYLGIPARCPYSAIPRESOSSCHA    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGCP**176*PLITGFPEP*AGLP    ARLYPRIPARGAGAAPPRYAVSMAPDPSAKH    WEASPEMOSKCHOKOKNNOTECENHYWFIO    RLINSTHLYACGTHAFOPLAGENITY     ARLYPRIPARGHAPISTIC     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN     ARTHYRICAN		]	ŀ				GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS
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FCDGRRQNGGTCVNRWNMYLCECPLRFGG   KNCEQGEWPASSIPPVTAAWEALLLDVPGTT   VRGLHIQVRQPLVVYAAFTVDSHRPLQETVL   RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP   ATVIISVPWYLGLMFRTIRKEDSVLMEATSGG   PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG   LRVTDGEWHHLLILLWG*TLPPAQGKTGA   SEDKVSVRRGFRGCMQVRGGCGGRGEACPS   QAAPRL		1	' '	'*'	<sup>*</sup>		
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RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP   AIVIISVPWYLGLMFATRKEDSVLMEATSGG   PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG   LRVTDGEWHHLLIELKNVKEDSEMKHLVTM   TLDYGMDQVSWHLHLLWG*TLPPAQGKTGA   SEDKVSVRRGFRGCMQVRGGCGGRGEACPS   QAAPRL     40		1		l l			1 -
PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG		i		ľ	i	1	RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP
LRVTDGEWHHLLIELKNVKEDSEMKHLYTM		]		ł		İ	ATVIISVPWYLGLMFRTR\KEDSVLMEATSGG
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42 1392 A 841 1 415 GSTHASGYDKTPDFILQVPVAVEGHIIHWIES KASFGDECSHHAYLHDQFWSYWNSLKHRTW QGIGTYASNLSQL*TLNAPFPELLLFRSLARTG FVLT*\RFGPGLVIYWYGFIQELDCNRERGILL KACFPTNIVTL  43 1393 A 845 358 92 PALSPAPVPQKKGSPLPLDPCLGPSSWLLSVG LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLLF QRPMLPPSHAGLARPPPEPISVP  44 1394 A 853 452 1 LPQYCFFPRLSPKSKLVKHSAL**PSALKPPTK SPRCIPRTSLYFTICC/PPALQL/SPIEDPPAIYRS PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG QVSCPPQPTLPREKPLPLHLRPPPRPAQPPLPR PLTFSTRRNVDPEIPERFR  45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR	41	1391	A	835	7	בעו ן	
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44 1394 A 853 452 1 LPQYCFFPRLSPKSKLVKHSAL**PSALKPPTK SPRCIPRTSLYFTICC/PPALQL/SPIEDPPAIYRS PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG QVSCPPOPTLPREKPLPLHIRPPPRPAQPPLPR PLTFSTRRNVDPEIPERFR  45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR		Ì					
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PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG QVSCPPQPTLPREKPLPLHLRPPPRPAQPPLPR PLTFSTRRNVDPEIPERFR  45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR	44	1394	A	دده	432	1	
QVSCPPQPTLPREKPLPLHLRPPPRPAQPPLPR PLTFSTRRNVDPEIPERFR  45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR		-			[		
PLTFSTRRNVDPEIPERFR  45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR			i		}	}	
45 1395 A 894 379 162 GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK 46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR		1	!				
QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR	15	1204	<u> </u>	904	270	162	
WLSMSMGK  46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR	43	1273	^	074	3/9	102	
46 1396 A 900 1 366 TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR			1		l	1	, ,
EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR	46	1204	- <u>,</u>	900	<del>                                     </del>	366	
	40	1370	^	1 300	1	. 500	1
VFLFHQLNIT**CLHFFTMTTFIAIPFSFLFLGR			l		ĺ		

<del></del>	1 050 10	1 1/	Lero	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	SEQ ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
NO: of nucl-	peptide	1100	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	į	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ľ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		}	peptide	sequence	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
	ļ	<del> </del>	<b>├</b>	sequence	<b></b>	D/KSLAMLPRLVSNSWPQVILPP
- 15	1207	<del>                                     </del>	-	162	2	OLONLASRGCL*SQLLRRLRRENRLNPGGGG
47	1397	A	944	102	2	CSEIAP\CTPAWVTQRDFFRKKK
	<u> </u>	<del> </del>	100		200	HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
48	1398	A	963	216	308	
49	1399	A	967	466	1	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK GRKHASRTARAHVFHPIRQSIRSPVRGRPGDP
	1	[	1			
		1				RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E
	1	ì	1		i	GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPG
_					<u></u>	AAAAQP**TPRCPAALRAGAHIGRVGRPY
50	1400	A	973	45	421	EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA
	ł	i	1			LNFMPLEMEPKMSKLAFGCQRSSTSDDDSGC
	1		1			ALEEYAWVPPGLRPEQIQLYFACLPEEKVPY
		ļ	i			VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSE
			1			E
51	1401	Α	992	2095	194	IRIRHEAARSCLGCAAGHVPAPGLRLLPTVRG
		1	1			PPGRRGPAAPGCVCY*SGESTFVSHVPQRMA
	Ì	ĺ	1			WPGSAPPRGFHPLQSQTSPSDTVSSPQLSKEE
		1				DGPGWEHPLSSSL*SLGQAGGNH*QPEELAG
	ì					WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSLS
				ļ		ESHAASNDPRNFVPNKMWKGLVKRNASVET
	ŀ	1	1	1		VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
	ļ	1		1		MEVTTEDTSRTDVSEPATSGVAADGVTSIAPT
	1	İ		1		AVASSTTAASITTAASSMTVASSAPTTAASST
	1	ł		ł		TVASIAPTTAASSMTAASSTPMTLALPAPTST
	1	Ì		1		STGRTPSTTATGHPSLSTALAQVPKSSALPRT
	1	1		ì		ATLATLATRAQTVATTANTSSPMSTRPSPSKH
	1	ì	l	ľ		MPSDTAASPVPPMRPQAQGPISQVSVDQPVV
		1		}		NTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAR
	1		ļ			EPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYT
	{	Ī		[		QRAAGPGTSQAPEQVETEATPGTDSTGPTPRS
		1	1	1		SGGTKMPATDSCQPSTQGQYMV/DHH*APHP
	1		-			GRGRQNSPSGGAVTRGDPFHHSLGFVCPAGL
	1	[	i	1		*ELQEEGLHPGGLLNQRDVCGLRNVRGAGA
		1				WREAWPLPRPFLLPLRPNQVLPNSFGAIEEIC
	1		ļ	}	!	OMLKHI
52	1402	A	994	1	462	ESGEFLVSFTLKKPTNVFHHINGMKFFNK/LIF
) <b>-</b>	1 - 1 - 1	1	1			*SHTDIAFYKIQHPFMLKALTKWA*EGT*PDR
				1		RYLH*SLRLNGEOLKTFPLRSGMR*G/CAILPL
	1		1			VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQE
	1		{		-	EK*FS*FVGDMNTCVENKKESKKLLE
53	1403	+A	1011	1	630	PEVIOOSAYDSKADIWSLGITAIELAKGEPPNS
ر د	1405	^	1011	, *	1 330	DMHPMRVLFLIPKNNPPTHCWRRLLESFKEV
				1	1	*LMLA*TKDPSI\RPTAKELLKHKFIVKNSKKT
		1		1		SYLTELIDREKRWKAEGHSDDESDSEGSDSES
		1	1			TSRENNTHPEWSFTTVRKKPDPKKVQNGAEQ
Ī	1	1				DLVOTLSCLSMITPAFAELKQQDENNASRNQ
1		1		1		AIEELEKSIAVAEAAGPG
<u> </u>	1	1	1000	<del> </del>	1222	ISIDA*KAFDKIOH/CFMITTLKKLGIDGKYLN
54	1404	A	1016	1	222	TIKAIDDRHTVSTILNVEKLKAFL*RSGTRQRF
		1	1	1	1	· · ·
		<b></b>	4	<del></del>	<del> </del>	PISGSGARI
55	1405	A	1033	3	366	HASVDGDEGSDDVYYYYTPAILRELQALNTA
1		1	1	1	1	EAAEHRPEEDRMLSEDPWRPAIMIKGYMPL
1		1	l l	1	1	HNIPHTEVIDVTGLNQSHLYQHLNKGTPMKT
		ĺ		L	<u> </u>	QKRAA\LYTWHVLEQLEILRQINQQSHGPG
56	1406	A	1044	5	429	SVLTLQTRSPSKPLS\RKLMDWEVVSRNSISE
		1			1	DRLETQSRASRSPPVTPNQSQETPVDGKPLAL
1			1			PPNQSQKNIRYHIHYLHLQYYLDRHISATLPIP
		1	1			SSSGIPTPIAVITDALTDLVELILGQPCSEESGR
	1	1	1	1		APGTLFLLAL
		<u> </u>		<u></u>	<u> </u>	APGTLFLLAL

NO. of   NO. of   NO. of   NO. of   NO. of   NO. of   No. of   N	250 15	CEOTO	1 14-4	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
mucleotide sequence certified by the corresponding of the corresponding	SEQ ID		1	,		_	
Segretaria   Seg			noa	1			
Sequence			<b>\</b>	1			
Page   Page			ĺ	1			
### ### ### ### ### ### ### ### ### ##	-	L LLLCC	1				
residue of peptide sequence   y=Tyrosine, X=Unknown, *Supp codon, peptide sequence   s	udice	ľ					T=Threonine, V=Valine, W=Tryptophan,
Peptide   Sequence		<b>{</b>		1	i		Y=Tyrosine, X=Unknown, *=Stop codon,
1407   A   1050   11   430   GAYAPETNGPPIMLVLTTDKIEGDVGIAGLYD   MHUSLPMAFLLRTLYRCTSYIIPVTHVLSTPS   TCLRRREKDGVIVDVLSDTASHINGFYPEEP   ADDTHPARLQGPTLRSQFMGPLKHKAFEERA   NIGUQRRILRED   STORT			į	1		}	/=possible nucleotide deletion, \=possible
1417   A   1050   11		1		1			
MHISLPMAFLLRILVRCTSYIPPTHYLSTYPE	57	1407	A	1050		430	GAYAFETNGFPIMLVLTTDKIEGDVGLAGLYD
ADDITHPARLOGETILSOPMOPLEHIKAFEERA   NUCLVORRIGED	٥,	• • • •	1			1	MH\ISLPMAFLLRTLVRCTSYIIPVTHVLSTPV
NILGLYORRIRLED		ĺ	1	1	(	ĺ	TCLRRREKDGVIVDVLSDTASNHNGFPVEEH
58         1408         A         1058         258         419         LKRRDTPVGANNRALSCTPLISLTLCALCPL.           59         1409         A         1064         3         425         KARSHTISLIGHQRMHTGERPYKCEGCGKIF           60         1410         A         1064         3         425         KARSHTISLIGHQRMHTGERPYKCEGCGKAFSGSC           60         1410         A         1065         204         419         GGPGFLAHTM           61         1411         A         1079         3         383         RFRARALCOPPHLVARROLLOLGOPPGCHY           61         1411         A         1079         3         383         RFRARALCOPPHLVARROLLOLGOPPGCHY           62         1412         A         1080         1         859         VERLWERROSSDPPREPASKCOMMEER           62         1412         A         1080         1         859         VVEELWSRESSSDPPREPASKSCOMMEER           62         1412         A         1080         1         859         VVEELWSRESSOSPPREPASKSCOMMEER           62         1412         A         1080         1         859         VVEELWSRESSSDPPREPASKCOMMEER           62         1413         A         1080         1         859         VVEELWSRESSSDPP		Į		i			ADDTHPARLQGPTLRSQPMGPLKHKAFEERA
PCLGCPTXATCRLYQTTVAVVF		ĺ	Ì			1	NLGLVQRRLRLED
PCLGCPTXATCRLYQTTVAVVF	58	1408	Ā	1058	258	419	LKHRDTPVVGANNRALSCTPLTSLTLCALCPL
KGSSSLNNINGRIHTGERPYKCNECGRAFSSRLSR							PCLGCPTXATCRLYQTTVAVVF
	59	1409	A	1064	3	425	KAFSFTTSLIGHORMHTGERPYKCKECGKTF
HHRIHTGEKPPHCNECGKVFSYHSALIHQRIH TGEKPYACKDVGK   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGSLADDHA    LAGIFTYNTDSWTTGYLLWEITSLGSLADDHA    A 1080		1,	1.		] -		
HHRIHTGEKPPHCNECGKVFSYHSALIHQRIH TGEKPYACKDVGK   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   GOPPOFELAHTHAGLQAPGPLLAPAGDEGDL   LLLAVQGCLADHLLTASWGGK/DPIPTKALG   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGYMPPGGCHY   LEGHETYNTDSWTTGYLLWEITSLGSLADDHA    LAGIFTYNTDSWTTGYLLWEITSLGSLADDHA    A 1080		1			1		
TGEKPYACKDVGK		1	1	j	ł		
LLLAVQQSCLADHLITASWGGK/DPIPTKALG		1		İ	1		
LLILAVQQSCLADHLITASWGGK/DPIPTKALG	60	1410	A	1065	204	419	l
EGGECIPITV		1	1	1	1	1	
			1		1	1	
LEENILIHRDIAARNCLISCAAPITRAATIGDF	61	1411	A	1079	3	383	
	OI.	1 ****	1	10//	] ]	303	
LEGIETYNTDSWTFGVLLWEIFSLGYMPYPGR TN		1			l	}	
1412   A   1080   1   859   VVEFLWSRRPSGSDPRPRRPASKCQMMEER   ANIMHMMKLSIKVLLQSALSLGRSLDADHA   PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFF   GPLELVEKLCPGASDIATSVRNLPELKTAVGR   GRAWLYLALMQKKLADYLKVLIDNKHLLSE   FYEPEALMMEEEGMVIVGLLVGLNVLDANIA   CLKGPDLDSQVQVIDFSLYLKDVQDLDGGKE   HERITDVLDQKNYVEELRHILSCTVGDLQTK   IDGGLEKTNSKLQERVSAATDRICSLQEEQQQL   REQNELIR   SFAKHKRHTGEKPFICLECGKAFTSSTILTK   HRRHTGEKPYTCGECGKAFRQSALLYVHRRI   HTGGKPYTCGECGKAFRQSALLYVHRRI   LLY   HTGGKPYTCGECGKAFRQSALLYHTGGKPCALLY   HTGGKPYTCGECGKAFRQSALLYHTGGKPCALLY   HTGGKPYTCGECGKAFRQSALLYHTGGKPCALLY   HTGGKPYTCGECGKAFRQSALLYHTGGKPCALLY   HTGGKPYTCGECGKAFRQSALLYHTGGT   HTGGKPTTCGECGKAFRGTTHFANNFSPALTTRVINFSLE   HVLPNPQLLCCDILLYKALT   HTGGKPYTCGECGKAFT   HTGGKPYTCGECGKAFT   HTGGKPTTCGECGKAFT   HTGGKPTTCGECGKTGGT   HTGGKPTTCGECGCATTCGGT   HTGGKPTTCGCGCTTTTT   HTGGKPTCGCTTTT   HTGGKPTTCGT   HTGGKPTTCGCCGKTGGT   HTGGKPTTTT   HTGGKPTTCGCT   HTGGKTTTT   HTGGKPTTCGCTTT   HTGGKPTTCGT   HTGGKTTT   HTGGKPTTCGT   HTGGKTTT   HTGGKPTTTT		}		1		1	
1412   A   1080   1   859		1	1				
ANI,MMM,MISIKVLLQSALSLGRSLDADHA   PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFF   GPLELVEKLCPEASDIATSVRNLPELKTAVGR   GRAWLYLLAMQKKLADYLKVLIDNKHILLSE   FYEPEALMMEEGGMYVGLLVGLNVLDANIA   CLKGEDLDSQVGVIDPSLYIKDVQDLDGGKE   HERITDVLDQKNYVEELNRHLSCTVGDLQTK   IDGLEKTNSKLQERVSAATDRICSLQEEQQQL   REQNELIR	62	1412	Ι Δ	1080	<del>                                     </del>	859	
PLQQFFVVMEHCLKHGİ,KVKKSFIGQNKSFF GPLELVEKLCPEASDIATSVRNLPELKTAVGR GRAWLYLALMQKKLADYLKVLIDNKHILLSE FYEPEALMMEEGEMVIVGLLVGLNVLDANIA CLKGEDLDSQVQVIDFSI,VKDVQDLDGKGK HERITDVLDQKNYVEELNRHLSCTVGDLQTK IDGLEKTNSKLQERVSAATDRICSLQEEQQQL REQNELIR 63 1413 A 1083 2 615 SSFAKHKRIHTGEKPFICLECGKAFTSSTITTK HRRIHTGEKPYTCGECGKAFTRQSANLYAHKKIHTGEKP YKCKECGKAFKSYYSILKHKRTHTRGMSYEG DEC/QRSLN/RSSILSNHKIHRHEMSYEG DEC/QRSLN/RSSILSNHKIHRHEMSYEG DEC/QRSLN/RSSILSNHKIHRHEK/PLKCEKCE KAFNITSICCRIKKN  64 1414 A 1084 946 1 KKQDLSSSLTDDSKNAQAPLALTESHLATLA SSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHIS SSESIAQSIDISQDKLRRHHVPQQCNKMPITAD LVAPILRRTLEVGNSHIMKDWLGGSEVNPLW TALLFILCHSGSTSGSWHILGAQQDQCKISPS FFSWLTTGLTTQQRTAIENATVAFFLQCISC HIPNNOKLMAQVI.CELFQTSPQRGNLPTSGNI SGFIRRLFLQUMLEDEKVTMFLQSPCPLYKG RINATSHVQIPPMYGAGMKFRTLHLPVSTTL SDVLDRVSDTPSITAKLISKQKDDKKKK  65 1415 A 1087 103 324 PRAFFFVHTEMIVG/RVQNIHLFTLQVLEDRA LTMSVGSSLWSTYLIHVANLPVSTLL SDVLDRVSDTPSITAKLISKQKDDKKKK  66 1416 A 1095 3 493 HETCSVTHIVSFSIPFINPSHPASTPGHTENEQ PSL/WFDRGKFYLTTEGSSRGPSPLTMGAQD TLPVAAAFTETVNAYFKGADPSKCIVKITGE MVLSFPAGITRHFANNPSPAALTFRVINFSRLE HYVLPNPQLLCCDNTQNDANTKEFWYNMPNL MTHLK  67 1417 A 1098 57 356 LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYYFLLDLCCSDILRSAICFPFVFNSVKNGST	02	1412	] ^	1000	} <b>*</b>	( 00)	
GPLELVEKLCPEASDIATSVRNLPELKTAVGR   GRAWLYLALMQKKLADYLKVLIDNKFILLSE   FYPPEALMMEEGMVIVGLLVGLNVLDANL		i	1	1		1	
GRAWLYLALMQKKLADYLKVLIDNKHLLSE   FYEPEALMMEEGMVIVGLVGLNVLDANL\  CLKGEDLDSOVGVIDFSLYLKDVQDLDGGKE   FYEPEALMMEEGMVIVGLVGLNVLDANL\  CLKGEDLDSOVGVIDFSLYLKDVQDLDGGKE   HERITDVLDQKNYVEELNRHLSCTVGDLQTK   IDGLEKTNSKLQERVSAATDRICSLQEEQQQL   REQNELIR     63		1	1	l	l	1	
FYEPEALMMEEĞGMYIVGILVGLNVLDANI.\ CLKGEDLDSQVGVIDFSLYLKDVQDLDGGKE HERITDVLDQKNYVEELNRHLSCTVGDLQTK IDGLEKTNSKLQERVSAATDRICSLQEEQQQL REQNELIR SSFAKHKIHTGEKPFTCLECĞKAFTSSTTLTK HRRIHTGEKPYTCEECGKAFTSSTTLTK HRRIHTGEKPYTCEECGKAFRQSAILYVHRRI HTGEKPYTCEGCGKTFRQSANLYAHKKIHTGEKP YKCKECGKAFKSYSILKHKKTHTIGMSYEG DEC/QRSLN/RSSILSNHKIHNEEK/PLKCEKCE KAFNHTSICCRHKKN  64 1414 A 1084 946 1 KKQDLSSSLTDDSKNAQAPLALTESHLATLA SSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHIS SSESIAQSIDISQDKLRRHHVPQQCNKMPITAD LVAPILRFI.TEVGNSHIMKDWLGGSEVYPLW TALLFLCSGSTSGSWNLGAQQDQCKISFS FFSWLTTGLTTQQRTAIENATVAFFLQCISC HPNNQKLMAQVLCELFQTSPQRGNLPTSGNI SGFIRRLFQLMLEDEKVTMPLQSPCPLYKG RINATSHVQIPPMYGAGHKFRTLHLPVSTTL SDVLDRVSDTPSITAKLISKQKDDKKKK 65 1415 A 1087 103 324 PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDRA LFTMSVGSSLWSTYLHVMALP/DRELLKPNA SVALHKLSNALV  66 1416 A 1095 3 493 HETCSVTHIVSFSLPFLNPSHPASTPGHTENEQ PSLVWPDRGKFYLTFEGSSRGPSPLTMGAQD TLPVAAAAFTETVNAYFKGADPSKCIVKITGE MVLSFPAGITRHFANNPSPAALTFRVINFSRLE HVLPNPQLLCCDNTQNDANTKEFWVNMPNL MTHLK  67 1417 A 1098 57 356 LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYFFLLDLCCSDILRSALCFPFVFNSVKNGST				1	1		
CLKGEDLDSQVGVIDFSLYLKDVQDLDGGKE				1			1
HERITDVLOKNYVEELNRH.SCTVGDLQTK   IDGLEKTNSKLQERVSAATDRICSLQEEQQQL   REQNELIR     63	J	}	]	)			
63 1413 A 1083 2 615 SSFAKHKRIHTGEKPFICLECGKAFTSSTTLTK REQNELIR  85 AKHKRIHTGEKPFICLECGKAFTSSTTLTK HRRIHTGEKPYTCEGEGKTFRQSANLYVHRRI HTGEKPYTCGDEGKTFRQSANLYVHRKIHTGEKP YKCKECGKAFKSYYSILKHKRTHTRGMSYEG DEC/QRSLN/RSSILSNHKIHNTEEK/PLKCEKCE KAFNHTSICCRHKKN  64 1414 A 1084 946 1 KKQDLSSSLTDDSKNAQAPLALTESHLATLA SSSQSPEAIKQLLDSGLPSILLVRSLASFCFSHIS SSESIAQSIDISQDKLRRHHVPQQCNKMPITAD LVAPILIFLTEVGNSHIMKDWLGGSEVNPLW TALLFILLCHSGSTSGSHNLGAQQDQCKISFS FFSWLTTGLTTQQRTAIENATVAFFLQCISC HPNNQKLMAQVLCELFQTSPQRGNLPTSGNI S\GFIR\RLFLQLMLEDEKVTMFLQSPCPLYKG RINATSINVIGIFMYGAGHKFRTLHLPVSTTL SDVLDRVSDTPSITAKLISKQKDDKKKK  65 1415 A 1087 103 324 PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDRA LFTMSVGSSLWSTYLIHVMALP/DRELLKPNA SVALHKLSNALV  66 1416 A 1095 3 493 HETCSVTHIVSFSLPFLNPSHPASTPGHTENEQ PSLVWFDRGKFYLTFEGSSRGPSPLTMGAQD TLPVAAAFTETVNAYFKGADPSKCIVKITGE MVLSPPAGITRIFRANNPSPAALTREVNIPSRLE HVLPNPQLLCCDNTQNDANTKIEFWVNMPNL MTHLK  67 1417 A 1098 57 356 LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYYFLLDLCCSDILRSAICPFVFNSVKNGST			1	1			
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MVLSFPAGITRHFANNPSPAALTFRVINFSRLE HVLPNPQLLCCDNTQNDANTK\EFWVNMPNL MTHLK  67 1417 A 1098 57 356 LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYYFLLDLCCSDILRSAICFPFVFNSVKNGST				1	1	1	1
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67 1417 A 1098 57 356 LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYYFLLDLCCSDILRSAICFPFVFNSVKNGST							
PYYFLLDLCCSDILRSAICFPFVFNSVKNGST	67	1417	A	1098	57	356	
		1	'			1	
	{			1	1		WTYGTLTCKVIAFLGVLSCFIITAFMLFCISVT

0E0 ID	OI OUG	Met	SEQ	Predicted	Predicted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of		под	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ			corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq.	uence	(	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		Į.	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	residue of	sequence	Y=1 yrosine, X=0nknown,stop codon,
	1		į	peptide		/=possible nucleotide deletion, \=possible
	)	}	1	sequence	ì	nucleotide insertion
	+	<del> </del>	+	<del>  -'</del>	<del>                                     </del>	RYL
	<del> </del>	<del></del>	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH
68	1418	A	1100	1 .	1320	YEREGMQDWKTASGQSEEATQQSSQKPQPH
	1	1	}	1	1	YTTYQSSSFLKYSSESHLLAWRENSSEGSFQF
		ĺ	1	l .		PGRSRARPPRTRQQRRGAAAGPGRGAVRLG
	(	[		į.	1	HPQSAAQPQLRAAARIPESPAAFPAQPRPGSA
						HPQSAAQPQLKAAAAT LSI AATTAQTA SON
	1	1	}	}	1	RNSDASGPASLSRTLGRASSPRPPQAPDVTAP
	1	1		]		SPAALAPRAARGGSRAAALAGAEAEEPLRTL
		1				APRPTRAAAPPPPPPPPPPPPCAPPPVRCVSR
	1	1	1	ľ	1	RARAPPWR/PAATGPPP/RPVAPSRKLGSARAP
	1	ļ	ł	1	ŀ	APALOIRKGTSSGLPGRGGGSGPGNNLSSVA
	1	}	}	1	}	GNWRGSSFAVERPGMAKYOGEVQSLKLDDD
	[	1	1	ţ		SVIEGVSDOVLVAVVVSFALIATLVYALFRNV
	1	}	1	}	}	HONIHPENQELVRVLREQLQTEQDAPAATRQ
	1	1	1	Į.	1	QFYTDMYCPICLHQASFPVETNCGHLFCGSLT
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69	1419	TA.	1107	2	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA
0)	1,	1	]	j	]	FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF
	1		1			LTKEATSVYHDMSIDSPMKLESLTDIIQKKIEE
	Ì	1	ĺ	ſ	1	TNGOFLIGOREESLP/SS/CGPHSLMVTIKWSS
	1		l l	1	İ	RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
		1		<del></del>		ALRRLHYVRATKVFLSFRRPFWREEHIEGGH
70	1420	A	1111	698	23	SNTDRPSRMIFYPPPREGALLLASYTWSDAAA
	1	1	<b>.</b>	· I	\ -	AFAGLSREEALRLALDDVAALHGPVVRQLW
	- }	j			1	AFAGLSREEALKLALDDVAALHOI VINQUI
	l l	- (	l l		Į.	DGTGVVKRWAEDQHSQGGFVVQPPALWQT
	[	1	- 1			EKDDWTVPYGRIYFAGEHTAYPHGWVETAV
	ì					KSALRAAIKINSRKGPASDTASPEGHASDMEC
Ì	)	}	}	)	}	QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL
	1	1		ŀ		ONTTHTRTSH
L		4	-1		385	OKOTLONGYLDSSMDILYLGSLPPELQVSSDE
71	1421	A	1119	2	100	PPGPPEQAGLSQFHLEPETQNPETTEEIQSSALC
1	.	}	}	}	}	QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL
	1	)		1		EGVHSSTEQKAPAQQLPAFEEILAPLLIHHE
l	į.		[	1		EGVHSSTEQKAPAQQEPAPELICAT BETTATE
72	1422	A	1127	1	906	HAQYVGPYRLEKTLGKGQTGLVKLGVHCIT
\ '~			Į	1	ł	GQKVAIKIVNREKLSESVLMKVEREIAIL\RLI
			j.		-	EHPHVLKLHGVYENKKYFPPDELTSGPSMLA
	1	1		1		OVSPHOKLSARRSWDLLSGFPRYLVLEHVSG
)	1	1	1	1	ì	GELEDYLVKKGRLTPKEARKFFRQIVSALDF
1	- 1		1	1	ì	HSYSICHRDI KPENLLLDEKNNIRIADFGMAS
1	1	- 1	1	1	1	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR
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	1	- [	ļ	i	1	KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEK
(	Ţ	ļ		Į.		LSLEQIQKHPWYLGGNFIS
73	1423	HA	1128	- <del>    </del>	802	LRNALDVLHREVPRVLVNLVDFLNPTIMRQV
/3	1423	^	1123	1.	1	FI GNPDKCPVOOA/MLEPLGSKTETLDLRAE
1	1	}	Ì		l	MPITCPTONEPFLRTPRNSNYTYPIKPAIENW
1	1	ı	1			SDELCTEWKASNSVPTSVHOLRPADIKVVAA
1	1	1	1	1	1	LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG
	Ī	ŀ	1	1		GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG
1	i i	}	}	}	<b>\</b>	TAGLNVAAEGARARDMPAQAWDLVERMK
1	[		1		i	IAGENVAAEGAKAKUMITAQAWDEVENWA
1	1	- 1	1	- {	<b>\</b>	SPDINLEKDWKLVTLFIGGNDLCHYCENPEA
1			J			HLATEYVQHIQQALDILSE
L	- 122E		1139	60	480	FREPCLLVPGDHOPLREASWLA/LPPIGLWG1
74	1424	/ ^	1139	1 00		DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG
	}		1	1		VI GMRDTIPOEHPWESTPDLCFCRDPEEIEVE
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1	- !	- 1				EQUANDAMITTATIONA
L	}	}	1	L		AADPAPVHTTAHPKGA PFPHQHPQEPKGSCWPQSALRGQCPGPVLG
					413	■ CPEPHOHPOEPAK GSCWPOSALKOUCTUT VLU
75	1425	l A	1147	2	[ 413	TTTSDLCSLQVPVSSHRNPLLDLAAYDQEGR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	ļ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	į	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	иелсе		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	[	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	(	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide	·	/-possible nucleotide deletion, \-possible
<b> </b>	<u> </u>	<b></b>	<del> </del>	sequence	<u> </u>	nucleotide insertion
1	1			Į		RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ
	J	j		)		DDESGQKKLHGLQAILVHEASGTTAITATAT
76	1426	-	1155	38	410	GYQESHLSSAR PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK
76	1426	A	1133	ا ا	710	PDCKEIWIFWWGDEPNLVVQYIMNCMLWK
	!	ļ				KDSGKMAFPMNVGRC/FFKEIHNLLERCLMD
	[			1	ļ	KNFVLIGKWFVRPYYKDEKPVNKSEHLSCAF
	1					T
77	1427	A	1162	526	350	RFPQGLEDVSTYPVLIEELLSRGWSEEELQGV
1 ''	1 177	1	****			LRGNLLRVFRQVEKVQEENKWQSPLED
78	1428	A	1171	1	1293	MAESASPPSSSAAAPAAEPGVTTEQPGPRSPP
1.0	0	١	l	1 -		SSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQT
,			}	1		TSPRNWCIKMVCNPWFECVSMLVILLNCVTL
]	J	1	l	J		GMYQPCDDMDCLSDRCKILQVFDDFIFIFFA
	1			<b>[</b>		MEMVLKMVALGIFGKKCYLGDTWNRLDFFI
			1	i		VMAGMVEYSLDLQNINLSAIRTVRVLRPLKA
1	1	[	1	{		INRVPSMRILVNLLLDTLPMLGNVLLLCFFVF
			1	ĺ		FIFGIIGVQLWAGLLRNRCFLEENFTIQGDVAL
		1	1	1		PP\YYQPEEDDEMPFICSLSGDNGIMGCHEIPP
-	1	}	ł	ł		LKEQGRECCLSKDDVYDFGAERQDLNASGL
1		!				CVNWNRYYNVCRTGSANPHKGAINFDNIGY
)	1	J	j	}		AWIVIFQVITLEGWVEIMYYVMDAHSFYNFI
	}			ŀ		YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSFP
		ļ	L		- <u></u>	GVAAESLLLRGWVLWLPGGG
79	1429	A	1175	1	405	PNOFFKOMFPOLPGGPLGPIKAENDYGAYLN
(		l	1			FLSATHLGGLFPPWPLVEERKLKPKASQQCPI
1 .						CHKVIMGAGKLPRHMRTHTGEKPYMCTICE
	1	ł	1	ĺ		VRFTRQDKLKIHMRKHTGERPYLCIHCNAKF
90	1420	<del>  </del>	1102	25	198	VHNYDLKNHMR  ENDIELSOOLSOOGERGASOCESERARTI DNET
80	1430	A	1182	25	170	EMNELSQQLSQQGGRGASQCPSPPAPTLPNPT PLCQLQLQRVNTGLPTPPCHPGAGAA
81	1431	A	1186	254	583	KTVLDVGAGTGILSIFCAQAGARRVYAVEAS
01	1431	^	1100	) 254	,,,,,	AIWQQAREVVRFNGLEDRVHVLPGPVETVEL
	}	!	1			PEOVDAIVSEWMGYGLLHESMLSSVLHARTK
		J	1			VVKDGGFFLPXSSELFM
82	1432	A	1187	2	716	DFVDAARNLPLESTKSPAEPSKSVPSLE\DPRA
\	1	1	1/	[ -	. • •	SSQGLPSQGPVQNQGRRGEQRPKKF/TVIQHT
		1				SSFEKSDSLEQPSGLEGEDKPLAQFPSPPPAPH
	1	1	{			GRSAHSLOPKLVROPNIQVPEILVTEEPDRPD
		ĺ	1			TEPEPPPKEPEKTEEFQWPQGSQTLAQFPVEK
		1		Į	ļ	LPPKKKRLGLAKMAQSSGESSFESSVPLFRSP
				j		SQESNVSLSGSSRSALFERDDHGKAEAPSPSF
				}		DMGPKPLGTHMLTV
83	1433	A	1188	517	804	ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLC
	[	[	[			WGRGHGCGQEALSTSHGYHLFCALLTGFLFA
	ļ	l		ļ		SHLPERLAPGRFDYIGHSHQLFHICAVLGTHF
l _ i	1	l	l	l		Q
84	1434	A	1192	45	476	LGDVGFWVERTPVHEAAQRGESLQLQQLIES
		]				GACVNQVTVDSITPLHAASLQGQARCVQLLL
						AAGAQVDARNIDGSTPLCECLRLGQHRVCEA
		Ì				LAVLRGQGQPSPVHSVPPARGLHXREFRMC*
			L			GFLFDVGXNLEAHEFHFGEP
85	1435	Α	1194	69	410	KRSEEASAPPFPLGGTGAAPTRASLPEQILLPR
	}					SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ
		ł		ľ		HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT
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86	1436	Α	1215	3	405	LPSHTCGNPGRLPNGIQQGSTFNLGDKVRYSC
1				1	1	NLGFFLEGHAVLTCHAGSENSATWDFPLPSC
1	}		(	1	[	RADDACGGTLRG/AEWHHLQPPLPLG/ATKN

SEQ ID No. of nucl- outdoor peptide conde sequence (A-Alanine C-Cysteine, Downson of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide outdoor of peptide peptide peptide of peptide peptide peptide of peptide outdoor of peptide pep							
mucle eutide seq uence uence users of the corresponding uence uence users of the corresponding to the sequence peptide sequence peptide sequence sequence sequence users of peptide sequence seq			,	1 7			
uence USSN vence 19349 corresponding to last amino acid residue of peptide residue of peptide sequence sequence 1944 and per sequence 1950 peptide 1950 peptide sequence 1950 pe		1	hod	T .		h .	
1419   1223   1   1223   1   1224   1245   3   1227   2   349   1441   A   1245   3   1237   1242   1442   A   1246   5   362   349   1442   A   1246   5   362   349   1442   A   1246   5   362   349   1442   A   1246   5   362   349   1442   A   1246   5   362   349   1447   A   1246   5   362   344   348   358			ļ	1			
uence   914   anj to first anino acid residue of peptide residue of peptide sequence   7-Th-Incomie, V-V-Nine, W-Tryproblan, Y-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible uncledide deletion, 'possible nucledide insertion   NADICTWILLAGE (DTIAL). VFIDE QLED GYDFL   X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible uncledide deletion, 'possible nucledide insertion   NADICTWILLAGE (DTIAL). VFIDE QLED GYDFL   X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible uncledide deletion, 'possible nucledide insertion   NADICTWILLAGE (DTIAL). VFIDE QLED GYDFL   X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). VFIDE QLED GYDFL   X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, **-Stop codon, Y-Poysible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosible nucledide insertion   NADICTWILLAGE (DTIAL). X-Tryrosine, X-Unknown, Y-Tryrosible (DTIAL). X-Tryrosible			1				
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		1		1		sequence	
NADCTWTILAELGGTTALVFIDFQLEDGYDFL   EVTGTEGSSLW      87		ļ	1	1		ļ	
87				ļ	sequence		
1437   A   1216   226   964   GTARFOPM\GFGANRAGRI.PSI.VI\GVILV\GYV\GFY\WSISSRH\LI_GEV\AFI\GVILV\GFY\GFY\GFY\GFY\GFY\GFY\GFY\GFY\GFY\GFY		i	ŀ	ļ	1		
		Ĺ					
RTEVARGRIEKRNSDLFAVVGHAGETTRPEG	87	1437	Α	1216	226	964	
GRIRPPQOPAAGOROPREEMEDIA VILQNN				ł		ļ	VIVVLAFNYWSISSRHVLLQEEVAELQGQVQ
SISYOMADĪIHLKEQLAELRQEPELRQEDQLQD   YRKNNTYLVKRELYESPGQOMKELRA,	l	ļ	1	ļ		1	RTEVARGRLEKRNSDLFAVVGHAQETDRPEG
				1			GRLRPPQQPAAGQRGPREEM\EDDKVKLQNN
EENIKKI ADOFILEEQK QÜTÖKIĞ SÜĞ KÖRÜKEL IN NOVYPKIN KVAENVA ADKNEEPSSNHIPHG					[		ISYQMADIHHLKEQLAELRQEFLRQEDQLQD
NNQVYPKNIFKVAENVÄDKNEEPSSNHIPHG   1438		ĺ	ĺ	(	1	ĺ	YRKNNTYLVKRLEYESFQCGQQMKELRAQH
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92 1442 A 1246 5 562 VFDEENILNELNDPLREEIVNFNCRKLVATMP LFANADPNFVTAMLSKLRFEVFQPGDYIIREG AVGKKMYFIQHGVAGVITK SSKEMKLTDGS YFGEICLLTKGRRTASVRADTYCRLYSLSVD NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN SILLQKFQKDLNTGVFNNQENEILKQIVKH  93 1443 A 1249 180 901 TVPPPFGGFSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPSSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT							
92 1442 A 1246 5 562 VFDEENILNELNDPLREEIVNFNCRKLVATMP LFANADPNFVTAMLSKLRFEVFQPGDYIIREG AVGKKMYFIQHGVAGVITKSSKEMKLTDGS YFGEICLLTKGRRTASVRADTYCRLYSLSVD NFNEVLEEYPMMRRAFETVAIDRIDRIGKKN SILLQKFQKDLNTGVFNNQENEILKQIVKH  93 1443 A 1249 180 901 TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPSSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		1	[				
LFANADPNFVTAMLSKLRFEVFQPGDYIIREG AVGKKMYFIQHGVAGVITKSSKEMKLTDGS YFGEICLLTKGRRTASVRADTYCRLYSLSYD NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN SILLQKFQKDLNTGVFNNQENEILKQIVKH TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPSSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT	00	·	<del></del>	1.015	<u> </u>		
AVGKKMYFIQHGVAGVITKSSKÈMKLTDGS YFGEICLLTKGRRTASVRADTYCRLYSLSVD NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN SILLQKFQKDLNTGVFNNQENEILKQIVKH  73 1443 A 1249 180 901 TVPPPPGGPSPAPLHFKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPSSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT	92	1442	A	1246	3	362	
YFGEICLLTKGRRTASVRADTYCRLYSLSVD NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN SILLQKFQKDLNTGVFNNQENEILKQIVKH  93 1443 A 1249 180 901 TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPASSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		)	1	ļ	ļ		,
93 1443 A 1249 180 901 TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPASSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		1	ŀ	}			
93 1443 A 1249 180 901 TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPASSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		<b>!</b>	1			1	
93 1443 A 1249 180 901 TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGRKASCSTAGSGSRGLPPASSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		1	1				
PGRKASCSTAGSGSRGLPPASSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT		L	<u> </u>	<u> </u>			
KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT	93	1443	A	1249	180	901	1
		1	)	}			PGRKASCSTAGSGSRGLPP\SSPMVSSAHNPN
				] .			KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT
		ľ	ì	]			ERPGAERPSLLPNGKENSSGTPRVPPASPSSHS

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG GGGGGGVQNGPPASPTLAHEAAPLPAGRPRP TTNLFTKLTSKLTRRVADEPERIGGPEVTRRP
94	1444	A	1261	3	385	RQEDHLSPGGRGCSEL KFSQWGLTKPKLSNASP/WISLVKKLMKKWS VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL DFNHFYAMDETHHKCLVLRIQEAFGNKLCPA CR
95	1445	A	1282	2	550	GPRDNPG\EDPRFEIVEHFGIAWFTFELVARFA VAPDFLKFFKNALNLIDLMSIVPFYITLVVNL VVESTPTLANLGRVAQVLRLMRIFRILKLARH STGLRSLGATLKYSYKEVGLLLLYLSVGISIFS VVAYTIEKEEN\EGLATIPACWWWATVSMTT VGYGDVVPGTTAGKLTASACILA
96	1446	A	1294	1	1456	QLLPPSNRENAGLLVGRCLCSAALRPVGDLIT SSGQVAVRNAPQAGSAKAGKGKFQDNFEFIQ YFKKFFDANCNEKDYNPVAAGQGQETEVAP SIVAPVLNKPNQCPEGYICVKAGRNPNYGYT SFDTFSWAFLSLFRLMTQDYWENLYQLTLRA AETTYMIF/LV/LVILLGSLYLVTLILAV/VAMA YEEQNQATLEEAEQKEAEFQQMLEQLKKQQ EAAQQAATATASEHSREPSAAGRLSDSSSEAS KLSSKSAKERRNRKKRKQKEQSGEEKDED EFQKSESEDSIRRKGFFSIEGNRLTYEKRYSS PHQSLLSIRGSLFSPRNSRTSLFSFRGRAKDV GSENDFADDEHSTFEDNESRRDSLFVPRRHGE RRNSNLSQTSRSSRMLAVFPANGKMHSTVDC NGVVSLVGGPSVPTSPVGQLLPEVIIDKPATD DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR ORAMSIASILTNTVE
97	1447	A	1295	2	2057	IQTQLPTKSSQQLRKGGNCVRCKMQMNFIAE EVLLKYRITFYNNNKGPNMLYIEIKAFVHFMI NRYLSYGSGPKRFPLVDVLQYALEFASSKPV CTSPVDDIDASSPPSGSIPSQTLPSTTEQQGALS SELPSTSPSSVAAISSRSVIHKPFTQSRIPPDLP MHPAPRHITEEELSVLESCLHRWRTEIENDTR DLQESISRIHRTIELMYSDKSMIQVPYRLHAV LVHEGQANAGHYWAYIFDHRESRWMKYNDI AVTKSSWFELVRDSFGGYRNASAYCLMYIN DKAQFLIQEDLIKTGQPLVGIETLPPDLRDFV EEDNQRFEKELEEWDAQLAQKALQEKLLAS QKLRESETSVTTAQAAGDPKYLEQPSRSDFSK HLKEETIQIITKASHEHEDKSPETVLQSAIKLE YARLVKLAQEDTPPETDYRLHHVVYYFIQNQ APKKIIEKTLLEQFGDRNLSFDERCHNIMKVA QAKLEMIKPEEVNLEEYEEWHQDYRKFRETT MYLIIGLENFQRESYIDSLLFLICAYQNNKELL SKGLYRGHDEELISHYRRECLLKLNEQAAELF ESGEDREVNNGLIIMNEFIVPFLPLLLVDEMEE KDILAVEDMRNRWCSYLGQEMEPHLQEKLT DFLPKLLDCSMEIKSFHEPPKLPSYSTHELCER FARIMLSLSRTPADGR
98	1448	Ā	1304	118	453	SGPSSRAIYLHRKEYSONLTSEPTLLOHRVEH LMTCKQGSQRVQGPEDALQKLFEMDAHGRV WSQDLILQVRDGWLQLLDIETKEELDSYRLD SIQAMNVALNTCSYNSILS
99	1449	Ā	1306	3	1660	CGYFCHTTCAPQAPPCPVPPDLLRTALGVHPE TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS

SEQ ID NO: of nucl- eotide seq-	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496	Predicted beginning nucleotide location correspondi	Predicted end nucleotide location corresponding to last amino	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence		-	914	ng to first amino acid residue of peptide sequence	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP TTCTVLLLAESEGERERWLQVLGELQRLLLD ARPRPRPVYTLKEAYDNGLPLLPHTLCAAILD QDRLALGTEEGLFVIHLRSNDIFQVGECRRVQ QLTLSPSAGLLVVLCGRGPSVRLFALAELENI EVEVPKIPESRGCQVLAAGSILQARTPVLCVA VKRQVLCYQLGPGPGPWQRRIRELQAPATVQ SLGLLGDRLCVGAAGGFALYPLLNEAAPLAL GAGLVPEELPPSRGGLGEALGAVELSLSEFLL LFTTAGIYVDGAGRKSRGHELLWPAAPMGW GYAAPYLTVFSENSIDVFDVRRAEWVQTVPL KKVRPLNPEGSLFLYGTEKVRLTYLRNQLAE KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE EQQKQQRREMIKDPFVRSKLISPPTNFNHLV
100	1450	A	1318	918	190	HVGPANGRPGARDKSP SLCVPGPVDTGTFAVMSVMVGSVTFSLAPQA LNDSMINETARDAARVQVASTLSVLVGLFQV GLGLIHFGFVVTYLSEPLVRGYTTAAAVQVF VSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKL PQSKVGTVVTAAVAGVVLVVVKLLNDKLQQ QLPMPIPGELLTLIGATGISYGMGLKHRFEAG\ PPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGK IFALRHGYRVDSNQVWVMRDV
101	1451	A	1353	220	445	DWPDLFTYPLIGSPKCFQSARPE\RMYRRTVR SSHGNHALQEVLPRSGHGTEFTKQKHLEAAD HGHPPARMSIFSR
102	1452	A	1363	542	2	AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGEN WIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRY CVIIHPMSCFSIHKTRCAVVACAVVWIISLVA VIPMTFLITSTNRTNRSACLDLTSSDELNTIKW YNLILTA\LLCLPLVIVTLCYTTIIHTLTHGHAN \DSCLKQKARRLTILLL
103	1453	A	1371	2	410	CHSTESSSDFILPGDYLLGGLCPLHSGCLQV\C SFNEHGYHLFQAMRLAVEEINNSTALLPNITL GYQLYDVCSDSANVYATLRVLSLPGQHHIEL QGDLLHYSPTVLAVIGPDSTNRAATTAALLSP FLVPMLLEQ
104	1454	A	1376	3	432	NSRVEDRS/NMSLWTQNITVCPVRNVTRDGG FGPWSPWQPCEHLDGDNSGSCLCRARSCDSP RPRCGGLDCLGPAIHIANCSRNGAWTPWSSW ALCSTSCGIGFQVRQRSCSNPAPRHGGRICVG KSREERFCNENTPCPVPIF
105	1455	A	1379	2	396	GLGLLYLIFAAVEGVMRVIGGSNHLAVVLDD IILAVIDSIFVWFIFISLAQTMKTLRLRKNTVKF SLYRHFKNTLIFAVLASIVFMGWTTKTFRIAK CQSDWMERWVDDAFWSFLF\SLILIVIMFLW RPSA
106	1456	A	1383	1	432	EDGHGGWSSRCLVDHAEEGHREPWKRLCIW QRGGHEIRFAFYFPGHPLLSPQICLAPETPPRG CPPVSSLHFISLQ/RLPRDCQELFQVGERQSGL FEIQPQGSPPFLVNCKMTSGTFWTCRTDSRVF QNANPSNAAHSEDQPTP
107	1457	A	1386	719	558	FFFVTRSHSVAQAECSGVFTAHRSLDLVGSSN YPALSLQSSWDHRHTWLIFAFL
108	1458	A	1397	631	2	RVAISLLCAAIFISFMVQSAGKRWPTGVMLM VVVLFAFLYSWPIQALLPTYLKTDLAYNPHT VANVLSFSGFGAAVGCCV/GGFLGDWLGTRK AYVCSLLASQLLIIPVFAIGGANVWVLGLLLF

SEQ ID SEQ ID Met SEQ Predicted Predicted end Amino acid sequ	ence (A=Alanine C=Cysteine,
	d, E=Glutamic Acid,
	e, G=Glycine, H=Histidine,
	=Lysine, L=Leucine,
	N=Asparagine, P=Proline,
uence 914 ng to first acid residue Q=Glutamine, R	=Arginine, S=Serine,
	-Valine, W-Tryptophan,
	Unknown, *=Stop codon,
	otide deletion, \=possible
sequence nucleotide insert	tion
FQMLGQGIA	GILPKLIGGYFDTDQRAAGLG
FTYNVGALGO	GALAPIIGALIAQRLDLGTALAS
LSFSLTFVVIL	RNRRPGKSLVR
109 1459 A 1402 15 387 VLVALPDT\V	<b>FSETVVTEVLGHRVTLPCLYSS</b>
WSHNSNSMC	WGKDQCPYSGCKEALIRTDGM
RVTSRKSAKY	RLQGTIPRGDVSLTILNPSESDS
GVYCCRIEVPO	GWFNDVKINVRLNLQRASTT
110 1460 A 1421 3 350 HEDLSSLLTRO	GSGNQERERQLKKLISLRDWM
LAELAFPVGV	LATCA*SLLSC*YCVILFPCSCF
FFHSPDALFSL	LLLSCYFPSYCFFYYLFFSSSPL
CLLLASSPFPL	FILLASL
111 1461 A 1426 2 344 FTSTMTKPFE	CESEQPA*ATLAFGAQTSTTAD
	LNNSSSSSSTPATSAGGGIFGSS
TSSSNPPVATE	VFGQSSDPVSSYGFVNTAESST
SDSLLFSQDSK	
112 1462 A 1434 46 372 TTSWTTSCTR	SCT*SGASSGPGWTPRTTWWR
SRRSSQRTCSI	RACSGAWSRTW*RSS*TSSSSC
STSCSSSSRS	CGRPGGPLGARGVHITSCLNSC
MSSSTTSSTTS	
113 1463 A 1439 3 292 HEDIMTHYDR	LVDE*ALNAGKQRYEKMISG
MYLGEIVRNII	LIDFTKKGFLLRGQISEMLKTR
	LIVCVLLFYVSFYLFQSCINFVL
114 1464 A 1463 1 396 KQQAVPEPHS	STTTPQEQEQNWYGQDLLNLQ
QRTKVHLPGH	IKTGPAVAKDTPEPVKKEFTVP
ATSQGP*SPFS	EEPPLPPSNEEVPPTLPP*EPQS
EDP*KNA*LK0	QMHAATTHWQQHQQHQVGC
QYHGIMQ	
	SCHWGVTQKRRAL*VYSFEEG
	PLEKDSRIRFGFLTVSNLGVEN
	EILNPEVNPGFFFLTLWKQGEN
NYCN	
	SYSTCNVSSGFLAGQSHNIHLQ
	WLQHFLDTNQLDANCIPFQEF
	SLQEFTRAAGTAGQLLYSNLQ
HLKWNGDSLI	
	VTERFPWQNPLPVNRGQAQR
	VPLQAQKLVSSHKPGQNQKHK
	VCMPLNNTQKSKQPLPSAPEN
	NEESL*RPWALEDFEIGRPLG
KGK	ELECTION OF PER II DAVIDE TO
1 1	FYEKNOGGLFELILRAKDEFNS
	AKHFIRPLTGRDP*KPFPCDQPL
	LDNNIHQAASEPINNNFAESKR
	RHMRKLFMGANLEGPGPTVS
H	not the opening tents to the
	RSLIRGPFDHDLKPNAATRDQL
	LTYEEQDLGWKFRYYLTNQE
	/NWDLPQEAKQALELLGKWK
	LSSHYTNPTVRRYAVARLRQA
DDEDLLMYL	717 4 C) OIG : C! CTC =
	TVLAGMNSAGLSFGGGAGKY
	PSENV WELDLKRFGALQSSRT
	MPLMYDLKVPHWDFQTGRQL
	AQGARWMEKHGFERPKYFVP
] ] ] ] ] ] ] ] ]	EV LEVEDINGENTVECEVECCE
PDKDLLALEQ	
EAVCVIDMSS	FTEFEITSTGDQALEVLQYLFS
EAVCVIDMSS NDLDVPVGHI	FTEFEITSTGDQALEVLQYLFS VHTGMLNEGGGYENDCSIARL
EAVCVIDMSSI NDLDVPVGHI NKRSFFMISPT	FTEFEITSTGDQALEVLQYLFS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	Į.	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
- <b>-</b>	ĺ	ſ		amino acid	of peptide	T-Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł		i	peptide	· ·	/possible nucleotide deletion, \possible
				sequence	ĺ	nucleotide insertion
						MTPDHFPSLFCKEMSVGYANGIRVMSMTHT
			1	<u>L</u>	l	GEPGFMLYIPIEYRWGFTMLSTLVSNS
121	1471	Α	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDQN
						WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE
		j	j			MLVAHTHTVEEHTGTHLQYVSWPDHSVPDD
	<u> </u>	<u> </u>	<u> </u>			SSDFVEFEN
122	1472	Α	1533	121	329	LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT
		l	İ	1	1	WDPGTDTALGWSKQPSQSYTLFES*VGSGYII
			<b></b>	L	L	DNFFLA
123	1473	Α	1547	111	408	DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE
	1	ĺ	İ	1		RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA
		l l	1			AKHGHSPAVQVLLAQWQDINEMNEKQQTPL
101		<u> </u>		ļ.,		HVAADRG
124	1474	Α	1555	1	745	MTFDDDDKNTYGVALVWKKFQTQSLRLSDL
	l	1	}	1		HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP
		ļ		l		YVKFRLGHQKYKSKIMPKTLNPQWREQFDF HLYEERGGVIDITAWDKDAGKRDDFIGRCOV
	]	j	ļ			DLSALSREQTHKLELQLEEGEGHLVLLVTLT
			1	ļ		ASATVSISDLSVNSLEDQKEREEILKRYSPLRI
			l			FHNLKDVGFLQVKVIRAEGLMAADVTGKSD
	1	1	[			PFCVVELNNDRLLTHTVYKNLNPEWNKVFTL
	İ	1	1		1	*VALVWKKFQTQ\$LRL\$DLHRK\$HLWRGIV\$
	1		1	l	1	ITLIEGRDLKAMDSNGLSDPYVKFRLGHQKY
	i		İ	i		KSKIMPKTLNPQWREQFDFHLYEERGGVIDIT
	i .	}	1	ļ		AWDKDAGKRDDFIGRCQVDLSALSREQTHK
	i	l	ł		ł	LELQLEEGEGHLVLLVTLTASATVSISDLSVN
			1			SLEDQKEREEILKRYSPLRIFHNLKDVGFLQV
	1	ł	1	}	}	KVIRAEGLMAADVTGKSDPFCVVELNNDRLL
		Ì	1	l		THTVYKNLNPEWNKVFTL
125	1475	A	1556	57	509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA
	1		1		į	CGGLDNICSIYNLKTREGNVRVSRELPGHTGY
	]	İ				LSCCRPLDDSQIVTSSGDTTCALWDIETAQQT
	ļ		1	1	i '	TTFTGHSGDVMSLSLSPDMRTFVSGACDASS
				<u> </u>		KLWDIRDGMCRQSFTGHVSDINAVS
126	1476	A	1592	3	178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL
			ļ		ļ	EMLPTCDLADQHNIKFHYAFALNR*ER
127	1477	Α	1612	1	497	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS
	Į.		1	l		VLGAYISFGVPSSHLLTASVMSAPASLAAAKL
	1		1	)		FWPETEKPKITLKNAMKMESGDSGNLL*AAT
	ļ		1		Ì	QGASSSISLVANIAVNLIAFLALLSFMNSALA WVGNMFDYPQLSFELICSYIFMPFSFMMGVE
	)	1	}	]	1	WPDSFM
128	1478	A	1619	286	486	CCMNSKAQESVFKNVLCNPPALSEMPDVKA
120	14/8	^	1019	200	+00	EDEVDFRASSISEEVAVGSIAATLKMKQGPM
	)		}	j		TOAINR
129	1479	A	1627	1	395	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI
147	17/3	^	102/	1.	","	MGLCIISIDRYVGVSYPLRYPTIVTQRRGLMA
	1					LLCVWALSLVIYIGPLLGWRHPAPEDETICOI
	1	1	1			NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYRV
	[	1	1	ĺ	1	AKTE
130	1480	A	1638	2	466	DPRVRTKIVNRKTTIYEIQDKTGSMAVVGKG
1		1		<b>!</b> ~		ECHNIPCEKGDKLRLFCFRLRKRENMSKLMS
		1			Į .	EMHSFIOIOKNTNORSHDSRSMALPOEOSOHP
1	]	Į.				KPSEASTILPESHLKTPOMPPTTPSSSSFTKVT
		1	ī	]		KDKDIK*LLFNLYSSVEILPEVLHLKT
		Ì				
131	1481		1651	607	3	LAEGGDVFDCVLNGGPLPESRAKALFROMVE
131	1481	A	1651	607	3	
131	1481	A	1651	607	3	LAEGGDVFDCVLNGGPLPESRAKALFRQMVE

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- cotide seq-	peptide seq- uence		in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid residue of peptide sequence	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TDIPKMLWQQQKGVSFPTHLSISADCQDLLK RLLEPDMILRPSIEEVSWHPWLAST**KQWQV LSNKVGGESKPKKKK
132	1482	A	1656	150	48	LVAKSLLYCGCLFFLLQLAKNVGNNSFNDIM EANLTSPSPKPTPSSDM*VFLIY*TYFGAWHV VDAQ
133	1483	A	1660	3	406	RKHIKLLIQKLSDVP*ECQNNQL*KLTEICEKE KKEFKKKMDDQRPEKITEA*SKDKSPMEEEK TEMIRSYIQEVGRYIKRLEEAQSKRLEKLREK HKEIRQPILDEKPKGEGSSSFLSETCHEDTSWF PNFTP
134	1484	A	1666	1276	466	PGSTHASARITIY*L*IILSNATEVDNNFSKPPP FFPAGAPPASSSSSSSSSSPPTVSTAPPLIPPPGF PPPPGAPPPSLIPTIESGHSSGYDSRSARAFPYG NVAFPHLPGSAPSWPSLVDTSKQWDYYARSS SSSSSSSSSSSSSPRDRDRER*RTRERERERDHS PTPSVFNSDEERYRYREYAERGYERHRASRE KEERHRERRHREKEETRHKSSRSNSRRRHESE EGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE STEATPAE
135	1485	A	1673	1	417	PTRPVNSSQAFALVYYTLGALGGNLIAHMGL GYRYWAGIGVLQSCESALTHYRLVANHVAS DISLTGGSVVQRIRLPDEVENPGMNSGMLQE DLIQYYQFLAEKGDVQAQVGLGQLHLHGGR GV*ONHORAFDYFNLAA
136	1486	A	1678	525	9	ANTSLSSAAVSAVSPPPCRTSTATTLPPPMPSF FCVFPSPSMSPSPSEFLSCIASVSRVHSLSSSSS GSSSTASSLNFSAIMGSSSATASWVLSTASTPP CPSALPSSPAQES*SLAASSSAWPVAGISPSGA CTFPAGSASGAAKAPSPSWRCPSFRALFSLLD SSSLSL
	1487	A	1680	1	2999	AHRDEIQRKFDALRNSCTVITDLEEQLNQLTE DNAELNNQNFYLSKQLDEASGANDEIVQLRS EVDHLRREITEREMQLTSQKQTMEALKTTCT MLEEQVMDLEALNDELLEKERQWEAWRSVL GDEKSQFECRVRELQRMLDTEKQSRARADQ RITESRQVVELAVKEHKAEILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMKATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YIVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eatide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	1	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
			Ţ · · · · · ·			YGRRSRTDDLKWSRLPLAFAYREPYLFVTHF
	İ			†		NSLEVIEIQARSSAGTPARAYLDIPNPRYLGPA
	]	}		1	1	ISSGAIYLASSYQDKLRVICCKGNLVKESGTE
	L	L				HHRGPSTSRR*PASPLPQYQGQRAFLQGRRK
138	1488	A	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV
			1	l		PLCCLGGAAGRL*ARSGKSGLRRRRAHAGPP
	]	1		]	]	PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS
	ļ		1	1		CWTRGCQTTARTAAAAAAPGPAGRRPPGGA
		Į	İ	ļ		PQNGSCAASASQEAAAPPPMCPPGRRWAVAS
	L	ļ	<u> </u>		ļ	PPETRCPAAPGTRCRRLEAA
139	1489	Ä	1693	3	376	LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE
				1		FIETKALGCAWFSLCYYLVLYFESSHKVDFVF
				1	1	IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR
		<u> </u>	<u> </u>		<u> </u>	RWAGIAKGVGTQKIIGRVHLGEQKALGL
140	1490	A	1704	3	376	ERTNKFIKELIMDGKNLIAATKSLSVAQRKFA
	Ì	1				HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL
	(	l	ł	1	l	KNLEEQREIMVS*EGCKLISQLSRGKKIWIWK
141	1401	<del>  _,</del>	1543	<del>  ,</del>		LVLVEVVKHLSLGTVVHCNGKMRFPEP
141	1491	A	1743	1	362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ
	1		ŀ	1	1	DKLELELVLKGSYEDTQTSFLGTASAFRFHY
	}	1	j	1	1	MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV
140	1492		1769	<u> </u>	406	PLRPLTIVKEVTMDVPAPNVRGLNWMG
142	1492	Α	1769	1	406	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS
	-	1	1			LSLASSTVGPGGQIVHTETTEVVLCGDPLSGF
	1	1	1	1	1	GLQLQGGIFATETLSSPPLVCFIEPDSPAERCG LLQVGDRVLSINGIATEDGTMEEANQLLRDA
		1		j	· ·	ALAHKVV
143	1493	<del> </del> A	1789	<u> </u>	447	OMLRNGGDONTVPDYHFADRIRELL*PTEDO
143	1493	A	1709	<b>1</b> *	} ***	KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA
		i		ĺ		NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA
	ļ	1	1			SDFIARQGTLIQVPSSAGEVECYKICSCGQSGL
-	ĺ	Į	ł			LENCMEMHCMDLPTDTSALVR
144	1494	A	1814	<u> </u>	404	PGRRFRPRLSQAGTDSGS*VFPDSFPSAPAEPL
	,	•-		1 -	'*'	PYFLOEPODAYIVKNKPVELRCRAFPATOIYF
	]		<b>!</b>	ļ	<u> </u>	KCNGEWVSQNDHVTQEGLDEATGLRVREVH
				ĺ		IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK
						SRRAYVRI
145	1495	Α	1827	26	448	XVEEKHADTWRSXCLSDFFFHAAKXLCXE*N
	1	1		ĺ	ĺ	CGDAISLSVGDHFGKGNGLTWAEKFQCEGSE
		ŀ		1		THLALCPIVQHPEDTCHSREVGVVCSRYTDV
	1	1		ĺ	ĺ	RLVNGKSQCDGQVEINVLGHWGSLCDTHWD
		1		l		PEDARVLCRQLNCGTAL
146	1496	A	1828	574	333	QHEGGDLRRRQLGEIQLTVRYVCLRAASAC*
				i		SMAAET*HHVPASGADPYVRVYLLPERKWA
	<u> </u>	<u></u>			L	CRKKTSVKRKTLEPLFDET
147	1497	Α	1855	1	372	ERLVLTSEHCLVLTLFWPSWTYHTLLLSRQH
	!	ľ		1		VRRUPKLTHAEHDHLASIMNKLLTNYDNLFE
	1	1.				TSVTYSMG*HGAPTGSEAGANWNH**LHAH
	]					YYPPLLRSDTVRKFMVGSQMLAQAQRDLTPE
	L	<u> </u>				Q
148	1498	Α	1879	568	7	LLSALDDKGGTQPSASFSNAPTIVCVTACPAG
	1	1				IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN
	1	1				GIEGRLTADQLNSATACIFAAEVAIKESERFN
	1	1			,	GIPALSVPVAEPIRHAEALMQQALTLKRSDET
	1	1				RTVQQDTQPVKSVKTELKQALLSGISFAVPLI
***	L	ļ.,—	1			VAGGTQVA*AV*RQGISSLHDVQVRTWNS
149	1499	l A	1880	611	24	GLNSENALSNEAMERGWQCLRLFAERLQDIP
		• -		1		
	}	•				PSQIRVVATATLRLAVNAGDFIAKAQEILGCP VQVISGEEEARLIYQGVAHTTGGADQRLVVD

			1050		<del></del>	( A
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide	location	1 =
eotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ŀ	İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ļ		Į.	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i i		ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l		ļ	peptide	}	/-possible nucleotide deletion, \-possible
	ļ	ļ	}	sequence	ł	nucleotide insertion
						IGGASTELVTGTGAQTT*LFSLSMGCVTWLER
		ļ	l	1		YFADRNLGQENFDAAQKAAREVLRPVADEL
	1	1	Ì			RYHSWKEVRGASVTVQALQEIMMAQGMDE
	i .	l	l		ĺ	RITMEIWPVD
150	1500	A	1894	2	750	GRVDFFHTDYRPLIRDSNNYVLDEQTQQAPH
130	1300	\ \frac{1}{2}	1074	<b> </b>	1 130	LMPPPFLVDVDGNPHPTKYQRLVPGRENSAD
			İ	ł		EHLIPOLGYVATSDGEVIEQIISLQTNDNDERS
	J	]	1	j		
	Ì	ĺ	,		ļ	PESSILDGMIRQLQQQQDQRMGADQDTIPRG
			j	!		LSNGEETPRRGFRRLSLDIQSPPNIGLRRSGQV
	(	ĺ	į.	[	[	EGVRQMHQNAPRSQIATERDLQAWKRRVVV
		ļ		ļ		PEVPLGIFRKI.EDFRI.EKGEEERNI.YIIGRKRK
	1	1	1	1	Í	TLQLSHKSDSVGLVSQSRPRTCRRKYP
151	1501	Ä	1900	141	785	GKTIQIQTTMQNKYKTVQKQYKTIPKNKKA
					1	MEMOIKKOFODTCKVOTKOYKALKNHOLEV
		1	1	1	1	TPKNEHKTILKTLKDEOTRKLAILAEOYEOSI
	1	ĺ	[	1	1	NEMMASQALRLDEAQEAECQALRLQLQQEM
		1	i	1		ELLNAYOSKIKMOTEAOHERELOKLEORVSL
	1	1	ł .	i		RRAHLEOKIEEELAALOKERSERIKNLLEROE
	İ		1			REIETFDMESLRMGFGNLVTLDFPKEDYR
	1.55	<del> </del>	1 224 2 -	<b> </b>	200	
152	1502	A	1915	2	377	LVRLLDTQRDGLQNYEALLGLTNLSGRSDKL
	1	]	j	]		RQKIFKERALPDIENYMFENHDQLRQAATEC
	1					MCNMVLHKEVQERFLADGNDRLKLVVLLCG
	İ	•	1			EDDDKVQNAAAGALAMLTAAHKKLCLKMT
	i	(	1	[	<u> </u>	QVTT
153	1503	Α	1921	1	237	AYQSLRLEYLQIPPVSRAYTTACVLTSAAVQL
		1	ì	1		ELITPFOLYFIPELIFKHFOIWRLITNFLFFVPFG
	ļ	)	J	1	1	FNFLLYMIFLYT
154	1504	A	1928	2	354	EMVEGGEGKMCINTEWGGFGDNGCIDDIRTR
			1	-	}	YDTEVDEGSLNPGKQRYEKMTSGMYLGEIV
			ł			ROILIDLTKQGLLFRGQISERLRTRGIFETKFLS
	i	ł	ł			QIESDRLALLQVRRILQQLGLD
155	1505	A	1929	2	369	TEIAKIKMEAKKKYEKELTMFQNDFEKACQA
123	1303	^	1929	4	309	KSEALVLREKSTLERIHKHQEIETKEIYAQRQ
		i	1	ł		
		1	l			LLLKDMDLLRGREAELKQRVEAFESYQLELK
	<u> </u>		<u> </u>			DDYIIRTYRLIEDDRINIQISGHWQESP
156	1506	A	1935	1	270	VTRKLPIFIVDAFTARAFRGSPAADCLLENEL
			1	1		DEDMHQKIAREMNLSETAFIRKLHPTDNFAQ
	<u></u>	L	<u></u>	L	L	RSCFGLIWFTPTTDLQILTSSILPSIL
157	1507	A	1936	584	305	ESKVNNEKFRTKSPKPAESPQSATKQLDQPTA
		1	1	}	i	AYEYYDAGNHWCKDCNTICGTMFDFFTHMH
		ì	1	1	1	NKKHTQGQFQKSSDFQKEELQQTFLPPERQG
158	1508	À	1939	1	423	TTHRLNVTAEPPCTSMPIYWMPDVPHRCTTA
			1	Į	1	NTCPVDLTDYCAONGFYCLVYGFLPYGSLED
		]		Į.		RLHCOTOACPPLSWPORLDILLGTARAIOFLH
	1		}	ļ	]	ODSPSLIHGDIKSSNVLLDERLTPKLGDFGLA
	1			l		
160	1.500	<del></del> -	1054	<u> </u>	401	RFSRFAGSSPIQSSM
159	1509	A	1974	3	401	HTSTARLLHRGAGKEAVTSDGYTALHLAAR
	ļ					NGHLATVKLLVEEKADVLARGPLNQTALHL
		]		1		AAAHGHSEVVEELVSADVIDLFDEQGLSALH
		1	}	1	J	LAAQGRHAQTVETLLRHGAHINLQSLKFQGG
	ļ			l	_	HGPAATLLR
160	1510	A	1982	2	417	KFLKDLEKQYNKEEPHLSEIGSCFLQNQEGFA
-	1	i -	1	[	[	IYSEYCNNHPGACLELANLMKQGKYRHFFEA
	1	]		ĺ		CRLLQQMIDIAIDGFLLTPVQKICKYPLQLAEL
		ì	!	1		LKYTTQEHGDYSNIKAAYEAMKNVACLINER
			1	}	1	KRKLESIDKIA
141	1511	-	1004	4	770	RETGSVSLSPSGLEGAESYAVSPILYSSPDVKE
161	1511	A	1984	**	170	
	I	I	1	1	I	LWLETLQGQRHSHTGVKSTPGQSAAILMKLR
	]	ı	,	i		SSHNASKTLNANNMETLIECQSEGDIKEHPLL

6 <del>6</del> 5	1 000 V	1 14	1 650	1 10-231-2-1	I The office of the state of	Amino pold games as (A - Alasia - O O
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of peptide	noa	in NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-					corresponding	I=Isoleucine, K=Lysine, L=I.eucine,
eotide	seq-	ĺ	USSN	location	, , ,	1
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	l	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V-Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			[	peptide	{	/-possible nucleotide deletion, \-possible
	L	<u> </u>	<u> </u>	sequence		nucleotide insertion
			-			ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
	į.		1		i	PASDFSGALETDLKASLFDQPLSIICGDSDTLP
				ļ		RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
						KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
	1					RKLLSSDLFEEWMGALEMQDEEDRIEALK
162	1512	A	1986	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
ļ.	İ				ľ	KFQGRWGTVCDDNFNIDHASVICRQLECGSA
	ļ		1	<b>!</b>	}	VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
	ł	ł	1	1	1	CKHQGWGKHNCDHAEDAGVICSSKD
163	I513	A	2001	419	187	AVDLSIDESSLTGETTPCSKVTAPQPAATNGD
103	13.5	١.,	1 2001	'''		LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
				ļ.	1	FGDIINLSTFVVHS
164	1514	A -	2012	284	597	SLLCLFPGTSTVVCKPIVIETOLYVIVAOLFGG
104	1314	1^	2012	204	1 371	SHIYKRDSFANKFIKIQAIEILKIRKPNDIETFKI
				İ	i	
ļ		1		ļ	1	ENNWYFVVADSSKAGFTTIYKWERETGFYSH
1/5	1515	<b>L</b> .		<u> </u>	1 102	QSFTR
165	1515	A	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
	1		ſ	1	!	NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
İ	1		1		,	DTHWRVAHERDELWRAQIVATTVMLERKLP
	1		1	ł	1	RCLWPRSGICGREYGLGDRWILRVEDRQDLN
		L				RQRIQRYA
166	1516	A	2019	2	927	CCQREGLGLKAVVQILLSHGRNGLPGEPASS
1	ì	1		ŀ	1	QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
				ĺ		NKNMVTERLQNVMVLEQCFSDSSSLYRFLTY
Ì	ĺ	1	1	İ	ľ	SYLLAFNVWLLLAPVTLCYDWQVGSIPLVETI
	ĺ	ĺ	Ī		1	WDMRNLATIFLAVVMALLSLHCLAAFKRLE
		1	1	1		HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
l	}	1	1	ł		VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
		ł		1		LIVSTVLLLLLFSWKTVKQNEIWLSRESLFRS
)	ļ		}	J		GVQTLPHNAKVHYNYANFLKDQGRNKEAIY
		1	l l	Ì		HYRTALNNNKAWDYLCWRFRKTLIDLP
167	1517	A	2025	696	71	AAASAASSLTVTLGRLASACSHSILRPSGPGA
	ļ	1	1	(		ASLWSASRRFNSQSTSYLPGYVPKTSLSSPPW
	ì			1	1	PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
	ŀ	l	1	ļ		GRLFAVVHFASRQWKVTSEDLILIGNELDLA
		ļ	1	Į		CGERIRLEKVLLVGADNFTLLGKPLLGKDLV
	1		J	1	1	RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
			1	[	1	TTPOTVLRINSIEIAPCLL
168	1518	À	2046	2	366	HLOVAARVFMPLQAVDSAPKPLKGQAQAPQ
	1			l -	1	RLQGAARVFMPLQAQVKAKASKPLQMQIKA
		1	1	1		PPRLRRAARVLMPLOAOVRAPRLLOVOSOVS
}	1	1	}	1	1	KKQQAQTQTSEPQDLDQVPEEFQGQDQVLR
169	1519	Ā	2049	1	945	ONLEDREVLNGVOTELLTSPRTKDTLSDMTR
107	לוכו	^	2049	l <b>'</b>	343	
		1	1	J	1	TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
			1	{	1	EDNSRSKREGLFHENECIVKINNVDLVDKTFA
				İ	1	QAQDVFRQAMKSPSVLLHVLPPQNREQYEKS
	1		1	!		VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
		1	1	1	1	NLTGTDSPETDASASLQQNKSPRVPRLGGKPS
	)		1	)	ļ	SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
			1		1	TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
	1		1	]	1	SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
	L		l			ETASLVIARQEGHFLPRELVMFRSQSH
170	1520	Ā	2050	363	1	PVATHLTKILNSDEHAVVISSAKTLCETVKDF
				}	1	VAKVEKTYDKTLENAVVADAVASKCSVLNE
			1			KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV
			1		1	ESSSEESLGESKEOLGDDVTKPSSOKA
171	1521	A	2055	139	675	IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
_ · · ·		1.	-000	1	1	DAOFVDVIHSDTDALGYKEPLGNIDFYPNGG
					ļ.	LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL
L	<u> </u>		1	<u> </u>	<u> </u>	PPALACIELITEOGIA IL VODITAVOA I PI POOP

NO: of nucleotide sequence  No: of nucleotide sequence  NO: of nucleotide sequence  No: of nucleotide sequence  No: of nucleotide sequence  No: of nucleotide sequence  No: of nucleotide sequence  No: of nucleotide sequence  No: of nucleotide sequence, N=Proline, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, N=Asparagine, N=Asparagine, N=Arginine, S=Serine, O=Glutamine, N=Asparagine, N=Arginine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparag	050 50	T 000 00	1.40-	TODO	Dundies - J	Dandint-J 1	A -inc said requests (A-A)-rine (-Custoin-
Incurior	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
Sequence   1949/96   1940			под	1			
		,	1	1		1	
1914   ng to first amino acid residue of peptide residue of peptide sequence			Ì				
minion acid residue of sequence   fraction		uence	}				
Fesidue of   pepide   sequence   Y-Tyrosine, X-Unknown, *-Stop Godon,   pepide   sequence	uence			914			1 \ 7 \ 7 \ 7
Poptide   Sequence   Poptide   Poptide   Poptide   Sequence   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCTITATYCDSYQDYRNGKCVSCGTSQKE   RESCRIPTYCHTYDITTWINNVR   RESPECTIVE   RESPECT							
				ļ		sequence	
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182 1532 A 2123 1 493 RTKTDVYILNLAVADLLLLFTLPFWAVNAVH GWVLGKIMCKITSALYTLNFVSGMQFLACISI DRYVAVTKVPSQSGVGKPCWIICFCVWMAAI LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS  183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF		í	}	1	1		
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DRYVAVTKVPSQSGVGKPCWIICFCVWMAAI LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS  183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF	102	1334	1 ^	2123	[ *	173	
LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS  183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF			1	1	1		
IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS  183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF		Į.		}	[		
183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF		1	}	1	]	J	
183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF			1		1		•
RSGNYFVTMFDDYSATLPLLIVVILENIAVCF		L	ļ	<del> </del>	<u> </u>		
	183	1533	A	Z140	ا ا	261	
VYGIDKFMEDLKDMLGFAPSRYYYYMWKYI			1	1	1		
			<u></u>	<u> </u>	<u>L</u>	L	VYGIDKFMEDLKDMLGFAPSRYYYYMWKYI

NO: of NO	D: of ptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutarnic Acid,
nucl- eotide seq seq-	ptide 1-	nod				
eotide seq seq- uer	1-	Ì	111			F=Phenylalanine, G=Glycine, H=Histidine,
seq- uer			USSN	location	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
		- [	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
Genee		- 1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
]		- 1	<b>'''</b>	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	5- <b>4</b>	/=possible nucleotide deletion, \=possible
		- 1	ļ	sequence		nucleotide insertion
<del></del>	-+					SPLMLLSLLIASVVNMGLSPPGYNAWIEDKAS
1		-				EEFLSYPTWGLAVCASLDVFAILPVPVAFIGR
		Į				RFSLIDDGAGPFCSAAYTTTGCRTPYL
184 153	34	A	2145	3	538	HELTVAAADRGQPPQSSVVPVTVTVLDVND
		- 1				NPPVFTRASYRVTVPEDTPVGAELLHVEASD
1		1				ADPGPHGLVRFTVSSGDPSGLFELDESSGTLR
i i	- 1	- 1				LAHALDCETQARHQLVVQAADPAGAHFALA
	- 1	-				PVTIEVQDVNDHGPAFPLNLLSTSVAENQPPG
						TLVTTLHAIDGDAGAFGRLRYHL
185 15:	35	A	2151	2	671	LDKLLDRMENYNIFNEYILKQVAATYIKLGW
į		ŀ				PKNNFNGSLVQASYQHEELRREVIMLACSFG
		- 1				NKHCHQQASTLISDWISSNRNRIPLNVRDIVY
		ŧ				CTGVSLLDEDVWEFTWMKFHSTTAVSEKKIL
]	-					LEALTCSDDRNLLNRLLNLSLNSEVVLDQDAI
	[	[				DVIIHVARNPHGRDLAWKFFRDKWKILNTRI
1		i				RQKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
J	1	<u>,                                    </u>	2152		400	E GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
186 15.	30 .	A	2153	2	400	HLALPDAQDILYTLEDNRNWVDSMIPQSPSPP
	- [				_	LDEONROWOGLLENLHVELTLDEEDSEGPEK
]	- 1					EGEGQTYFTSSKTLCGIVPQNTDSLGETGIHIC
İ İ						AHDKSP
187 15	37	${A}$	2158	227	442	FNCFRVASDSFLENSSLLIMILPLRNATQEFIIR
13.	"	**	21.70	251	174	PGAVAYTCNPSTLGGWGGWITRSGVRDQPG
	- 1	1				OHGGTPS
188 15	38	A	2167	3	486	AHLGGAWLTQRSLGSWAAPGPARAAKEVVA
100		· ·				CIPONOKMNIWRMKTSKHLQLLSFVLGAVSP
1 1	i	- 1				AVVVPYMMVLQENGYGVEEGIPTLLMAASS
i	1					MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
1	İ	l				LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
3						HSGA
189 15	39	A	2168	2	412	EFLSSNQITQLPNTTFRPMPNLRSVDLSYNKL
1				,		QALAPDLFHGLRKLTTLHMRANAIQFVPVRIF
				,		QDCRSLKFLDIGYNQLKSLARNSFAGLFKLTE
				!		LHLEHNDLVKVNFAHFPRLISLHSLCLRRNKV
L						AIVVSSLDW
190 154	40	A	2179	64	399	MRLNQNTLLLESFGXXRPYTSEHAPTYHQW
		ļ		İ		MKADELLRWTTSEPLTLEHEYAMQRTWLED
		1				AYECTFIVLDAEKRHAQPGATEESCMVGDVN
101		<u>,                                     </u>	2100	1	460	LFLTDLEDLTLGEIEVLIAEP CLDRAAGIRHERNVIYINETHTRHRGWLARR
191 154	<del>4</del> 1 .	A	2190	1	469	
		1				LSYVLFIQERDVHKGMFATNVTENVLNSSRV OEAIAEVAAELNPDGSAQQQSKAVNKVKKK
		ļ				AKRILQEMVATVSPAMIRLTGWVLLKLFNSF
		1				FWNIQIHKGQLEMVKAATETNLPLLFLPVHR
		l				SH
192 154	47	A	2197	26	157	PSKXGGIRLLLTGTQLYGRFGSAIAPLGDLDR
132   134	T#	r	4171	20	131	DGYNGEGREEPY
193 154	<del>43-  </del> -	Ā	2236	2	383	EYFPNSJWRSLFSTMDLGDIGFYTYRILQALS
133   134	-	^	2430	-	263	YTHSKGIMHRDVKPLNILCNSPRNKVILADW
i l		}				GLAEFYHPMRKYSVHVATRYYKSPEILLDYE
						YYDYSLDIWAVGVILLELLTLKLHVFEGGDN
1	- 1	- 1				EO
194 154	<del>44 - +</del>	A	2241	105	409	RKGVGKMPTSEGRPGOERSDWVTSYKVMGS
15		^ <b>`</b>	T1	103	,	NDSHTWVTVKNGSGDMIFEGNSEKEIPVLNE
i i	- 1	ľ			,	LPVPMGARYIRINPQSWFDNGSICMRMEILGC
		i		!		PLPDPNNY
1			2212	·	799	
195 15	45	A I	2245	1	672	MGVASDWTKRIEYQPGSGSMPLFPSIHLETCD

000 10	r aso to		1 650	I D 11-4-3	Dan di And and	A i-a acid acquarac (A Alonina C Custaina
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	1	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide -	seq- uence	ì	055N 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1		sequence	
				peptide	ĺ	/=possible nucleotide deletion, \=possible
	ļ		<u> </u>	sequence		nucleotide insertion
		ł	ĺ		1	KLCGASSGIIDLLPSPSAATNWTAGLLVDSSE
	1			1		MIFKFDGRQGAKIPDGIVPKNLTDQFTTTMW
		ł				MKHGPSPGVRAEKETILCYSDKTEMNRHHY
	(	ì		1		ALYVHNCRLVFLLRKDFDQADTFRPAEFHW
	ľ	ļ	ł	1		KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
		1	<u> </u>		·	ISLKPS
196	1546	Α	2256	1	396	FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
		1				GKVINKDLRHYLSLQFQKGSIDHKLQQVIRD
			1		1	NLYLRTIPCTTRAPRDGEVPGVDYNFISVEQF
	}	1	ł	ì		KALEESGALLESGTYDGNFYGTPKPPAEPSPF
	1				1	QPDPV
197	1547	A	2259	43	594	QLAIEIGVRALLFGVFVFTEFLDPFQRVIQPEEI
					1	WLYKNPLGQSDNIPTRLMFAISFLTPLAVICV
			1			VKIIRRTDKTEIKEAFLAVSLALALNGVCTNTI
		ľ	1	(	1	KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP
			ľ		ì	DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKL
						HCFTESGRGKSWRLCAAILPL
198	1548	A	2275	3	404	TCTTVVVIPRMLVDFLSESKTISLPECATOMFF
						FLGFASNNCFIMAAMSYDRYTAIHNPLQYHT
	l .		ì			LMTRKICLQMMMASWMVGFLFSLCIIVTVFN
	Į	}	ł	1		LSLCDLNTIQHYFCDISPVVSLACNYTFYHEM
			l .			AIFVLSA
199	1549	A	2315	<del>                                     </del>	375	LTOMFFIHALSAIESTILLAMAFDRYVAICHPL
177	1347	1.	2313	ļ •	3,5	RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLI
			t		İ	KRLAFCHSNVLSHSYCVHQDVMKLAYADTL
	1					PNVVYGLTAILLVMGXDRMFISLSYFLII
200	1550	A	2334	2	409	PRVRPQORKMSFFFKTELGEKLVTKFLFETDF
200	1330	Α	2334	1	403	SDDPMLPSPDQLKKKAPFTNKKLKAHQTPVD
		1				ILKQKAHQLASMQVQAYNGGNANPRPANNE
			1	ļ	ł	EEEDEEDEYDYDYESLSDDNILEDRPENKSCH
	1		<b>}</b>			DOLOFEYKEEM
201	1551	A	2350	3	512	ISWEAQIAEIIQWVSDEKDARGYLQALASKM
201	1331	A	2330	١٠	312	TEELEALRSSSLGSRTLDPLWKVRRSQKLDM
	ļ	i	i	1		SARLELQSALEAEIRAKQLVQEELRKVKDAN
ļ			1	i		LTLESKLKDSEAKNRELLEEMEILKKKMEEK
İ	J	ļ	}	j	ļ	FRADTGKLMLCDSALFEYKYFSNECFYFLFD
	1		}			LIVTLEAPTEFQIQY
	1.550	<del>                                     </del>	1 2253	ļ.,	1000	
202	1552	Α	2351	1	1003	PSSYSSDELSPGEPLTSPPWAPLGAPERPEHLL
			ŀ			NRVLERLAGGATRDSAASDILLDDIVLTHSLF
ŀ	1		1	l	1	LPTEKFLQELHQYFVRAGGMEGPEGLGRKQA
						CLAMLLHFLDTYQGLLQEEEGAGHIKDLYL
		1				LIMKDESLYQGLREDTLRLHQLVETVELKIPE
		]	]		1	ENQPPSKQVKPI.FRHFRRIDSCI.QTRVAFRGS
			1		1	DEIFCRVYMPDHSYVTIRSRLSASVQDILGSV
						TEKLQYSEEPAGREDSLILVAVSSSGEKVLLQ
	1		J		J	PTEDCVFTALGINSHLFACTRDSYEALVPLPE
		į	1			EIQVSPGDTEIHRVEPEDVANHLTAFHWELFR
	1 .			L	i	CVHELEFVDYVFHGE
203	1553	Α	2361	2	403	NNLNCAEPLFEQNNSLNVNFNTQKKTVWLIH
			1			GYRPVGSIPLWLQNFVRILLNEEDMNVIVVD
	1				1	WSRGATTFIYNRAVKNTRKVAVSLSVHIKNL
	[				1	LKHGASLDNFHFIGGSLGAHISGFVGKIFHGQ
	1	1	1	•	1	LGRITGLDP
204	1554	A	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSPQ
					1	AGSRLGAMRRCAREMDATPMPPAPSCPSERV
	1				1	T
205	1555	A	2400	543	745	AAVALRDISWOOPYPMDFYAGSSLOPWTVN
_05	.555	1 '`	2,000	1 3 . 3		HGQDRRPHAPGRPARGKVQEGSARPPSAVAC
		1	1		1	EDCSCR
	1	1		1	1	DECOOR

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence 122	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DLSPDSREDHPQGHRRLLPKRPVRGSLMPGH THHPCPVSSTTNDTPDQIWVSVGSLRMGTGG MGANASTSPRCWDLSSGNKKWIIQVPILASIV ESRGGLLATGVGGMCACVPRNQPLTGT LWTLYRHKOOVOHNHSNRLSCRPSOEDRAT
208	1558	A	2413	64	492	HTIMVLDKENTLS  VQGTGXXFIAFTEAMTHFPASPVWAGMFFL  MLINLGLGSMIGTMAGITTPIIDTFKVPKEMFT  GGCCVFAFLVGLLFVQRSGNYFVTMFDDYSA  TLPLTLIVILENIAVAWIYGTKKFMQELTEML  GFRPYRFYFYMWKFVSP
209	1559	A	2417	3	877	EKERLLDEWFTLDEVPKGKLHLRLEWLTLMP NASNLDKVLTDIKADKDQANDGLSSALLILY LDSARNLPIRYKTNEPVWEENFTFFIHNPKRQ DLEVEVRDEQHQCPLGNLKVPLSQLLTSEDM TVSQRFQLGNSGPNSTIKMKIALRVHLEKRE RPPDHQHSAQVKRPSVSKEGRKTSIKSHMSG SPGPGGSNTAPSTPVIGGSDKPGMEEKAQPPE AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA SDISLPIATQELRQRLRQLENGTTLGQSPLGQI QLTIP
210	1560	A	2422	35	456	REFAASDLEPFTPTDQPISPEAITQPSCIKRQRA AGNPGSLAATIDHKPCSAPLEPKIQASRNQRW GAVRAAESLTDIAEPASPQVHETPIDASQTQK VEPASKSRFTPELQAKVSHSRERALSTMDATP HHAQPQRGEG
211	1561	A	2431	1	764	RRYSOKLIOHTACOLLRTYPAATRIDSSNPNP LMFWLHGIOLVALNYQTDDLPLHLNAAMFE ANGGCGYVLKPPVLWDKNCPMYQKFSPLER DLDSMDPAVYSLTIVSGQNVCPSNSMGSPCIE VDVLGMPLDSCHFRTKPIHRNTLNPMWNEQF LFHVHFEDLVFLRFAVVENNSSAVTAQRIIPL KALKRGYRHLQLRNLHNEVLEISSLFINSRRM EENSSGNTMSASSMFNTEERKCLQTHRVTVH GVPG
212	1562	Α	2436	1	411	GIRGTTGHLGCPINDDPSLTLTVSWVMEDKPI YIGNGTKKEDDSLTIFAVAKRDHVSDTCGAC TDLDHNLDKGYLTVLGEQATPTNRLGALPKG RANRTRDLELTYLAERIVRLTWIPGDANNRPI TDYDCQIEEHQ
213	1563	A	2445		1294	MSSIGCLWVSRSSQIDGLTAEKSGPEKPHGT WLMPELHPKEQILELLVLEQFLSILPEELQIWV QQHNPESGESVTLLEDLEREFDDPGQQVPAS PQGPAVPWKDLTCLRASQESTDIHLQPLKTQ LKSWKPCLSPKSDCENSETATKEGISEEKSQG LPQEPSFRGISEHESNLVWKQGSATGEKLRSP SQGSFSQVIFTNKSLGKRDLYDEAERCLILT TDSIMCQKVPPEERPYRCDVCGHSFKQHSSLT QHQRIHTGEKPYKCNQCGKAFSLRSYLIHQR IHSGEKAYECSECGKAFNQSSALIRHRKIHTG EKACKCNECGKAFSQSSYLIHQRIHTGEKPY ECNECGKTFSQSSKLIRHQRIHTGERPYECNE CGKAFRQSSELITHQRIHSGEKPYECSECGKA FSLSSNLIRHQRIHSG
214	1564	A	2461	1	615	GIPGSTISSSRNIFLEDDLAWQSLIHPDSSNTPL STRLVSVQEDAGKSPARNRSASITNLSLDRSG SPMVPSYETSVSPQANRTYVRTETTEDERKIL LDSVQLKDLWKKICHHSSGMEFQDHRYWLR THPNCIVGKELVNWLIRNGHIATRAQAIAIGQ

muche odde sequence where the corresponding of the contemporary where the contemporary wher	SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
DISSN   Dication   Dissn   D				Į.			
156			!	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
156	seq-			09/496	correspondi	to last amino	
Page   Page			ļ	914	ng to first		
							T=Threonine, V=Valine, W=Tryptophan,
				ļ	residue of	sequence	
AMYDGRWLDCVSHIBOLFRDEYALLYRPLQV	}	ļ	ļ	i	peptide		
2932		<u> </u>		<u> </u>	sequence		nucleotide insertion
1565   A   2464   3   2932   GFGVRSSQDGMADVFVHLRTAWFRCSISGO   HGGRGHGRUCSSQDSMADVFVHLRTAWFT   CSLISGOHGGESVSYEDDDPAPASLLHVVA   AAPALTNFTARVLCTAPNNTOKEVPSOMS   AAPALTNFTARVLCTAPNNTOKEVPSOMS   AAPALTNFTARVLCTAPNNTOKEVPSOMS   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHSTVFVGVRISSC   TOPLICAVSTHATVFGVRISSC   TOPLICAVSTHA							
HOFGRIGRRVCSSQDSMADVFVHLRTAWFT							LFSVYCQLECSKLIL
CSLISEGOHGGESVSYEDDDAPASLLHVVAN AAPALINPITAPVICTAPNITACKEVYSGMISSC POPLICAVSIHSTYPOTRISC TPELICAVSTHSTVPSVCISSCTPDLITCAVSTH STYPOGYRISSCTPDLICAVSTHSTYPOTRISSC TPELICAVSTHATVYOCKISSCTPDLICAVSTHSTYPOTRISSC TPELICAVSTHATVYOCKISSCTPDLICAVSTHSTYPOTRISSC TPELICAVSTHATVYOCKISSCTPDLICAVSTHATYOCKISSCTPDLICAVSTH	215	1565	A	2464	3	2932	
AAPALINPTAPULCTAPNNTAQKEKPYSCMS   QRRAGVRISSTPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSTHSTYPGVRISSC   TPDLTCAVSHATYPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   ATVPGVRISSCTPDLTCAVSHA   TVPGVRISSCTPDLTCAVSCTPDLTCAVSHA   TVPGVRISSCTPDLTCAVSCTPDLTCAVSCTPDLTCAVS		ļ			<b>:</b>		
QRPAGVRISSRTPDLTCAVSTHSTVPQVRISSC   TPDLTCAVSHISTVPSVCISTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   STVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   ATVPQVRISSCTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   STVPQVRISSRTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSCTPDLTCAVSTH   TVPQVRISSRTPDLTCAVSH   STVPQ	ł	ł		ŀ		}	
TPDLTCAVSHISTYPPSVICSCTPDLTCAVSTHS   STVPGVRISSCTPDLTCAVSTHSTYPGVRISSR   TPDLTCAVSHATVPGVRISSCTPDLTCAVSHATVPGVRI			ł		ļ		
STYPGYRISSCTPDLICAVSTHSTYPGYRISSCTPDLICAVSHA	i	l	1				
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MLKCRVDNVNSQLQVLGDHLGNTNADIQMV KGVLKDATTLSLQTQMLRSSLEGTNAEIQRL KEDLEKADALTFQTLNFLKSSLENTSIELHVL SRGLENANSEIQMLNASLETANTQAQLANSS LKNANAEIYVLRGHLDSVNDLRTQNQVLRNS		1	1	i	1		APKIPRLVQATPAFMAVTLVFSLVTLFVVDH
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LKNANAEIYVLRGHLDSVNDLRTQNQVLRNS				1	1		KEDLEKADALTFQTLNFLKSSLENTSIELHVL
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	1			]	1		LEGANAEIQGLKENLQNTNALNSQTQAFIKSS

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
nucl-	peptide		in	nucleotide	location	
eotide	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
neuce			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
i	1		ĺ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ	İ			peptide	Į.	/=possible nucleotide deletion, \=possible
	ļ <u>.</u>			sequence		nucleotide insertion
!			1			FDNTSAEIQFLRGHLERAGDEIHVLKRDLKM
	İ	i				VTAQTQKANGRLDQTDTQIQVFKSEMENVN
	1	i	}			TLNAQIQVLNGHMKNASREIQTLKQGMKNA
			1	ļ		SALTSQTQMLDSNLQKASAEIQRLRGDLENT
L	l			L		KALTMEIQQEQSRLKTLHVVITSQEQLQRTQ
221	1571	A	2501	3	500	RVRLNNDGLSPLMMAAKTGKIĞIFQHIIRREV
	1		ì			TDEDTRIILSRKFKDWAYGPVYSSLYDLSSLD
	ł	}	ł		<u>}</u>	TCGEEASVLEILVYNSKIENRHEMLAVEPINE
		i	1		ľ	LLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
	Ì		1			AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
	}	1	1			GVLFFFTN
222	1572	Α	2508	3	395	DAHCQRKLAMQEFMEINERLTELHTQKQKL
	1		1		1	ARHVRDKEEEVDLVMQKVESLRQELRRTER
]	j	]	1	ì		AKKELEVHTEALAAEASKDRKLREQSEHYSK
			1		ŀ	QLENELEGLKQKQISYSPGVCSIEHQQEITKL
ļ	1		1			KTDLEKKS
223	1573		2544	2	412	NDPAIISNESAAVVHTIVNETLESMESLEVTK
	10.00	[		[ -		MVDERTDYLTKSLKEKTPPFSHCDQAVLQCS
	]		1	ļ		EASSNKDMFADRLSKSIIKHSIDKSKSVIPNID
i		İ				KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
1	1		ì		ì	LTHCSLSAA
224	1574	A	2552	401	1	GASLCFISTAFTVLTFLIDSCRFSYPERPIIFLSM
227	13/4	<b>1</b> • • • • • • • • • • • • • • • • • • •	2332	***	l *	CYNIYSIAYIVRLTVGRERISCDFEEAAEPVLI
	1	i	1		}	OEGLKNTGCAIIFLLMYFFGMASSIWWVILTL
			1	}	İ	TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
i	ľ	1	1	i	1	VK
225	1575	A	2563	724	1	MSARKERREKGEEEGEGEKDGDEDEKEEEKE
223	13/3	^	2303	124	1 '	GLGEEEKEAGKKKKKQEEKEKGAVYSR
ļ.	ł	Ì	ì	1	1	VARICKNDMGGSQRVLEKHWTSFLKARLNC
		ł	1			SVPGDSFFYFDVLOSITDIJOINGIPTVVGVFTT
1	İ	1	1		,	QLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTP
1		1			İ	DSVWTAVPEDKVPKPRPGCCAKHGLAEAYK
		Ì				TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
ſ	1	Í			1	KTRVRYRLTAISVDHSAGPYH
226	1576	A	2571	449	3	EGVLFVYGNYVGDVMNFEMAAEMAQEVAIP
226	13/6	^	23/1	449	3	TRTVLTTDDISSSPIEDRDGRRGVAGNFFIFKV
l	1	1	1	1		AGAACDRGMSLEACEAVTRKANRRTYTMG
		l	1		<u> </u>	VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE
Ļ		Ì				
227	1625	-	0555	<del> </del>	1107	RGVIREKMMPADAIVDHIMDRIFS
227	1577	A	2575	3	1197	VLSDLCLFYYRDEKEEGILGSILLPSFQIALLTS
ŀ		ļ	1	i	}	EDHINRKYAFKAAHPNMRTYYFCTDTGKEM
1		}	1		1	ELWMKAMLDAALVQTEPVKRVDKITSENAP
	1	l		1		TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE
ł	ł	l		1	1	KKALEAEKYGFQKDGQDRPLTKINSVKLNSL
		l		1		PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
1		l	1	1		LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ
	1	l		ł		LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS
		Ī		1	1	HRAQIMARYPEGYRTLPRNSKTRPESICSVTP
		l	1			STHDKTLGPGAEEKRRSMRDDTMWQLYEW
	]	J	1	1		QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT
l		ì	1	1	1	MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI
		l		1		QRGDVTIDRRHRAHHPKVK
228	1578	A	2583	3	330	LPFLGLGSVLPOGMVMASPEMNPTICSVFEA
		1	1		-	HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE
		J	]	ļ		KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
]		1				PTMGIKPHLWWVAA
229	1579	A	2589	1	448	DDKNAQGIKRHVKPTSGNAFTICKYPCGKSR
	,	' `		•	1	ECVAPNICKCKPGYIGSNCQTALCDPDCKNH
1	1	1	[	1	İ	GKCIKPNICQCLPGHGGATCDEEHCNPPCQH
L			1	<u> </u>	<u> </u>	S. C. C. C. C. C. C. C. C. C. C. C. C. C.

			1.450			7. 11
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	(	f	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	ł	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
l	ł	l	i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ŀ	}	peptide		/-possible nucleotide deletion, \-possible
	<u> </u>	L	L	sequence		nucleotide insertion
		ł	1			GGTCLAGNLCTCPYGFVGPRCETMVCNRHC
			i .			ENGGQCLTPDICQCKPGWYGPTCSTA
230	1580	A	2593	2	138	AVTFSVVFAYVADITQEHERSMAYGLVCMFI
İ		ĺ	í	[		LYLLYLLRNAFFLR
231	1581	A	2595	185	2	SGPYTDFTPWPTEEQKLLEQALKTYPVNPPER
		1	1	l	•	WEKIAEAVPGRTKKACIKRYKVADLRISK
232	1582	A	2596	<u> </u>	391	STVTGOPRRLLDTAGHQOPFLELKIRANEPGA
		1."		1	1	GRARRTPTCEPATPLCCRRDHYVNFQELGW
		i		1	<b>\</b>	RDWILLPEGYQLNYCSGQCPTHLAGSPGIAAS
		ŀ	i			FHSAVFSLLKANNPWPGRTSWCVPTARRPLS
		ŀ				LLYL
233	1583	A	2601	184	403	LLFSDEIIMAAPLRIADVTSGLIGGEDGRVYV
200	1505	^	2001	104	705	YNGKETTLGDMTGKCKSWITPCPEEKVNVLO
		[				NSIPYWERIT
024	1504	<del> </del>	2614	170	225	
234	1584	A	2614	178	335	PLTLCLPENNKPPQADAVPDKELTLPVDSTTL
		<del> </del>	1	<u> </u>		DGSKSSDDQKIISYLWEKTQ
235	1585	A	2616	2	896	DVLEVYGTGVASTRHEMGTLDKHKELEDLV
		<b>!</b>			ļ	AKFLNVEAAMVFGMGFATNSMNIPALVGKG
		}	1	1	ŀ	CLILRDEVNHTSLVLGARLLGATIGIFKHNYA
				1	]	QSLEKLLRDAVIYGQPRTRRAWKKILILVEGV
	ļ	1	ŀ	]		YSMEGSIVHLPQIIALKKKYKAYLYIDEAHSI
				ļ		GAVGPTGRGVTEFFGLDPHEVDVLMGTFTKS
			ļ		1	FGASGGYIAGRKARILSPPACLVPNTGSHSLH
	1	1		[	[	RLTRDLQMNEAMVALVTDRLQGWNSGEGN
	:		1			WDRADKFGDLVDYLRVHSHSAVYASSMSPPI
		ļ				AEQIIRSLKLIMGLDGTTQ
236	1586	A	2621	1	392	NTSSFPAQPSSPARPSLPHLSQHPSNPLLPLAS
				1		ADHPQCGRFLPLHEPEPLCPSPSLSYPTLVSS
	Ì	1	j	1	1	WSSPFSSHHGCPPGLYPFPTSPKTIQPPGLAQL
	ŀ	1	1			KMLCIPPGRQQLRGAQSMPGHGALSPLLLPP
	İ		1	1		A
237	1587	A	2628	398	1	DLVCKISGFGRGPRDRSEAVYTTMSGRSPAL
23,	130,	1.	2020	""	1	WAAPETLOFGHFSSASDVWSFGIIMWEVMAF
	Ī	ĺ	1	1	ĺ	GERPYWDMSGQDVIKAVEDGFRLPPPRNCPN
				i		LMHRLMLDCWQKDPGERPRFSQIHSILSKMV
	1	l	1	i	ĺ	QDPEPPNV
238	1500	A	2631	1	1104	WSPCSLTCGVGLQTRDVFCSHLLSREMNETV
۵۵	1588	<b>^</b>	2031	1 1	1104	
	1	1	1	J	}	ILADELCRQPKPSTVQACNRFNCPPAWYPAQ
		}	}	Į.		WQPCSRTCGGGVQKREVLCKQRMADGSFLE
		1	]	J		LPETFCSASKPACQQACKKDDCPSEWLLSDW
		1	1	1		TECSTSCGEGTQTRSAICRKMLKTGLSTVVNS
		1	ł	1		TLCPPLPFSSSIRPCMLATCARPGRPSTKHSPHI
				ĺ	[	AAARKVYIQTRRQRKLHFVGGGFAYLLPKTA
			ŀ	1		VVLRCPARRVRKPLITWEKDGQHLISSTHVT
	ł	1	ł	<b>!</b>		VAPFGYLKIHRLKPSDAGVYTCSAGPAREHF
			1	1	1	VIKLIGGNRKLVARPLSPRSEEEVLAGRKGGP
			}	Į.		KEALQTHKHQNGIFSNGSKAEKRGLAANPGS
	1			[		RYDDLVSRLLEQGAPCSSSKKKN
	l .		2636	i	678	MKPDNILLDEHGHVHITDFNIAAMLPRETQIT
239	1589	A		1 '	(	TMAGTKPYMAPEMFSSRKGAGYSFAVDWW
239	1589	A	1			
239	1589	A		ļ		,
239	1589	A		Į I		SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET
239	1589	A		ļ 		SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRPSQ
239	1589	A				SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRPSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK
239	1589	A				SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRPSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK
239	1589	A				SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRPSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE
						SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE KVNRDCI
239	1589	A	2639	389	3	SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRPSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE KVNRDCI ELLDPTTPMRTKCIELLYAALTSSSTDQPKAD
			2639	389	3	SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQ LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK GRLNCDPTFELEEMILESKPLHKKKKRLAKK EKDMRKCDSSQTCLLQEHLDSVQKEFIINRE KVNRDCI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, I.=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion EMANKELKQLRASYTESCIQEHYLPQVIDGTL
241	1591	A	2640	392	3	Y IRLTILRCVFMRLATICVLVFTLGSKITSCDDD TCDLCGYNQKLYPCWETQVGQEMYKLMIFD FIIILAVTLFVDFPRKLLVTYCSSCKLIQCWGQ QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM Y
242	1592	A	2642	405	ī	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT STTAMVMPIVEAVLQELVSAEDEQLVAGNSN TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK SPLMISQACI
243	1593	A	2646	412	2	CLAMIKGIQSSGKIIYFSSLFPYVVLICFLIRAF LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL VSFINFFTSVLATLVVFAVLGFKANVINEKCIT QNSETV
244	1594	A	2650	1	1271	MTTTLIGLLKTARLLRLVRVARKLDRYSEYG AAVLMLLMCIFALIAHWLACIWYAIGNVERP YLTDKIGWLDSLGQQIGKRYNDSDSSSGPSIK DKYVTALYFIFSSLTSVGFGNVSPNTNSEKIF SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS TSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSS PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE VVSDPASV
245	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW WESLLLLTAYFCYVVFMKFNVQVEKWVKQ MINRNKVVKVTAPEAQAKPSAARDKDEPTLP AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD PIIV
246	1596	A	2660	200	506	VLVLQMNYYQMLIIYYVLFFKVNEFLAFEGPI LLDMRIKHILIKTNQLSQATALAKLCSDHPEIG IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS NYFLS
247	1597	A	2678	3	267	DAWVKNDIFNQTERKQKISENLKHLASVRV VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF VSLSYLEIIFDPAQLCDSSEHIIS
248	1598	A	2687	1	404	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD ENDAVAEESRQVLTICAQFLKWKLPREVYSK DPWHIKPTEAGTICRFFEKKCKGKINILEQTL MYSKNPKL
249	1599	A	2692	1	440	FRRRRRRENDCAAQGARRHCRHLAECKLV SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK AIDLSRNQFQDFPEQLTALPALETINLEENEIV DVPVEKLAAMPALRSINL
250	1600	A	2693	459	21	LLPGSLGVPILHSQPWDPSPQCPHRAPSTPRRL PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG ISSCPDLKLTKSSTP
251	1601	A	2694	2	404	FVFDLKLRVPGFAALLIHGASSVPGPETVRLR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cystcine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	j	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	İ		914	ng to first amino acid	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1			of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
Ì			1	peptide		/=possible nucleotide deletion, \=possible
		<del> </del>		sequence		nucleotide insertion
1	1	ĺ	}			QKRKKKAPDHSSGRKEELVTTHTVDKLETKK
1		ļ	į.	į		PVGRVLCGLSGELLHSLLLPRRKTEKRALGSH
	!		1		,	RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
252	1602	A	2697	421	1	GAGDCL   PQKSHSGAYQCFATRKAQTAQDFAIIALEDG
232	1602	A	2097	421	¹	
1	1			]	[	TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
	1					VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
l	1	ļ	}			MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
253	1600		0600		401	NVROPPSIRAMRNIT
253	1603	A	2698	65	401	ACCOWRRTLIPAKSTTVSCTISTPHHPFRGSYS
1	1	1	ĺ			FDDHITDSEALSRSSHVFTSHPRMLKRQPAIEL
}	1				ļ	PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
1051	1/01	<b>-</b>	0200	400	-	AAFTNNIASSTIIL
254	1604	A	2699	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
1	1605	<del></del>	2762	! <del>,</del>		RVRGPWEAGPGVGY
255	1605	Α	2700	1 -	842	LQNREDSSEGIRKKLVEAEELEEKHREAQVS
1	!					AQHLEVHLKQKEQHYEEKIKVLDNQIKKDLA
					ļ	DKETLENMMQRHEEEAHEKGKILSEQKAMIN
i	İ	ĺ		1	[	AMDSKIRSLEQRIVELSEANKLAANSSLFTQR
	Ī			Ì		NMKAQEEMISELRQQKFYLETQAGKLEAQN
i	ļ	1	ř			RKLEEQLEKISHQDHSDKNRLLELETRLREVS
1		1	1	!	]	LEHEEQKLELKRQLTELQLSLQERESQLTALQ
1	ì	l	i		ļ	AARAALESQLRQAKTELEETTAEAEEEIQALT
	1.00	<b>.</b>	0001			VGLGSNIFRLLKASARMSVELALSILAHP
256	1606	Α	2701	2	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE
			İ			LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
l	l	l	1	}		YQWGVPPRDLAVLLCNKSNAFFSLGKWNEA
į		1	1			FVAAKECLQWDPTYVKGYYRAGYSLLRLHQ
257	1607	<del> -,</del> -	2702	_	200	PYEAARMFFEGLR
457	1607	Α	2702	2	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD
ļ	1	1	Į			FNPSFSFLDPRYSVGGDENIGTVTTLANILREF
			Ì			NPSLKGFSVGTGKETSPNAFLNQAVAGGRAE
	İ					DLPVQARRLVDLMKNDTRIHFQEDWKIITLFI GGNDL
258	1608	A	2709	1	1097	
230	1008	^	2709		1097	SVGARQGEARDRIRRFFPKGDLEVLQAQVERI MTRKELLTVYSSEDGSEEFETIVLKALVKACG
[	ĺ .	ĺ	j j			SSEASAYLDELRLAVAWNRVDIAQSELFRGDI
i	1	ļ		·		· · · · · · · · · · · · · · · · · · ·
		1	<b>!</b>			QWRSFHLEASLMDALLNDRPEFVRILISHGLS LGHFLTPMRLAQLYSAAPSNSLIRNLLDQASH
{	1	l				SAGTKAPALKGGAAELRPPDVGHVLRMLLG
	1	i				KMCAPRYPSGGAWDPHPGQGFGESMYLLSD
1	1	!				KATSPLSLDAGLGQAPWSDLLLWALLLNRA
1	1					QMAMYFWEMGSNAVSSALGACLILRVMAR
}	1	1	.		,	LEPDAEEAARRKDLAFKFEGMGVDLFGECYR
		[				SSEVRAARLLLRRCPLWGDATCLQLAMQAD
1		j				ARAFFAQDGVQSLPTQKWWGDMARR
259	1609	A	2721	1	403	VYLGAGPGLFFSNEGAKEGEKANIPKLMLPR
]	1007	1 **	] <b>-</b> ''-' ]		.03	GGFSQREMVTGERSPSPEEEEEEEEEGFGERA
						SCRRGLFRVRLTRVGLAAPSKASRGQEGDAA
			]		:	PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE
						GGLRVRLP
260	1610	A	2728	1	477	LLGGDLRYHLQQNVHFTEGTVKLYICELALA
	1.010	١.,		! <b>^</b>	'''	LEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN
	[	1				IATVVKGAERASSMAGTKPYMAPEVFQVYM
	(	-			-8-	DRGPGYSYPVDWWSLGITAYELLRGWRPYEI
	1		) l			HSVTPIDEILNMFKVERVHYSSTWCKGMVAL
		ľ				LRK
261	1611	A	2730	3	547	LTITDFILVLYRYYRSPLVQIYEIEQHKIETWR
				-		EIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIH
L	<del></del>	└		<u> </u>		

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	[	{		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	l		peptide	1 -	/=possible nucleotide deletion, \=possible
	ļ	1		sequence		nucleotide insertion
				<del></del>		RLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLP
			Ì	ļ		RPSFLYRTIQDLGIGTFRDLAVVLETAPILTAL
		ļ	1	1		DIFVDRRVSALAVVNECGTHPQDERLGLGW
		ł				GLGEPGSEERLFPAAITSR
262	1612	A	2733	3	431	GPEFPGSAKLVFLDLSYNNLTQLGAGAFRSA
			i			GRŁVKLSLANNNLVGVHEDAFETLESLQVLE
	1		1			LNDNNLRSLSVAALAALPALRSLRLDGNPWL
	ì	1	ł	1		CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
		1	1	ì	ļ	ESRRISLRACRRPASRV
263	1613	Α	2736	2	343	PARISGVDPPVRKATKGGENCSFEDNKNWQF
			1	1	ì	LWGLNGNFNFFKEPWGGRNNHAKGFRTTW
	i	1		ĺ		ARSSSQNNRTFQNNRNFLRLQRDSQKKGQFA
	ļ	ļ	]	1	}	RLISPLVNLPQSPGGLEFQYQAT
264	1614	A	2738	2	245	RAMLKCLREGQPPPSYNWTRLDGPLPSGVRV
		1				DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
				[	<u></u>	DTVDVLDPPEDSGKQVDL
265	1615	A	2752	2	388	AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
	ł	i	ł	ł		LAAVETTVLVLIFAVSLLGNVCALVLVARRR
	1					RRGATACLVLNLFCADLLFISAIPLVLAVRWT
	ļ		Į.	!		EAWLLGPVACHLLFYVMTLSGSVTILTLAAV
			i			SLER
266	1616	A	2755	192	1	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK
	ĺ		Ţ	f		LQGYLPLQDAFHIFQDPLTGDLPWPELILGLP
			į			V
267	1617	A	2760	434	714	ASRLEKQNSTPESDYDNTPNDMEPDGMGYM
	t	•	ĺ	[	ĺ	HRTSVPGEGLPRARDLAGLGQQKQFTTHTPF
	<u> </u>	l	1	<u></u>	L	LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
268	1618	A	2762	1	405	IACTFCGQDEWSPERSTRCFRRRSRFLAWGEP
	1	İ			}	AVLLLLLLSLALGLVLAALGLFVHHRDSPL
		1	1	]		VQASGGPLACFGLVCLGLVCLSVLLFPGQPSP
	ŀ	ł	ľ	ĺ		ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE
						LPLSWAE
269	1619	A	2772	3	243	TRPAEKIQYLVLFFVMSHPSQAYDKLSLSDHL
		ĺ		ł		LIAVLNLLRREVSEHGRHLQQYFNLFVMYAN
	Ĺ					LSKNLSFSEFCFDVSY
270	1620	A	2789	1	486	ELQSQQACTHTKETEQLRSQLQTLKQQHQQA
j	}	ľ	1		1	VEQIAKAEETHSSLSQELQARLQTVTREKEEL
				ļ		LQLSIERGKVLQNKQAEICQLEEKLEIANEDR
	ļ	]	1			KHALERFEQEAVAVDSNLRVRELQRKVDGIQ
						KAYDELRLQSEAFKKHSLDLLSKERELNGKL
		<u> </u>				RHLSP
271	1621	A	2795	1	568	KEKRVTVQLPTESIQKNQEDKLKMVPRKQRE
						FSGSDRGKLPGSEEKNQGPSMIGRKEERLITE
	1	ĺ		-		RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN
			[			FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE
		!		'		VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE
			L			SQRDDGKGALNIVEFLRKREELHQILSTVKQP
272	1622	A	2797	8	523	KCMQGKYAGAMESEPCVCTEADFDCDYGYE
		1				RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST
		Ì				GYRKVVSNNCTDGVREQYTAKPQKCPGKAP
						RGLRIVTADGKLTAEQGHNVTLMVQLEEGD
				!		VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV
				<u> </u>		YQNXGIXRXTVQVDNSLGS
273	1623	A	2801	72	395	HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS
						DEEGQNQLGIRIHQDIPLPPRRRELPALRTTNG
						KADSLNVSRNSVMQELSELEKQIQVIRQELQL
						AVSRKTELEEYH
274	1624	Α	2805	168	320	ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE
	ı	ı				IFIARNGVVGETLTHCKRV

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ĺ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
	]	ļ	ļ	residue of peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
275	1625	A	2812	208	321	GSLATCOLSEPLLWFILRVLDTSDALKAFHD
						MGKIIFQ
276	1626	Α	2813	41	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
	ļ	1				KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY
	1627		2017	3	410	QVGPVRRNGEAGPG VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
277	1627	A	2817	] 3	410	LFISYLHTPKHKQHEVLQAMGSILGITGEEME
		1		]		PLFQEEHGTATRWMTGWLEGGSKSVPKTPL
						GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
						LPPHNSPGKIK
278	1628	A	2821	238	457	GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
	_	ĺ				VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
		L	<u>L</u>		<u> </u>	PVDQNPRLV
279	1629	Α	2822	342	1	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
	ĺ					TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
					}	CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
280	1630	<u> </u>	2825	307	77	VPSQRHPTXPPPAS PSMVWSYHWGVKQKRLALCVFSFEEGGRRK
280	1630	A	2825	307	] ' '	CGOYWPLEKDSRIRFGFLTVTNLTGAVGEPG
		1				VAFQCDGQRRREPTC
281	1631	A	2827	81	381	KMGTAVWVPKEKEKRDKASQEGGDVLGAR
		}				QDCTPSLKSLVATGNLLDLEETAKAPLSTVSA
	Ī		}			NTTNMDEVPRPQALSGSSVVWVSGCVASRS
		ļ				VILSLTSG
282	1632	A	2830	471	160	KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
	Ì			i		TSSGKYNELGYPFGYLKASTTLTCVNLFVMP
						YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS YLKTLPPYYL
283	1633	A	2835	462	148	VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
203	1033	^	2033	102	170	MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
		ĺ				PLOCOMHPEESTOFSIKLOPPPVGRKNRERVE
						SSEESAP
284	1634	Α	2836	2	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
			ļ			DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL
						KSLAETVLNFPLDKSLLLRCSNWDAETLTED
	İ	1				QVIYAARDAQISVALFLHLLGYPFSRNSPGEK
285	1635	A	2843	20	271	KR PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
203	1035	^	2043	20	4/1	VCDRVSEDGINRQQAQEWCIKHGFELVELSP
	1	f .	1			EELPEEDGKCLCVRRKYGTYI
286	1636	A	2845	197	278	TAEDVLTVAYEHGVNLFDTAEVYAAGK
287	1637	A	2851	2	427	FVAEVRREWAKYMEVHEKASFTNSELHRAM
						NLHVGNLRLLSGPLDQVRAALPTPALSPKDK
		}	}	1		AVLQNLKRILAKVQEMRDQRVSLEQQLRELI
			Į į			QKDDITGSLVTTDHSQMKKLFEEQLKKYDQL
	1/5-	ļ			170	KVYLEQNLAAQDRVLCALT
288	1638	A	2859	2	469	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
						LGTSELLPAKNVGNNSFNDIMEANLPSPSPKP TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
			1			KLNELLEAIKSRDLLALIQVYAEGVELMEPLL
						EPGQELAETALHLAVRTADQTSLHLVE
289	1639	A	2861	2	454	FVASGGPATARMSDSQFFCVAEERSGHCAVV
	,			-	=	DGNFLYVWGGYVSIEDNEVYLPNDEIWTYDI
						DSGLWRMHLMEGELPASMSGSCGACINGKL
			1			YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
						ITDFEGQPPTPRDKLSCWVYKDRLIYFG
290	1640	A	2868	1	378	FRQGQLYKVFLHGSQGQVYHSQQVGPPGSAI
			1 1			SPDLLLDSSGSHLYVLTAHQVDRIPVAACPQF
		L	L	L	L	PDCASCLQAQDPLCGWCVLQGRCTRKGQCG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	<b></b>	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		Ī	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/-possible nucleotide deletion, \-possible
			<u> </u>	sequence		nucleotide insertion
	1	ł	l			RAGQLNQWLWSYEEDSHCLHIQSLLPGHHPR
			L			QE
291	1641	Α	2870		385	FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGAL
		ĺ	1			PFTPKSIRSHFQHVFVIVKVHNPCTENVCYSV
			ľ			GVSRSKDVPPFGPPIPKGVTFPKSAVFRDFLL AKVINAENAAHKSEKFRAMATRTRQEYLKD
			ļ.			LA
292	1642	A -	2877	3	188	RPTRPPPATTQSPESTMDTSLKKEKSAILDLYI
292	1042	^	20//	٦	100	PPPPAVPYSPRYVAVHCHGMLVSCWCHL
293	1643	A	2878	<u> </u>	427	REKEEEVEEEEDKVVKETEKEAEQEKEEDSL
293	1043	A	28/8	[ 1	427	GAGTHPDAAIPSGERTCGSEGSRSVLDLVNYF
		i	[	•	}	LSPEKLTAENRYYCESCASLQDAEKVVELSQ
				ľ		GPCYLILTLLRFSFDLRTMRRRKILDDVSIPLL
		ļ		•		LRLPLAGGRGQAYDL
294	1644	A	2879	109	245	QLCCFCFRQTTLIVYILSFIGMVIFTFTLDLRYI
			//	]	- '-	IVFVTGGVLG
295	1645	A	2880	3	320	LASSOHGILNNLSLLFSICKTCIRTMDHHCPRA
	10.0		-555	-		NNCVGEONHRFFCALHCKSKHFCIEFTLNTNF
	l			1		FNCFLPGAEKSTIDAPFSLQPFLQDSKYNTALS
						LSESISQ
296	1646	A	2892	209	363	SQYSHSLDYHLLQVTKNPFTLGDSSNPGQTE
			1		i	RLQEFSQKMDQVRGHWPVST
297	1647	A	2893	8	424	SPXTLXLDTFILLGIQDNILVLILATPPFMAGG
	[		i	ĺ		KLYSTMGRFLRDRKNPACREMAVVLLANLA
			!			QGDSLAARAIAVQKGSIGHLLGFLEDSLAAT
	•		ļ		!	QIQQSQASLLHMHNPPFEPTSVDMMRRACRA
			<u> </u>			LLALAKVDDNHSEF
298	1648	Α	2894	310	445	FWIYFPSFFMTGYLPLGFEFAVEITYPESEGTS
		L				SGLLNASAQVNL
299	1649	Α	2898	Ī	492	KIKAKNLTNYDLCSIFLGTSTLLVWVGVIRYL
				}	ł	GYFQAYNVLILTMQASLPKVLRFCACAGMIY
			ļ	)	ļ	LGYTFCGWIVLGPYHDKFENLNTVAECLFSL VNGDDMFATFAQIQQKSILVWLFSRLYLYSFI
						SLFIYMILSLFIALITDSYDTIKKFQQNGFPETD
					}	LOEF
300	1650	A	2901	T	445	PVWWNSLNGASEVIFSVHVKDGGSFPKTDST
300	1050	^	2701	<b>1</b> *	,,,,	TVTVRFVNKADFPKVRAKEQTFMFPENOPVS
	[	ĺ			İ	SLVTTITGSSLRGEPMSYYIASGNLGNTFQIDQ
						LTGQVSISQPLDFEKIQKYVVWIEARDGGVPP
	İ	]				FSSYEKLDITVLDVNDNAPIF
301	1651	Α	2902	162	433	THFICLPLGYCFPLLDKDLQLPSGFNCNFDFLE
'		1		'		EPCGWMYDHAKWLRTTWASSSSPNDRTFPG
	]	]	J			KPAVSEDMKELRPACSTYFNPRFPYKL
302	1652	Α	2909	2	412	GPQMLCKKIYFIWVTRSQCQFEWLADIMQEV
		1		}		EENDHQDLVSVHIYVTQLAEKFDLRTTMLYI
	J	}			İ	CERHFQKVLNRSLFTGLRSITHFGRPPFEPFFN
					,	SLQEVHPQVRKIGVFSCGPPGMTKNVEKACQ
		L				LVNRQDRAHFM
303	1653	Α	2914	291	453	KLNRWLCFFYSWSFOILLYEMVTLGAPPYPE
	<u> </u>	L	<u></u>			VPPTSILEHLQRRKIMKRPSSCS
304	1654	Α	2926	179	354	PGVPSQALRKAESLKKCLSVMEAKVKAQTAP
		<u>L</u>				NKDVQREIADLGEVGAASLPPSSGPGA
305	1655	A	2938	135	438	GMGYLHAKGILHKDLKSKNVFYDNGKVVIT
		!				DFGLFSISGVLQAGRREDKLRIQNGWLCHLA
		l	1		1	PEIIRQLSPDTEEDKLPFSKHSDVFALGTIWYE
		L	ļ			LHAREWP
306	1656	Ā	2944	2	329	VRWNSCVNCSCAFGNGASLSTSLGESSGCLW
	1					EIGKWLSCSLLSFPSPLAVLIITFCIVTVLGREA LTKGALWAVFLLAGSALLCAEVTGVIWROPE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ļ	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ţ	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	Į.	/=possible nucleotide deletion, \=possible
			<b>_</b>	sequence		nucleotide insertion
	L	ļ—	1.000	<u> </u>	l-,	SKTKLSFKVSSSA
307	1657	A	2950	2	411	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL
						PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ
	1	1	1	1	-	PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT CTAENAVGRARRRVHLTILVLPVFTTLPGDRS
	-	ł	]		ļ	LRLGDRLWLR
308	1658	A	2951	1	407	PTRPPRVRFDNEFDAESORKRTTSVSKMERM
300	1038	^	2931	<b>'</b>	107	DSSLPEEEEDEDKEAINGSGNAENRERHSESS
		l				DWMKTVPSYNQTNSSMDFRNYMMRDETLEP
		ŀ			ł	LPKNWEMAYTDTGMIYFIDHNIKTITWLDP
	1	1				RLCKKAKAPEDC
309	1659	A	2954	2	179	ODFLTLTLTEPTGLLYVGAREALFAFSMEALE
309	1097	Α	2554	-	177	LQGAVRGGAVGGSRACQRARPRGAVLG
310	1660	Α-	2959	i	419	QDMMERAIIDTFVGHDVVEPGSYVQMFPYPC
310	1000	<u> </u>	1 2,3,	1 *	1 717	YTRDDFLFVIEHMMPLCMVISWVYSVAMTIO
	1		1	ļ		HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI
		1		į.	Į.	TGFVQLSISVTALTAILKYGQVLMHSHVVIIW
	Į	ŀ	Į.		ł	LFLAVYAVATIMFCF
311	1661	A	2963	3	465	MKPOMPGLGAPNGYGPGRGRAGVPGGPERR
*				-		PWVPHLLPFSSPGYLGVMKAQKPGAGEGMK
	ŀ	ì				POKPGLRGTLKPOKSGHGHENGPWPGPCNA
			1	1	ł	RVAPMLLPRLPTPGVPSDKEGGWGLKSQPPS
		ŀ	1			AVQNGKLPGHQPPNGYGPGAEPGFNGGLEPQ
		İ		İ	ł	KI
312	1662	Α	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM
		ļ	j		1	HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV
	1	1		1	[	EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS
					1	ACTVTCGVGTQVRIVRCQVLLSFSQSVADLPI
		<u> </u>		ļ		DECEGPKPA
313	1663	A	2969	2	430	VVADNČROGYLDALRFLERRGLTKEPVLWT
	ļ.	Ĭ				LVSKEPPAPADGNWDAGCDQRRKGGLSLNW KVPHVQVKDVPNFEQLSPELEAALKKACTRD
	j	ļ	}		]	PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYF
				ŀ		RSRRLVVWLPDVPADLWWMQ
314	1664	A	2971	422	33	LDXSHNALQRLRPGWLAPLFQLRALHLDHNE
314	1004	^^	1 23/1	722	} 33	LDALGRGVFVNASGLRLLDLSSNTLRALGRH
			i	i		DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA
	ſ		í	[	[	LSHLYLGCNELASFSFDHLHGLSATHLLTLDL
						SSNRM
315	1665	Ā	2973	1	525	ITVSTHASGSPFGLEPQSGWLWVRAALDREA
						QELYILKVMAVSGSKAELGQQTGTATVRVSI
					1	LNQNEHSPRLSEDPTFLAVAENQPPGTSVGRV
	]		}	1	}	FATDRDSGPNGRLTYSLQQLSEDSKAFRIHPQ
	1	1	1			TGEVTTLQTLDREQQSSYQLLVQVQDGGSPP
	L	<u></u>	<u> </u>	L		RSTTGTVHVAVLDLNDNT
316	1666	A	2978	2	400	ELVVELVSAGKSGPERNTYEVQVVTGNVPKA
	-	1				GTDANVYLTIYGEEYGDTGERPLKKSDKSNK
						FEQGQTDTFTTYAIDLGALTKIRIRHDNTGNR
	1	1		}		AGWFLDRIDITDMNNEITYYFPCQRWLAVEE
	L.,,,,	<del> </del>	1 2000	ļ		DDGQLSRE
317	1667	A	2981	3	440	VLNCQGRPTRPVRINGDGQEVLYLAESDNVR
	!	ł	1		}	LGCPYVLDPDDYGPNGLDIEWMQVNSNPAH
		İ	1	1		HRENVFLSYQDKRINHGSLPHLQHRVRFAAS
	İ	1			·	DPSQYDASINLMNLQVSDTATYECRVKKTTM
310	1660	<del>  </del>	1 2005	110	414	ATRKVIVTVQARPAVPMCWTEGQ
318	1668	A	2995	119	414	LPEKEPPIIRKSSSLKVTKCLFTEQPKPIIILRFA
			1	1		ENYDARI.LRIDIANTLREQVQELFNKTYGKQ RRTPGEGHVAAVDREVAGFPVPAEGISGETIH
210	1660	-	2999		222	GFFAYTYGRLVVVEDLHSGAQQHWSGHSAEI
319	1669	A	_ <b>4</b> 999	2	332	GLLVI I I DKT A A KENTHOOYOO MAQAHOYEI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  STLALSHSAOVLASASGRSSTTAHCOIRVWD
320	1670	_	3000	693	322	VSGGLCQHLIFPHSTTVLALAFSPDDRLLVTL GDHDGRTLALWGTGHL IDESTGLIITVNYLDYETKTSYMMNVSATDOA
320						PPFNQGFCSVYITLLNELDEAVQFSNASYEAA ILENLALGTEIVRVQAYSIDNLNQITYRFDAY TSTQAKALFKIDAITVRGWGQGAPFFPI
321	1671	A	3001	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPC GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR WNQKRYEALGEIITKYVYELLEKDCNSKKVS
322	1672	A	3007	192	447	ERVRNSLFPGRGDSQCACCPSSPVWVFLETGF LFPWLFLQVEVIKKAYMQGEVEFEDGENGK DGAASPRNVGHNIYILAHQLARH
323	1673	A	3019	18	245	KELLFYHLIVNNINFFNTRYAKIHIPILASVSEH QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND ERVFGKRGF
324	1674	A	3020	523	797	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI YLFIFFEMESHSVTHAGVQRHNLNSLQPLPPG FKRFSCLCFI.SSWNYRGAPPGPANF
325	1675	A	3022	2	156	NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL GNHKAFKKELRQCRWQVGAL
326	1676	A	3023	38	172	KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT FCLNKEALKDEFE
327	1677	A	3027	I	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC GFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ EGDLVEVVLSASATFEDFQIRPHALTVHSYRA PAFCDHCGEMLFGLVRQGLKCDGCGLNYIK RC
328	1678	A	3030	13	569	ITRPTISCQRPGPGLAAGMLPYTVNFKVSART LTGALNAHNKAAVDWGWQGLIAYGCHSLV VVIDSITAQTLQVLEKHKADVVKVKWAREN YHINIGSPYCLRLASADVNGKIIVWDVAAGV AQCEIQEHAKPIQDVQWLWNQDASRDLLLAI HPPNYIVLWNADTGTKLWKKSYADNILSFSF D
329	1679	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG RGEAVYQIGVEDNGLLVGLAEEEMRASLKTL HRMAEKVGADITVLREREVDYDSDMPRKITE VLVRKVPDNQQFLDLRVAVLGNVDSGKSTL LGVLTQGELDNGRGRARLNLFRHLHEIQSGR TSSISFEILGFNSKGEVHGINGTQWGQTLRMG W
330	1680	A	3040	3	397	LCSTLLLLTIPSWVLSQITLKESGPTLMKPTET LTLTCTFSGFSLNTSGVGVAWIRQPPGKALE WLALIYWDDDKRYSPSLNDRLTIAKDTSRNQ VVLTMTNMGPVDTATYYCAQFARGARGSN WFDPWGQ
331	1681	A	3043	3	1509	AGIRHEAPPITSNRHRRQIDRGVTHLNISGLK MPRGIAIDWVAGNVYWTDSGRDVIEVAQMK GENRKTLISGMIDEPHAIVVDPLRGTMYWSD WGNHPKIETAAMDGTLRETLVQDNIQWPTG LAVDYHNERLYWADAKLSVIGSIRLNGTDPI VAADSKRGLSHPFSIDVFEDYIYGVTYINNRV FKIHKFGHSPLVNLTGGLSHASDVVLYHQHK QPEVTNPCDRKKCEWLCLLSPSGPVCTCPNG KRLDNGTCVPVPSPTPPDAPRPGTCNLQCFN GGSCFLNARRQPKCRCQPRYTGDKCELDQC

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC TQQVCAGYCANNSTCTVNQGNQPQCRCLPG FLGDRCQYRQCSGYCENFGTCQMAADGSRQ CRCTAYFEGSRCEVNKCSRCLEGACVVNKQS GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT MNSKMMPECQCPPHMTGPRCEEHVFSQQQP GHIASILIP
332	1682	A	3045	3	952	TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT LSSLRLQCRSQSDDGPIMWVRPGEQMIPTAD MPKSPFKRRSMNEIKNLQYLPRTSEPREVLF EDRTRAHADHVGQGFDWQSTAAVGVLKAV QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ LDLHEPPVSQCVQWVDEAKLNQMRREGIRY ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW HIRLKQYHPVVEATQNTESNSNMDCGLTGKR ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP PASE
333	1683	A	3046	497	167	SACSTGPELPGRATRSLTRPANQKGCDGDRL YYDGCAMIAMNGSVFAQGSQFSLDDVEVLT ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG CSSKTWKVAPFVRAWWRP
334	1684	A	3053	37	276	VITDLEEQLNQLTEDNAELNNQNFYLSKQLD EASGANDEIVQLRSEVDHLRREITEREMQLTS QKQVRRVNKVVRSLEDF
335	1685	A	3054	2	846	WDAWGDWSDCSRTCGGGASYSLRRCLTGR NCEGQNIRYKTCSNHDCPPDAEDFRAQQCSA YNDVQYQGHYYEWLPRYNDPAAPCALKCH AQGQNLVVELAPKVLDGTRCNTDSLDMCISG ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC RLVRGQSKSHVSPEKREENVIAVPLGSRSVRI TVKGPAHLFIESKTLQGSKGEHSFNSPGVFVV ENTTVEFQRGSERQTFKIPGPLMADFIFKTRY TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT CGGG
336	1686	A	3058	54	347	VVGKQEAGAHSDSCCLLHTPPRLTPAHSRKA LRNSRIVSQKDDVHVCIMCLRAIMNYQVSRG AWDWRLGSPACPHWGLHKLPRLWDPLSLYP VLCWGT
337	1687	A	3059	2	709	ILTSLVELTRFETLTPRFSATVPPCWVEVQQE QQQRRHPQHLHQQHHGDAAQHTRTWKLQT DSNSWDEHVFELVLPKACMVGHVDFKFVLN SNITNIPQIQVTLLKNKAPGLGKVNGLRLCPF LEDHKEDILCGPVWLASGLDLSGHAGMLTLT SPKLVKGMAGGKYRSFLIHVKAVNERGTEEI CNGGMRPVVRLPSLKHQSNKGYSLASLLAK VAAGKEKSSNVKNENTSGTRK
338	1688	A	3060	85	384	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK DKVYGVADSCTSLLSGRNRCKLGLLSLHETIL SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDE EELNP
339	1689	Α	3063	236	362	CFLCLSGDFMVMTIFFNVSRRFGYVAFQNYV PSSVTTMLSWV
340	1690	A	3065	3	1249	DLWQFTPLHEAASKNRVEVCSLLLSYGADPT LLNCHNKSAIDLAPTPQLKERLAYEFKGHSLL QAAREADVTRIKKHLSLEMVNFKHPQTHETA LHCAAASPYPKRKQICELLLRKGANINEKTKE FLTPLHVASEKAHNDVVEVVVKHEAKVNAL DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPN

NO: of No: of No: of No: of Incide cotide couldered folded to the contract of	SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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	seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
Peptide   Pept	uence	ł		914	ng to first		
Peptide   Pept				t		of peptide	
					residue of	sequence	
IISLQGFTALQMGNENVQOLLQEGISLGNSE    DRQLIEARKAGDVETVKKLTVSWNCED  GRQSTFILHFAAGYNRVSVYEYLLQHGQJWNCED  GRQSTFILHFAAGYNRVSVVEYLLQHGQJWNADKDGGLVPIHAACSYOHTVSVAELLVKHG  AKDRGGLVPIHAACSYOHTVSVEYLLQHGQJWNADKDGGLVHINACSYOHTVSVEYLLQHGUNDIQDIA  GRAALDAAKKGCLARVKKLSSPDNVNCR TOGRISTPILHAGK    GVILPSFORQLFADHAAGESYTSERNYQTDIA  GDAALLDAAKKGCLARVKKLSSPDNVNCR TOGRISTPILHAGK    GVILPSFORQLFADHAAGESYTSERNYQTDIA  GGAALDAAKKGCLARVKKLSSPDNVNCR TOGRISTPILHAGK    NYNYDRDSEESSVIKLLSYNIDGILSEKYHT RTVKFLRSATIPVVELMDVQGGRLDMEVGF    RRVAFTANDVAGAFDMVCTMLEKRVRHKIYLCSKDD  RBDGRYQGYCDAMMLHNLSPLRNMPRAIS  HLRMQLMRDJASNPDLDGYMAKTRIL  AYSGVRPLVASDDDPSGRNVSRGIVLLDS  RDDGRYQGYCDAMMLHNLSPLRNMPRAIS  HLRMQLMRDJASNPDLDGYMAKTRIL  AYSGVRPLVASDDDPSGRNVSRGIVLLDN  AYSGVRPLVASDDDPSGRNVSRGIVLDN  AND STANDAM RRLGGTRRCTTADLALPGSQEPAKVP  DDNRVTJAEVDLLRGEGKLAVKGOVRRAAC  LGASRAQVLWFVLLPGALPELTGLRIGLGW  WSTLYABELJAATRGLGFM  ALSKINSTRNLLL  AYSGVRPLVASDDPSGRNVSRGIVLDN  ALSKINSTRNLLL  AYSGVRPLVASDDPSGRNVSRGIVLDN  ALSKINSTRNLLL  AYSGVRPVLVASDLJAARTGLGFM  ALSKINSTRNLLLL  AYSGVRPVLVASDLJAARTGLGFM  ALSKINSTRNLLLL  AYSGVRPVLVASDLJAARTGLGFM  ALSKINSTRNLLLL  AYSGVRPVLVASDLJAARTGLGFM  ALSKINSTRNLLLL  ALSKINSTRNLLL  ALSKINSTRNLLLL  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTRNLT  ALSKINSTR		}	1	ļ		ł	
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*RQGFPMLPRLVSNSWAQTVHPPRPPKVLDL QA  361 1711 A 3135 56 1449 PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPSQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALL WTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT		_					
361 1711 A 3135 56 1449 PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT							
AD*RGSRM/PPRAPASPTGP/APGGKKVRGR VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT				<u></u>		1	
VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALL WTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT	361	1711	A	3135	56	1449	
GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALL WTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT			1				
GPORQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALL WTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT							
PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALL WTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT		1	ł				
APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT			]				
GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT							
PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT		ľ	ĺ				ſ
SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT			)				
GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT	l t		]			'	
F/LIPSPT*MSPALVIOPPVPPTOMGLRISGLPR				'			GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
			!				F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPR
QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP	L	L	L	L			QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion  RNQSPLGNDTLSSGLPMGPRRQVWPLARVG
362	1712	A	3136	1270	274	GHISSPREPQVLKKPLWGQTDIAGVGSASLYP DNL  RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ HNTWQLSRVYPSDLRTDSSNYNPQELWNAG CQMV*GGSRDWEEGVEEQQVGNKFSSDGR VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE GSIVDPLVKVQIFGVRLDTARQETNYVENNG FNPYWGQTLCFRVLGPDFPMLRFGKMDYDW KSRNDLLGKTPCPGTCMQQGYRHIHLLSKDG ISLRPASIFVYICIQEGLEGDES
363	1713	С	3139	60	248	MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA PAMNESPLAPHLHQHLVFSVFQVLTILIGV**
364	1714	A	3140	57	418	SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV GLTSGLIQHFHSPSSCQFPLLRGPPFPRQPPLGI SGASLCPVLSPPR*PLQPSSL
365	1715	A	3145	122	413	LLPYPSLFVFLRQCHFVT\RLECNGVVSAHCN LHLPGSSDSPASAS*VAGTTGVCHHTRLIF\VF LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL QA
366	1716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKUN FIKIKKLCIEGYY/NREPQNGRKIFANYVS\DK GLMATIYEELLKUSNKLIQ
367	1717	A	3152	3	2367	QKLKQNQPKRAHVEDGĞSRSKQĞNEQSKKT PIEKSDFAAATHPRAFYLSKPDETPNAWMSD SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS TDVSPNQVLTLDPTLHMKPKQQISGIQPHGLP NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSTFPSVYTITSNDISVNTVDEENTVMVAS ASVSQSQLPGTANSVPECISLTSLEDPVILSKIR QNLKEKHARHIADLRAYYESEINSLKQKLEA KEISGVEDWKITNQILVDRCGQLDSALHEATS RVRTLENKNNLLEIEVNDLRERFSAASSAKI LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF ENAYKLSDDKEAQLKQENKMFQDLLGEYES LGKEHRRVKDALNTTENKLDAYTQISDLKR MISKLEAQVKQVEHENMLSLRHNSRIHVRPS RANTILATSDVSRRKWLIPGAEYSIFTGQPLDT QDSNVDNQLEETCSLGHRSPLEKDSSP/GSSST SLLIKKQRETSDTPIMRALKELDEGKIFKNWG TQTEKEDTSNSLL*/INPRQTETSVNASRSPEK CAQQRQKRLNSASQRSSSLPSNRKSSTPTKR EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN DFEYTAKIRTLAETERFFDELTKEKDQIEAAL SRMPSPGGRITLQTRLNQVKCLSLNLL
368	1718	A	3163	2	2350	EFKSGGCGAGLVAAGAVLVLYPASRAGERT RVPGSPAPSSLPLHSPGACGTEVDMDPQRSPL LEVKGNIELKRPLIKAPSQLPLSGSRLKRRPDQ MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TVPQTQGQTTAQKVSKKTGPRCSTAIATGLK NQKPVPAVPVQKSGTSGVPPMAGGKKPSKRP AWDLKGQLCDLNAELKRCRERTQTLDQENQ

			·	, . <u></u>	<del></del>	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ł	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	соптевропфі	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ļ	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ		1	peptide	-	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
						QLQDQLRDAQQQVKALGTERTTLEGHLAKV
	ŀ	1	}			OAOAEOGOOELKNLRACVLELEERLSTOEGL
			1	,	ļ	VOELOKKOVELOEERRGLMSQLEEKERRLOT
			1			SEAALSSSOAEVASLROETVAOAALLTEREER
	l .					LHGLEMERRRLHNQLQELKGNIRVFCRVRPV
	ſ	1	1			LPGEPTPPPGLLLFPSGPGGPSDPPTRLSLSRSD
	1		ł			ERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDE
	1	{	Ì			VFEEIAMLVQSALDGYPVCIFAYGQTGSGKTF
	1	į.				TMEGGPGGDPQLEGLIPRALRHLFSVAQELSG
	1					QGWTYSFVASYVEIYNETVRDLLATGTRKGQ
	1		1			GGECEIRRAGPGSEELTVTNARYVPVSCEKEV
			}	1		DALLHLARQNRAVARTAQNERSSRSHSVFQL
		1	1	ĺ	l	QISGEHSSRGLQCGAPLSLVDLAGSERLDPGL
	1	1	1	i		ALGPGERERLRETQAINSSLSTLGLVIMALSN
		ļ	1		]	KESHVPYRNSKLTYLLONSLGGSAKMLMFV
	ļ	ì	1			NISPLEENVSESLNSLRFASKVEPSVLFGTAQS
		l	ł	ł	ļ	NRKWKTDPDLCVCVCVCVCVCVCVCVCVP
	]		1			MSMYRVRGGRVAGGCFIGWRAPCPRAIK
369	1719	A	3165	365	12	GYTSOGRWIDIERGPLTANTESLHENNFNALP
309	1 1/19	^	2103	303	12	
	1		1			GYIRKIE*I*IYKKN*INFGGVGLLNIVKISILS/K
	Į.	ł	ł	ŀ		IYRFDAIPVKILTRFFINLDKLILKFVLKTKIAK
	<u> </u>					NRIKTFYIMRRKKLGDSS
370	1720	Α.	3170	393	42	GASISPSAVIDGVEGLKPMQEQEAQEAGPCLD
	l		1			*HMAPEQWVAPR\RLLFRLIFSVLHALIIAAAA
j	1 .	j	1	}	}	QSSAEEDEDPRN*GQSSEDQAPNQNGLIVIVH
			ŀ			RVHVPLGAAATVPVHRSHFPR
371	1721	A	3173	770	510	GNGGCGLSQIPPSHLGAFSRGSLLSRG\DPRGP
8					[	PPHPVIFFVFVVE\QGFTVLARMVSIS*PCDPP
	i		ļ	ļ		ALASQSAGITGVSHLARPQNLYF
372	1722	A	3180	381	76	RVLIIIDNVPAHSSPQKREISQEFQLEIRHLP*S
] " " "	] ~ ~ ~ ~	] 11	] 3.00	} "	~	PDLAPSGCFLFLNLKNIFK\GTHFSLVDNVKK
	1	ŀ				TVSTWLH/SQNAQFYKDRLNGWYHCLQKCL
	İ					QHY*AYVEK
373	1723	A	3181	410	14101	RREVAGPEGKGLLLASAHTMLTPPLLLLLPLL
3/3	1/23	A	3191	410	14101	SALVAAAIDAPKTCSPKOFACRDOITCISKGW
	1			1		
						RCDGERDCPDGSDEAPEICPQSKAQRCQPNE
	Í	1	Į.	j	1	HNCLGTELCVPMSRLCNGVQDCMDGSDEGP
		i				HCRELQGNCSRLGCQHHCVPTLDGPTCYCNS
	1	1				SFQLQADGKTCKDFDECSVYGTCSQLCTNTD
	l		ł	İ		GSFICGCVEGYLLQPDNRSCKAKNEPVDRPP
		1	ł			VLLIANSQNILATYLSGAQVSTITPTSTRQTTA
	I	[		[		MDFSYANETVCWVHVGDSAAQTQLKCARM
l	1	1	1	1		PGLKGFVDEHTINISLSLHHVEQMAIDWLTGN
	ļ					FYFVDDIDDRIFVCNRNGDTCVTLLDLELYNP
	I	1				KGIALDPAMGKVFFTDYGOIPKVERCDMDG
	1	Į	1	}	]	ONRTKLVDSKIVFPHGITLDLVSRLVYWADA
		1	]			YLDYTEVVDYEGKGROTIIQGILIEHLYGLTVF
		1				ENYLYATNSDNANAQQKTSVIRVNRFNSTEY
	J	1	1	] .	j .	QVVTRVDKGGALHIYHQRRQPRVRSHACEN
		1				
	}	1				DQYGKPGGCSDICLLANSHKARTCRCRSGFS
	l	J				LGSDGKSCKKPEHELFLVYGKGRPGIRGMD
	l					MGAKVPDEHMIPIENLMNPRALDFHAETGFI
		1				YFADTTSYLIGRQKIDGTERETILKDGIHNVE
		i	]			GVAVDWMGDNLYWTDDGPKKTISVARLEK
	1	1	1			AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW
	1	i				TDWEEDPKDSRRGRLERAWMDGSHRDIFVT
		i				SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI
	1	1	i	ĺ		LLNGTDRKIVYEGPELNHAFGLCHHGNYLFW
	1	1	1			TEYRSGSVYRLERGVGGAPPTVTLLRSE\RPPI
	1	l	1	L	l	1211300 TACONIO TONATI TIDONODIGITI

[ 050 to 1	Landin	<u> </u>	000	70 - 41 - 4 - 3	Tn. 3: 4-3	A de la constant de l
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ľ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I≈Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ł	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
i	i	Į		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł			peptide		/=possible nucleotide deletion, \=possible
	l			sequence	L	nucleotide insertion
						FEIRIMYDAQHQQVGSNKCRVNNAGCSSLCL
	ļ					ATPGSRQCACAEDQVLDADGVTCLANPSYVP
						PPQCQPGEFACANSRCIQERWKCDGDNDCLD
	ļ		į			NSDEAPALCHOHTCPSDRFKCENNRCIPNRW
!	1	}	ļ		ļ	LCDGDNDCGNSEDESNATCSARTCPPNQFSC
	İ					ASGRCIPISWTCDLDDDCGDRSDESASCAYPT
	Ì		1			CFPLTQFTCNNGRCININWRCDNDNDCGDNS
}	ł	1	!			DEAGCSHSCSSTQFKCNSGRCIPEHWTCDGD
i	i	i				NDCGDYSDETHANCTNQATRPPGGCHTDEF
Į.			Ì			
j	ļ	ļ	1			QCRLDGLCIPLRWRCDGDTDCMDSSDEKSCE
i	1	1	1	1		GVTHVCDPSVKFGCKDSARCISKAWVCDGD
1		1		]	1	NDCEDNSDEENCESLACRPPSHPCANNTSVC
J	J	1	ļ			LPPDKLCDGNDDCGDGSDEGELCDQCSLNN
	1	į.				GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT
	i					CQIQSYCAKHLKCSQKCDQNKFSVKCSCYEG
J	1	J	J	]		WVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLH
		1				KGDYSVLVPGLRNTIALDFHLSQSALYWTDV
	ł					VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG
				}		LAVDWIAGNIYWVESNLDQIEVAKLDGTLRT
1		1	ĺ			TLLAGDIEHPRAIALDPROGILFWTDWDASLP
	1		}			RIEAASMSGAGRRTVHRETGSGGWPNGLTV
	i	l	l			DYLEKRILWIDARSDAIYSARYDGSGHMEVL
1		ŀ	[			RGHEFLSHPFAVTLYGGEVYWTDWRTNTLA
1						KANKWTGHNVTVVQRTNTQPFDLQVYHPSR
	1		1	Į		QPMAPNPCEANGGQGPCSHLCLINYNRTVSC
		i	ĺ	ĺ		ACPHLMKLHKDNTTCYEFKKFLLYARQMEIR
						GVDLDAPYYNYIISFTVPDIDNVTVLDYDARE
			1		ļ	QRVYWSDVRTQAIKRAFINGTGVETVVSADL
ſ	ĺ		ĺ		*	PNAHGLAVDWVSRNLFWTSYDTNKKQINVA
						RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY
						WTDGDNISMANMDGSNRTLLFSGQKGPVGL
	ļ	1	-			AIDFPESKLYWISSGNHTINRCNLDGSGLEVID
	1					AMRSQLGKATALAIMGDKLWWADQVSEKM
			•			GTCSKADGSGSVVLRNSTTLVMHMKVYDESI
			Į.			QLDHKGTNPCSVNNGDCSQLCLPTSETTRSC
	1					MCTAGYSLRSGQQACEGVGSFLLYSVHEGIR
						GIPLDPNDKSDALVPVSGTSLAVGIDFHAEND
		Í				TIYWVDMGLSTISRAKRDOTWREDVVTNGIG
1			Ì			RVEGIAVDWIAGNIYWTDQGFDVIEVARLNG
1				!		SFRYVVISQGLDKPRAITVHPEKGYLFWTEW
1	1	1				GQYPRIERSRLDGTERVVLVNVSISWPNGISV
1		!	}	'		DYQDGKLYWCDARTDKIERIDLETGENREVV
1	Į.					LSSNNMDMFSVSVFEDFIYWSDRTHANGSIK
1.		1				RGSKDNATDSVPLRTGIGVQLKDIKVFNRDR
1						3
			]	<b>i</b>		QKGTNVCAVANGGCQQLCLYRGRGQRACA
	{	ſ	1	:	1	CAHOMLAEDGASCREYAGYLLYSERTILKSI
		1				HLSDERNLNAPVQPFEDPEHMKNVIALAFDY
		1				RAGTSPGTPNRIFFSDIHFGNIQQINDDGSRRIT
1	ſ	ľ	ľ			IVENVGSVEGLAYHRGWDTLYWTSYTTSTIT
1	1	l				RHTVDQTRPGAFERETVITMSGDDHPRAFVL
		ł				DECQNLMFWTNWNEQHPSIMRAALSGANVL
1	[	ſ	[			TLIEKDIRTPNGLAIDHRAEKLYFSDATLDKIE
	1	l				RCEYDGSHRYVILKSEPVHPFGLAVYGEHIF
	1	l				WTDWVRRAVQRANKHVGSNMKLLRVDIPQ
1	1	ļ				QPMGIIAVANDTNSCELSPCRINNGGCQDLCL
1						LTHQGHVNCSCRGGRILQDDLTCRAVNSSCR
1	Į.			1		AQDEFECANGECINFSLTCDGVPHCKDKSDE
1		1	1	i	1	KPSYCNSRRCKKTFRQCSNGRCVSNMLWCN
		ļ				GADDCGDG\$DEIPCNKTACGVGEFRCRDGTC
1		ł				IGNSSRCNQFVDCEDASDEMNCSATDCSSYF
L	1		L	L	L	TT. ST. C. C. DODD. (DDD. D. D. CONTIDOUS II

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion
						RLGVKGVLFQPČERTSLČYAPSWVCDGAND CGDYSDERDCPGVKRPRCPLNYFACPSGRCIP MSWTCDKEDDCEHGEDETHCNKFCSEAQFE CQNHRCISKQWLCDGSDDCGDGSDEAAHCE GKTCGPSSFSCPGTHVCVPERWLCDGDKDCA DGADESIAAGCLYNSTCDDREFMCQNRQCIP KHFVCDHDRDCADGSDESPECEYPTCGPSEF RCANGRCLSSRQWECDGENDCHDQSDEAPK NPHCTSPEHKCNASSQFLCSSGRCVAEALLCN GQDDCGDSSDERGCHINECLSRKLSGCSQDC EDLKIGFKCRCRPGFRLKDDGRTCADVDECS
						TTFPCSQRCINTHGSYKCLCVEGYAPRGGDP HSCKAVTDEEPFLIFANRYYLRKLNLDGSNY TLLKQGLNNAVALDFDYREQMIYWTDVTTQ GSMIRRMIILNGSNVQVLIHRTGLSNPDGLAV DWVGGNLYWCDKGRDTIEVSKLNGAYRTVL VSSGLREPRALVVDVQNGYLYWTDWGDHSL IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTE RIYWADAREDYIEFASLDGSNRHVVLSQDIPH IFALTLFEDYVYWTDWETKSINRAHKTTGTN KTLLISTLHRPMDLHVFHALRQPDVPNHPCK VNNGGCSNLCLLSPGGGHKCACPTNFYLGSD
						GRTCVSNCTASQFVCKNDKCIPFWWKCDTE DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTN PAFICDGDNDCQDNSDEANCDIHVCLPSQFK CTNTNRCIPGIFRCNGQDNCGDGEDERDCPE VTCAPNQFQCSITKRCIPRVWVCDRDNDCVD GSDEPANCTQMTCGVDEFRCKDSGRCIPARW KCDGEDDCGDGSDEPKEECDERTCEPYQFRC KNNRCVPGRWQCDYDNDCGDNSDEESCTPR PCSESEFSCANGRCIAGRWKCDGDHDCADGS DEKDCTPRCDMDQFQCKSGHCIPLRWRCDA DADCMDGSDEEACGTGVRTCPLDEFQCNNT
						LCKPLAWKCDGEDDCGDNSDENPEECARFV CPPNRPFRCKNDRVCLWIGRQCDGTDNCGD GTDEEDCEPPTAHTTHCKDKKEFLCRNQRCL SSSLRCNMFDDCGDGSDEEDCSIDPKLTSCAT NASICGDEARCVRTEKAAYCACRSGFHTVPG QPGCQDINECLRFGTCSQLCNNTKGGHLCSC ARNFMKTHNTCKAEGSEYQVLYIADDNEIRS LFPGHPHSAYEQAFQGDESVRIDAMDVHVKA GRVYWTNWHTGTISYRSLPPAAPPTTSNRHR RQIDRGVTHLNISGLKMPRGIAIDWVAGNVY WTDSGRDVIEVAQMKGENRKTLISGMIDEPH
						AIVVDPLRGTMYWSDWGNHPKIETAAMDGT LRETLVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSKRGLSHPFSIDV FEDYIYGVTYINNRVFKIHKFGHSPLVNLTGG LSHASDVVLYHQHKQPEVTNPCDRKKCEWL CLLSPSGPVCTCPNGKRLDNGTCVPVPSPTPP PDAPRPGTCNLQCFNGGSCFLNARRQPKCRC QPRYTGDKCELDQCWEHCRNGGTCAASPSG MPTCRCPTGFTGPKCTQQVCAGYCANNSTCT VNQGNQPQCRCLPGFLGDRCQYRQCSGYCE NFGTCQMAADGSRQCRCTAYFEGSRCEVNK CSRCLEGACVVNKQSGDVTCNCTDGRVAPS
·						CLTCVGHCSNGGSCTMNSKMMPECQCPPHM TGPRCEEHVFSQQQPGHIASILIPLLLLLLLVL VAGVVFWYKRRVQGAKGFQHQRMTNGAM NVEIGNPTYKMYEGGEPDDVGGLLDADFAL

NO: of NO: of hod ID NO:   beginning   nucleotide   D-Aspart	tic Acid, E=Glutamic Acid,
	lalanine, G=Glycine, H=Histidine,
	cine, K=Lysine, L=Leucine,
	ionine, N=Asparagine, P=Proline,
	mine, R=Arginine, S=Serine,
amino acid of peptide T=Threor	nine, V=Valine, W=Tryptophan,
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ine, X=Unknown, *=Stop codon,
	e nucleotide deletion, \=possible
1	e insertion
1 1 1 1 1 1	NFINPVYATLYMGGHGSRHSLASTD
	GRGPEDEIGDPLA
	AGKIPEESKALSLLAPAPTMTSLMPG
	PTPNPLTTLGVSLSSLGAIPAAALDPNI
	PQPPLMGNVDPSKIDEIRRTVYVGNL
	ADQLLEFFKQVGEVKFVRMAGDET
	FVEFADQNSVPRALAFNGVMFGDRP
	NNAIVKPPEMTPQAAAKELEEVMKR
	SFISAAIEPGWLHSTSLCNDFLGCF*RR
	*APCTICGTFHLCLIINWDL*LF*AYTA
	RVWKEQ*KKRR\RSRSHTRSKSRSSSK
	RSQSKHRSRSHNRSRSRQKDRRRSK RSKSRERRKSRSRSHSRDKRKDTREKI
	/KEKDREKEREREKEREKERGKN
1	CREKDREKDKEKDREREREKEHEKD
	EKEODKEKEREKDRSKEIDEKRKKDK
	RSYNASRRSRSSSRERRRRRSRSSSRS
	IKRKSSRSPSPRSRNKKDKKREKERD
	ERERSTSMRKSSNDRDGKEKLEKNST
S	
	TRAILQEFQWDIIRHPPL\SPNLALSG
	KSLRGTHFSSVKK\TTLTWLNSODP
	P*SPDLQIPSSFRNGLNDWYHHSQKC
PDLDGA	
376 1726 A 3199 931 418 GV*WCI	DLGSPQPPPPGFKQFCLGRSSSWDYR
HVPPHP	ANFVFLLETGFLHAGQAGL\GDPPAS
ASQSAG	GITGVSHTWPKNHLIFYACLVIRSKRI
K	
	SRGSPLSPQSSIDSELSTSELEDDSISM
	DLTDVQIMARLQEESLRQDYASTSAS
	SVSLSSGKKGTCSDQEYDQYSLEDEE
	PPQPRLPRCSPFQRGIPHSQTFSSIREC
	QYFPSNNYQQQQYYSPQAQTPDQQP
	OK/PPKKYA*PSPDAKYNCH**QH\SSP
	SQSFDSSLHGAGNGISRIQSCIPSPGQL
	SVGHFPVSIRQPLKATAYVSPTVQGSS VGLQLYSNTGIPTPNKAAASGIMGRS
	LAINGSNLPRSKIAQPVRSFLQPPKPL
	RDGNWRDGCY
	SRPSVLRGDHLFALLSSETHQEDPIT
	HKVELDRVKLSFSMSLLSRFVGWG*
	Y/TFNRQPLRV\QHRALELTGRWLLW
	VAPRDVPLLPSDVKLKLYDRSLESNP
	MRHIVTGTTRPAPYIIFGPPGTGKTVT
	QVVKHLPKAHILACAPSNSGADLLC
	ILPSSIYRLLAPSRDIRMVPEDIKPCCN
	GEYVFPAKKKLQEYRVLITTLITAGR
	PIDHFTHIFIDEAGHCMEPESLVAIAG
	ETGDPGGQLVLAGDPRQLGPVLRSPL
TQKHGI	LGYSLLERLLTYNSLYKKGPDGYDPQ
	NYRSHPTILDIPNQLYYEGELQACA
DVVDRE	ERFCRWAG\LPRQGFPIIFHGVMGKD
	PSFFNPEEAATVTSYLKLLLAPSSKK
GKARLS	SPRSVGVISPYRKQVEKIRYCITKLDR
ELRGLD	DIKDLKVTCCSTVTPCLPCAPTCPLP
	issprprptpaalnraralpepltpgd [
	VDGIRKPACLTNTSCHS
1 000	VXLWFPPFL*GSFKPTKGHTXCVXIK
	AXDSXPGRQIAXXRQGGKVETTTAL

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide seq-	peptide seq- uence		in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
иелсе			914	ng to first amino acid residue of	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	ļ		ļ <u>.</u>	peptide sequence		nucleotide insertion  XKOSNNKGTRASSYXEPDAXEQWKFPHKKL
						QLPGXTHE
380	1730	A	3207	187	507	GGTGHPHPARPPLSGVGGCQCSHSKPWTAGS PEQRDHPAPHKQIEAGQGLPGPQAWGG*KGP AXLLPGPGGGPGPVASLEARAQASSGVTPNG GGRTYPYPTFSSGE
381	1731	A	3225	l	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSF*GESL/ EMQLITSLGLQEFDIARNVLELIYAQTLVWIGI FFCPLLPFIQMIMLFIMFYSKNISLMMNFQPPS KAWRASQMMTFFIFLLFFPSFTGVLCTLAITI WRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRP GYLWVVWIYRNLIGSVHFFFILTLIVLIITYLY WQITEGRKIMIRLLHEQIINEGKDKMFLIEKLI KLQDMEKKANPSSLVLERREVEQQGFLHLGE HDGSLDLRSRRSVQEGNPRA
382	1732	A	3238	256	38	LLMIKVSSTCFSCHLHHHHHHHHHHHHQGHNS LFFSLKSSSNSSTLPVYLSYNIILVFSKCLVFDF LFSNACL
383	1733	A	3241	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFFKAD KVTMLWNKKATAVLVIASTDVDKTGASYYG EQILHYIATNGESAVVQLPKNGPIYDVVWNS
						SSTEFCAVYGFMPAKATIFNLKCDPVFDFGTG PRNAAYYSPHGHILVLAGFGNLILQI*AD/IMK VWNVKNYKLISKPVASDSTYFAWCPDGEHIL TATCAPRLRVNNGYKIWHYTGSILHKYDVPS NAELWQVSWQPFLDGIFPAKTITYQAVPSEVP NEEPKVATAYRPPALRNKPITNSKLHEEEPPQ NMKPQSGNDKPLSKTALKNQRKHEAKKAAK QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK
384	1734	A	3242	3	678	NQLEKIQKETALLQELEDLELGI IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES
385	1735	A	3243	3190	664	FNI VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL
						KEEEILPEPGSETPTVASEALAELLHGALLRR GPEMGYLPGPPLGPEGGEEETTTTIITTTTT TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL GLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRL HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPR NDTCPELPPPEWGWRTASHGDLIRGTVLTYQ CEPGYELLGSDILTCQWDLSWSAAPPACQKI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  MTCADPGEIANGHRTASDAGFPVGSHVQYRC LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC ALKYEPCLNPGVPENGYQTLYKHHYQAGESL RFFCYEGFELIGEVTTTCVPGHPSQWTSQPPLC KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
386	1736	A	3250	5725	3984	SNPLYEAGDTREYEVSI GTSTVTMATKKHFSIILNLLGMLLKKDNQDT RKLLMTWALEVAVVMKKSETYAPLFCLPSF HKFCKGLLADTLVEDVNICLQACSSLHALSSS LPDDLLQRCVDVCRVQLVHRGTCIRQAFGKL LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE RLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIR SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
						RLVLLLQYLENLEKLMYNAYEGCANALTSPP KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA GQPAVTVRHGFDLLTEMKTTSLSQGNELEVSI MMVVEALCELHCPEAIQGIAVWSSSIVGKHL LWINSVAQQAEGRFEKASVEYQEHLCAMTG VDCCISSFDKSVLTLASAGCKSASLKHCLNGE SRKSVLSKPTDSSPEVINYLGNKACECYISTA DWAAVQEWQNAIHDLKKSTSSTSLNLKADF NYIKSLSSFESGKFVECTEQLELLPGENINLLA GGSKEKIDMKKLLRNM
387	1737	A	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF LKYVHNL*AENYKTLMK*INEDLNKQRDVPY S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET NMQ
388	1738	A	3260	685	428	PQWLGLQVYALPPANFVFFVEMRSTILAQTG FELLDSSDLPASASKSAGITCMSHHARTLSLK *WPFCLSATQEKFC*PASEGVAW
389	1739	A	3269	1	332	LDGYHTPIYMLNRIIRLPAAL*IISDQTGHALTI LTRLETQMINADYQNKLTLDYLLTTDREVYE PFNLTNYCLIIIHNQRLGAYDLG*V*Q/KLAHV PVQV*HGFDPEAMFR
390	1740	A	3270	2	372	GRCHDONKGKS\DGPDAQAEACGGESTYQEL LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
391	1741	A	3273	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ HVFTFFQEELTRSQEGMKLGENFLMFAMPP DDSKESKGK*FFQEMLDIMKAISDMMGKCTY PVLKEDAPRQHVETFFQVGINQKSRGHEVRR KFPDVCHAPR
392	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK RFSYLSLPSSW\DYRHVLPRQANFCIF/M*RRG FTMLARMVSIS*PRDLPALASQSAGITGVSHH APPQMDFTFALLCFALKGCLPRQKEGGTLNLI
393	1743	A	3283	385	3	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVVIC LLTVMGNLLLLVVINADSCLHTPMYFFLGQL SFLDLCHSSVTAPKLLENLLSEKKTISVEGCM A*VFFVFATGGTESSLLAVMAYDRYVAIRTR G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC LDNCPEGLEANNHTMECVSIVHCEVSEWNP WSPCTKKGKTCGFKRGTETRVREIIQHPSAKG NLCPPINETRKCTVQRKKCQKGERGKKGRE

00010	Lecom	E X des	Lero	Deadisead	Donalistad and	Amino acid sequence (A=Alanine C-Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	peptide	ļ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	seq- uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	dence	[	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uclice			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ		-	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	j	]		peptide	3-40-11-0	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	<del> </del>		<del> </del>	2040000		RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN
						KOOO
395	1745	A	3286	1	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS
			3200	-		WICLSMVILTHSLKTFHRNWDWESEYTLFMS
						ALKVNKNNAKLWNNVGHALENEKNFERAL
	j	ļ			1	KYFLQATHVQPDDIGAHMNVGR
396	1746	A	3293	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL
				j -		IAFMKQRRMGLNDFIQKIANNSYACKQ
397	1747	A	3295	12	401	AEPACGASSCTPPSLRSSSSQSVGPLRPGRPL
	ĺ	i	ł		Ì	WSEACAFL*AAAPQGPASPCCGLPSGFPRVW
	1	İ	i	,		AQCCPPGGALRFPEGLGSVLSPRRCPQVSRGS
			1	}		GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA
	}		ŀ		ł	GLT
398	1748	A	3300	1912	2768	KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS
						MLRKLPKVTCRDVLPEIRAICIEEIGCWMQSY
					Į	STSFLTDSYLKYIGWTLHDKHREVRVKCVKA
	ľ		Ì	1		LKGLYGNRDLTARLELFTGRFKDWMVSMIV
	ł		ł	ĺ	ł	DREYSVAVEAVRLLILILKNMEGVLMDVDCE
						SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI
	Į.				ł	RTMGGREQRQSPGAQRTFFQLLLSFFVESKSH
				1	Ì	SVTQAGVQWQFSAHRDLCLPGSSNSHVSASR
	ĺ			ĺ	ł	VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL
						VSNS
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE
	İ	l	ł	}	1	SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI
						CLSTHTQ*FTALPADLLTWTQSNVSLHISYLAI
			1			PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
	J		J	Ì		GRAVALLHLIASGLTSIQTNTASSKPPIWGY\L
	ļ		Ì			STQTSFISPPPLCLSRTYPNPAHATMVGQVPQ
						SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV   LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN
						SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGS
	ľ				1	N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL
	}			ļ	]	TGAALAGSYPIWENENTLSWLPTFTYNFCLST
	j	i	1			PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI
			1	}	ļ	NILPPNOTILISVEASISSSPIRNKWALHLITLLT
	i					GLGITAALGTGIAGITTSITSYOTLFTTLSNTVE
		1		[		DMHTSITSLQRQLDFLVGVILQNWRVLDLLT
					-	TEKGGTCIYLQEECCFCVNESGIVHIAVRRLH
		1			1	DRAAEL*HQVADSWWQGSSLLRWIPWVAPF
				ł	1	LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ
		1		ţ		ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPR
						P
400	1750	A	3303	2	453	THWRHSSGVPGSTTARRRRELEIATSDNQE
		}		1		YYNRLCQEVTNRERNDQKMLADLDDLNRTK
		1				KYLEERLIELLRDKDALWQKSDALEFQQKLS
	*	l				AEERWLGDTEANHCLDCKREFSWMVRRHHC
					<u> </u>	RICGRIFCYYCCNNYVLSKHGGKKERCC
401	1751	A	3304	1	626	MAPQHSSLDDKVPQQASTVCFEFQDILQHSQ
						CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP
	]		ļ	}	1	EKIVLRALKDSRAGMPEQDKDPGVQENPDD
		1			ļ	QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP
		1			1	GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR
		1				NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEG
	L		L	L		LSLSTQILG*QKPSKYIPSLCKR
		1	2205	1678	172	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA
402	1752	A	3305	1070	•	
402	1752	A	3303	1070		PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF
402	1752	A	3303	1070		

SEQ ID NO: of nuct- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion  GAQLKAPLSPLAFRMEDTEALPLTPILYPTCQ FFFF-IFLNIFLLAFSSPGSQPLLNSPPSFVCWSR GFMEMNGRGELVESLKRFCASTRLPPTPLLLF PEEEATNGREGLLRFSSWPFSIQDVVQPLTLQ
403	1753	A	3307	44	447	VQRTLVSVTVSDASWVSELL\WSLFVPFTVY QVRWLRPVHRQLGEANEEFALRVQQ\LVAKE LG\QTGTRLTPA\DKAEHMKRQRHPR\LRPQS AQSSFPPSPWVLSS\SDVQTGQTLGFREFKESF CPHVAIGVFIPERPWPKTGCCKTLTHLILL*G GPVSFSCPE\DIHPRGT*VPTQQASGLPSFPSYG PARGGVL*HPSAQQPLTFA\KSS\WARAGRAL QERKQ\ALYEYARRFTERRAPGGLD DPSPSLLAVALGLRAGERTRSGPGSSSPSGGIS
403	1733	Â	3307	<del>44</del> 	447	GGASAGLASSPECACGRSHFTCAVSALGECT CIPAQWQCDGDNDCGDHSDEDGCILPTCSPL DFHCDNGKCIRRSWVCDSDNDCEDDSDEQD CPPRECEED
404	1754	A	3311	409	1	PRHGWGRRVLGRDRPRLQKVKKSVKAIYIPG QDHVQNEEIYARVLDKFGSNFLSRDNADLGT AFVKFSTLTK*LSALLKNLLQGLSRNVIFTLDS LLKGDLKGVKGDLKKPFDKAWKDYETKFAK IEKEKREREWR
405	1755	A	3322	12	458	AAVPVENPWDDPRVRPRVRIFTWEDCIAGQA KVLCNDSYGVTIDWSPKGAFIRLTSQSVGNG HPASKENDQMVDTIKNTTKVPIIWTYGDMVE PRPQMIRPAVGAKHKELWKILMALKKIKIWE GKYTKPSQYNPNYMLELAHNDSVW
406	1756	A	3324	1	426	LSMLSTISTEHRLSVLWPIWYCCHCPTHLSAV MCVLLWALSLLQSILEWMFCSFLFSDVDSDN WCQILDFLTAVWLIFLIUVLCGFTLVLLVRIIC GSQKMPLTRLYVTILLTGLVFLFCSLPLSIQ*F LLYWIEKDLDDL
407	1758	A	3338	213	1841	SGDLSPAELMMLTIGDVIKQLIEAHEQGKDID LNKVKTKTAAKYGLSAQPRLVDIIAAVPPQY RKVLMPKLKAKPIRTASGIAVVAVMCKPHRC PHISFTGNICVYCPGGPDSDFEYSTQSYTGYEP TSMRAIRARYDPFLQTRHRIEQLKQLGHSVD KVEFIVMGGTFMALPEEYRDYFIRNLHDALS GHTSNNIYEAVKYSERSLTKCIGITIETRPDYC MKRHLSDMLTYGCTRLEIGVQSVYEDVARD TNRGHTVKAVCESFHLAKDSGFKVVAHMMP DLPNVGLERDIEQFTEFFENPAFRPDGLKLYP TLVIRGTGLYELWKSGRYKSYSPSDLVELVA RILALVPPWTRVYRVQRDIPMPLVSSGVEHG NLRELALARMKDLGIQCRDVRTREVGIQEIH HKVRPYQVELVRRDYVANGGWETFLSYEDP DQDILIGLLRLRKCSEETFRELGGGVSIVREL HVYGSVVPVSSRDPTKFQHQGFGMLLMEEA ERIAREEHGSGKIAVISGVGTRNYYRKIGYRL QGPYMVKMLK AIASPRAAGIRHELTSTMAAGKNKRLTKGGK
408	1/38	A	3333	3	407	AJASPRAAGIRHELTSTMAAGKNKRLTKGGK KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG LKGRVFEESLADLQND\TDGYLLRVI*VAFTT ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPLH DDFARKVKMLKKPKFELRKLMELHGEGSS
409	1759	A	3338	7	1252	PRWRNSARDEILLSFPQNYYIQWLNGSLIHGL WNLASLFSNLCLFVLMPFAFFFLESEGFAGLK KGIRARILETLGMLLLLALLILGIVWVASALID NDAASMESLYDLWEFYLPYLYSCISLMGCLL

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	}	USSN	location	corresponding to last amino	I-Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence		09/496 914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
dence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		İ		peptide	į   •	/=possible nucleotide deletion, \=possible
		l	1	sequence		nucleotide insertion
						LLLCTPVGL\SRMFTVMGQLLVKPTILEDLDE
	ł		1		ľ	QIYIITLEEEALQRPTKWAVFIRW/KYNIMELE
			[		ļ	QELENVKTLKTKLERRKKASAWERNLVYPA
		ļ		1		VMVLLLIETSISVLLVACNILCLLVDETAMPK GTRGPGIGNASLSTFGFVGAALEIILIFYLMVS
}		1	1		į	SVVGFYSLRFFGNFTPKKDDTTMTKIIGNCVS
					Ì	ILVLSSALPVMSRTLGITRFDLLGDFGRFNWL
						GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE
ŀ			i			LFKALGLHKLHLPNTSRDSETAKPSVNGHQK
					Ĺ	AL
410	1760	A	3339	127	1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLL
	Ì			1		WLALACSPVHTTLSKSDAKKAASKTLLEKSQ
					}	FSDKPVQDRGLVVTDLKAESVVLEHRSYCSA
					ļ	KARDRHFAGDVLGYVTPWNSHGYDVTKVFG SKFTQISPVWLQLKRRGREMFEVTGLIIDVDQ
	1	l	ł	i		GWMRAVRKHAKGL\P*CLGSCLRTGLTMISG/
						YVLDSEDEIEELSKTVVQVAKNQHFDGPVVE
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				ļ		GFSLMTYDYSTAHQPGPNAPLSWVRACVQV
						LDPKSKWRSKILLGLNFYGMDYATSKDAREP
]				ĺ	]	VVGARYIQTLKDHRPRMVWDSQVSEHFFEY KKSRSGRHVVFYPTLKSLQVRLELARELGVG
				1		VSIWELGQGLDYFYDLL*VGIAASAVDVFFSK
						PWSE
411	1761	A	3342	74	2701	VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK
İ	1	i			}	FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF
	1	}				EATQDDMVTVPKSPPAYARSSDMYSHMGTM
	}				1	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV
	l	ŀ			ŀ	PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS   AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA
						GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE
						ELKLSSTDLRSHAWYHGRIPREVSETLVQRN
	]		ļ	j		GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN
						KVVVKAGESYTHIQYLFEQESFDHVPALVRY
						HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS
						YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM
	1	[		[		TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDOIPDLHSPMSPISESPSSPAYSTVTRVHA
		1				APAAPSATALPASPVARRSSEPQLCPGSAPKT
		[				HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS
	ł		1			GHYCQLQPPVRGSREWAATETSSQQARSYGE
						RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP
}						ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA
	ļ					RTLARHVTKVDCLVARILGVTKEMQTLMGV
	1	1				RWGMELLTLPHG\RKLRLDLLERFHTMSIML
	l	1				AVDILGCTGSAEERAALLHKTIQLAAELRGT
						MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN
		ĺ	[		İ	TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV
	1					EVVLAHLEAARTVAHHGGLYHTNAEVKLOG
	ŀ					FQARPELLEVFSTEFQMRLLWGSQGASSSQA
			L			RRYEKFDKVLTALSHKLEPAVRSSEL
412	1762	Α	3347	1	898	IDRAAECRTKPLPMAVSIRGNADSIVACLVLM
}						VLYLIKKRLVACAAVFYGFAVHMKIYPETYI
			]		'	LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL
						KRLCNRTALMFVAVAGLTFFALSFGFYYEYG WEFLEHTYFYHLTRRDIRHNFSPYFYMLYLT
		]		'		AESKWSFSLGIAAFLPQLILLSAVSFAYYRDL
l i	1					VFCWFLHTSIFVTFNKVCTSQYFLWYLCLLPL
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416 1766 A 3373 42 651 ROEKMGLGEIGASGVLRSMLKERKKONMKG NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS APGLGSPLHPLQPQQEASTCPSGTLQGREKAA PGQGRPL.CSL.WAGGAGAIPGERGAEGRGPSD QAPDPKSGPWLPPPGLGAPAEVRLHNVPHNL RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH  417 1767 A 3382 2 2061 EAQDPRAGGPLAGGREFAARDAPGNSLRPPS SPPJGWPGQLRLLPRVPGSELRCGKPERGRLP ASPPGKIRGWPPGISKRPGLGGKPERGRLP ASPPGKIRGWPPGISKRPGLGGKPERGRLP ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT WRPEARGPSVQSL.PPIFSPQSAQTTAR*RPGAP KNAGRCGGARGFRLSLGPPPGPPPAPALPAR ASAGAGAAAALAVGGVRGAGGARGTGGY GHCSGR/PTGRTGPPQPGPPPMPARPR*ASIS TRGSRRGPGSRPARAAAAAPRAGDHGRRPVRV HILRQHTAV*EFRLGDATAPPGGAAGPGAPAP PLGPGWDCALLPSPGPRSPRAVGCAEPEIWDP SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY PLKGPGLPPWGPRTGTGHVITVQPSGSCIEH SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP PQSWGLCGIGRRGGLGGPGLKRGETGGLL*9GC SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD HSSCEGHPDLHAGREMPAAPGLSELERVRFT VGCGGLASGISSASVSGLSPNRAGGPGQGDW EMYPVSWQTQESGGGG\GSPKTGR*VGMLQA GAGSLQGGTGDQVWGL WEDGPRG*DSPLPS GTGTEP*TTTSIPFFPQPSGYYPSRATLLPMPS Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEPLLNVETAFWSMWVTYPKK  418 1768 A 3398 304 2121 EEEEEEEDEDDDDNNEEEEFECYPFGMKVQV RYGRGKNQKMYEASIKDSDVEGGEVLLYLH YCGGWLNSCHASHKSI EITSILNGLQASESSAEDSEQEDERAQDMDN	415	1765	A	3369	431	315	
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SEQ ID	SEO ID	Met	SEO	Predicted	Predicted and	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	""	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	uciico		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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			<del></del>		L	

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence	1	09/496 914	correspondi ng to first	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
				amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
						VESTSGIVRTLRRLDRENVAQYVLRAYAVDK GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD
						VFVEENSPIGLAVARVTATDPDEGTNAQIMY QIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
						YVLVIQATSAPLVSRATVHVRLLDRNDNPPV LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP
						DISDSLTYSFERGNELSLVLLNASTGELKLSR
						ALDNNRPLEAIMSVLVSDGVHSVTAQCALRV TIITDEMLTHSITIRLEDMSPERFLSPLLGLFIQ
	1					AVAATLATPPDHVVVFNVQRDTDAPGGHILN VSLSVGQPPGPGGGPPFLPSEDLQERLYLNRS
						LLTAISAQRVLPFDDNICLREPCENYMRCVSV LRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGF
						TGDYCETEVDLCYSRPCGPHGRCRSREGGYT CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
						CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP AHSFITFRGLRQRFHFTLALSFATKERDGLLL
						YNGRFNEKHDFVALEVIQEQVQLTFSAGEST TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
						QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG
						VPDLPESFPVRMRQFVGCMRNLQVDSRHIDM ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC
						VNQWDAFSCECPLGFGGKSCAQEMANPQHF
						LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD GVLLQAITRGRSTITLQLREGHVMLSVEGTGL
						QASSLRLEPGRANDGDWHHAQLALGAIGGP GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV
						GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN SLDPSHGESINVEQGCSLPDPCDSNPCPANSY
						CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC EHQSVCTRKPSAPHGYTCECPPNYLGPYCET
						RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC NKTSGECHCKENHYRPPGSPTCLLCDCYPTG
		i				SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF AEVTTNGCEVNYDSCPRAŒAGIWWPRTRFG
		į				LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF NCTSITFSELKGFAERLQRNESGLDSGRSQQL
						ALLLRNATQIITAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL
						DTANKRHWELIQOTEGGTAWLLQHYEAYAS ALAQNMRHTYLSPFTIVTPNIVISVVRLDKGN
						FAGAKLPRYEALRGEOPPDLETTVILPESVFR ETPPVVRPAGPGEAOEPEELARRORRHPELSO
		! <b>!</b>				GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK RPIINTPVVSISVHDDEELLPRALDKPVTVQFR
						LLETEERTKPICVFWNHSILVSGTGGWSARGC
	i					EVVFRNESHVSCQCNHMTSFAVLMDVSRRE NGEILPLKTLTYVALGVTLAALLLTFFFLTLL
						RILRSNQHGIRRNLTAALGLAQLVFLLGINQA DLPFACTVIAILLHFLYLCTFSWALLEALHLY
[ ]					ĺ	RALTEVRDVNTGPMRFYYMLGWGVPAFITG LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP
		ļ				VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL
					ĺ	FHYLFATCNCIQGPFIFLSYVVLSKEVRKALK LACSRKPSPDPALTTKSTLTSSYNCPSPYADG
					.	RLYQP\YGDSAGSLHSTSRSGKSQPSYIPFLLR EESALNPG\QGPPGLGGIPGR/LCFLGRFKDQQ
						H\DS*TRDFDSDLSLEDDQSGSYASTHSSDSEE

COTO ID	CECTE	1 1/	COEA	Predicted	Dendinted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		Predicted end	
NO: of	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
						I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	1 ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '
seq-	uence		09/496	correspondi		M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
]			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
-				peptide		/=possible nucleotide deletion, \=possible
		L		sequence	<u> </u>	nucleotide insertion
	!					EEEEEEEAAFPGEQGWDSLLGPGAERLPLHS
1	1	[	Į.		[	TPKDGGPGPGKAPWPGDFGTTAKESSGNGAP
l			1	•		EERLRENGDALSREGSLGPLPGSSAQPHKGIL
		j	ł	ļ		KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE
						GSRGGPPSRPPPRQSLQEQLNGVMPIAMSIKA
L	1	<b>{</b>	1	Ì	· ·	GTVDEDSSGSEFLFFNFLH
425	1775	A	3429	155	1417	GEPAVQSCDCGCTQRSCPWLLVAPGLLSSSSS
		ŀ				RAASVREAEDAPLQPASIHPVSQGSRGPEGSL
		1				GSAECLPGDPLGARRATRAHSPVPGPPPSLPA
1		i		,		AGTAVKRGLQPG*GA/GATSTPGTGAATGGL
į.		1				CGPAWAAPSAVGPCCCCPSISTTPSQMRSARP
Ì		1	1	i	Ì	SLGCLPSWAS\PGTEHPPGPQGPGPS*DLCSV*
1	[					KREFQRGPWAGMVILHRISAADPARAPGPDS
1	1	1	1			NLQSALQQPATGCSEPAAVYSPPIGLWGA**P
			1			EYG*PQHSLPG*TAPADR*P\AGIKDRVYSNSI
1	l	ļ	ŀ	<u>!</u>		YELLENGORAGTCVLEYATPLOTLFAMSOYS
1	į.	1 '		i		QAGFSREDRLEQAKLFCRTLEDILADAPESQN
				1		NCRLIAYQEPADDSSFSLSQEVLRHLRQEEKE
						, , , , ,
	į					EVTVGSLKTSAVPSTSTMSQEPELLISGMEKP
40.	155	<u> </u>	2421	1	7.0	LPLRTDFS
426	1776	Α	3431	1662	369	AIWWLSWLQHDLLPTPTQVAIDFTASNGDPR
		ļ	1			SSQSLHCLSPRQPNHYLQALRAVGGICQDYD/
		1	1	1		SVGESGAGGNRQGGLAQRIPQLFLLPSDKRFP
		1	1	ļ		AFGFGARIPPNFEVG*MRGKEGDGGRVSQAE
	]		1		ļ	KAGPHCSRLALTG\SHDFAINFDPENPECEGK
	1			ł		RGDFHLPRLPADTLHTGAQTPLPRAQLPVPST
			Į.	İ		HPRPVFT\EISGVIASYRRCLPQIQLYGPTNVAP
						INRVAEPAQREQSTGQATKYSVLLVLTDGV
1				İ		VSDMAETRTAIVRASRLPMSIIIVGVGNADFS
Ī	İ	ĺ	1	ĺ		DMRLLDGDDGPLRCPRGVPAARDIVQFVPFR
						DFKDVSPPGPFRLKDSSASHPPKSDLRLPPFD
			!			VLLRTREPSWPP*SPTSPSDDPASPTLPLTPNHI
		1	1			TVPTL\AAPSALAKCVLAEVPRQVVEYYASQ
				i		GISPGAPRPCTLATTPSPSP
427	1777	A	3446 .	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW
	1					GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA
1						ASRPEASGDCRAGRETAMATLEKLMKAFESL
Ì	1					KSFQQQQQQQQQQQQQQQQQQQPPPP
	i					PPPPPPPOLPOPPPOAOPLLPOPOPPPPPPPPPP
1		1	ľ			GPAVAEEPLHRPKKELSATKKDRVNHCLTIC
		1				ENIVAQSVRNSPEFQKLLGIAMELFLLCSDDA
		1				ESDVRMVADECLNKVIKALMDSNLPRLQLEL
		[				YKEIKKNGAPRSLRAALWRFAELAHLVRPOK
!	i	ł				CRPYLVNLLPCLTRTSKRPEESVOETLAAAVP
		!				`
		1				KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI
		1				RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
		1				LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV
*		1				KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL
]	İ	1	1	}		TLHHTQHQDHNVVTGALELLQQLFRTPPPEL
		1				LQTLTAVGGIGQLTAAKEESGGRSRSGSIVELI
		1				AGGGSSCSPVLSRKQKGKVLLGEEEALEDDS
	1	1				ESRSDVSSSALTASVKDEISGELAASSGVSTPG
1		ļ	Į l	l .		SAGHDIITEQPRSQHTLQADSVDLASCDLTSS
						ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG
	·	1				TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD
1		İ				GTDNQYLGLQIGQPQDEDEEATGILPDEASEA
		Ī				FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF
		1				VLRDEATEPGDQENKPCRIKGDIGQSTDDDS
		!	ļ ,	]		APLVHCVRLLSASFLLTGGKNVLVPDRDVRV
		l				SVKALALSCVGAAVALHPESFFSKLYKVPLD
ı	ı .	1	l			OTTE TO THE TENTE TO THE TRAILED

SEQ ID SEQ ID Met SEQ Predicted Predicted end Amino acid sequence NO: of NO: of hod ID NO: beginning nucleotide D=Aspartic Acid, E=0	(A=Alanine C=Cysteine,
I ITO, OF 1 TO, OF 1 MORE   MORE   CONTINUE   MOREOVINO   1 D (MONTHS MORE)	Glutamic Acid.
	Glycine, H=Histidine,
eotide seq- USSN location corresponding I=Isoleucine, K=Lysin	
amino acid of peptide T=Threonine, V=Vali	
residue of sequence Y=Tyrosine, X=Unkn	
peptide /=possible nucleotide	deletion, =possible
sequence nucleotide insertion	
	NYIDHGDPQVRGATAILC
GTLICSILSRSRFHV	GDWMGTIRTLTGNTFSL
ADCIPLLRKTLKDF	ESSVTCKLACTAVRNCVM
	IIDVLTLRNSSYWLVRTEL
	LEAKAENLHRGAHHYTGL
	HLLGDEDPRVRHVAAASL
	GQADPVVAVARDQSSVYL
	SVSTITRIYRGYNLLPSITD
	VSHELITSTTRALTFGCCE
	/SLGWHCGVPPLSASDESR
	LLSSAWFPLDLSAHQDAL
	SLRSSWASEEEANPAATK
	LVPMVEQLFSHLLKVINIC
	KAALPSLTNPPSLSPIRRK
	LSPKKGSEASAASRQSDTS
	YHLPSYLKLHDVLKATHA
	KFGGFLRSALDVLSQILEL
ATLQDIGKCVEEIL	GYLKSCFSREPMMATVC
VQQLLKTLFGTNL	ASQFDGLSSNPSKSQGRA
	HYCFMAPYTHFTQALADA
SLRNMVOAEOENT	OTSGWFDVLQKVSTQLKT
	IAIHNHIRLFEPLVIKALKQ
1 1 1 1 1 1	LDLLAQLVQLRVNYCLL
	FEYTEVGQFRESEATIPNIFF
	QUGIPKUQLCDGIMASGR
	HDLFVLRGTNKADAGKE
	RLIQYHQVLEMFILVLQQ
]	~ ~
	SRQIADIILPMLAKQQMHI
	EILAPSSLRPVDMLLRSMF
	LWISGILAILRVLISQSTED
	ISCTVINRLRDGDSTSTLE
	TFSRFLLQLVGILLEDIVT
	FYCQELGTLLMCLIHIFKS
	FRSDGCGGSFYTLDSLNLR
	WCQILLLVNHTDYRWW
	STKLLSPQMSGEEEDSDLA
	GALILFCDYVCQNLHDSE
	SLSHEPPVQDFISAVHRNS
AASGLFIQAIQSRCI	ENLSTPTMLKKTLQCLEGI
	DRLLCTPFRVLARMVDIL
	LQSSMAQLPMEELNRIQEY
	YSLLDRFRLSTMQDSLSPS
	VSLETVSPDKDWYVHLVK
	GAELVNRIPAEDMNAFM
	LSLGMSEISGGQKSALFEA
	QQLPAVHHVFQPELPAEP
	DAALYOSLPTLARALAOY
	PPEKEKDIVKFVVATLEAL
	LQAGLDCCCLALQLPGL
	CSLIYCVHFILEAVAVQPG
	AISEEEEEVDPNTQNPKYI
	SLQSVLALGHKRNSGVPA
	LPLVNSYTRVPPLVWKLG
	PEIPVEFLQEKEVFKEFIYR
INTLGWTSRTQFEE	ETWATLLGVLVTQPLVME
QEESPPEEDTERTQ	INVLAVQAITSLVLSAMT
VPVAGNPAVSCLE	QQPRNKPLKALDTRFGRK
	VSKRENIATHHLYQAWD
	HEKLLLQINPERELGSMS
	GNSITPLREEEWDEFEEEE
TRESQV SILB V WEX	

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1 1100	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
)	]			peptide		/=possible nucleotide deletion, \=possible
<del></del>	<del> </del>	<del>  -</del>	+	sequence	<u> </u>	nucleotide insertion
1		1	1	ĺ	ĺ	ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL LELYSRWILPSSSARRTPAILISEVVRSLLVVS
J	)	}	1	ļ	1	DLFTERNQFELMYVTLTELRRVHPSEDEILAQ
		1			1	YLVPATCKAAAVLGMDKAVAEPVSRLLESTL
	}	1				RSSHLPSRVGALHGILYVLECDLLDDTAKQLI
į	ļ	1	1		1	PVISDYLLSNLKGIAHCVNIHSQQHVLVMCAT
						AFYLIENYPLDVGPEFSASIIQMCGVMLSGSE
	İ					ESTPSIIYHCALRGLERLLLSEQLSRLDAESLV
1	ļ	1	1 ,		1	KLSVDRVNVHSPHRAMAALGLMLTCMYTG
						KEKVSPGRTSDPNPAAPDSESVIVAMERVSVL
		1				FDRIRKGFPCEARVVARILPQFLDDFFPPQDIM NKVIGEFLSNQQPYPQFMATVVYKVFQTLHS
Į.	ļ		1			TGQSSMVRDWVMLSLSNFTQRAPVAMATWS
j		]				LSCFFVSASTSPWVAAILPHVISRMGKLEQVD
		1	1			VNLFCLVATDFYRHQIEEELDRRAFQSVLEV
150	ļ. <u></u>					VAAPGSPYHRLLTCLRNVHKVTTC
428	1778	Α	3449	3	430	NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA
		)				WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG
1	}	ł	} }			LPCVGDAAEYQDCNPQACPVRGAWSCWTS
			i 1			WSPCSASCGGGHYQRTRSCTSPAPSPGEDICL
429	1779	Ā	3464	583	3	GLHTEEALCATQACPEGWS DALDRRYLERCHPAAGGWVGEGE*ALCQKT/
			• • •		Ĭ	RFSGVLEPPLPSLKDGGRFPAWT*RSCSKSLR
			1		'	AAFTSQFFPSRRSRASPGSAP\GNGQNLTEQHP
						CPGSCDPQVLSASWM*VEHRSKFRPPP*NSTI
1		l	} {			PPES/RS*QGGTVQTGQHSSGREAGSWRARGR
}			)		ļ	NAGRR*KGGGKIGTKQGAVRARKECRGEMA
430	1780	A	3473	2802	270	SGETDSE
1	1760	Α.	34/3	2602	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKA
			1			HLSIQKLLKER\Q\QLPVFKHRDSIVETLKRHR VVVVAGET\GSGKSTQVPHFLLEDLLLNEWE
!			1 1	ŀ	}	ASKCNIVCTQPRRISAVSLANRVCDELGCENG
i i			ii	ſ	ľ	PGGRNSLCGYQIRMESRACESTRLLYCTTGV
i						LLRKLQEDGLLSNVS/HMFIVDEV\HER\SVOS
			l i			DFLLIILKEILQKRSDLHLILMSATVDSEKFST
1 1	100			l	1	YFTHCPILRISGRSYPVEVFHLEDHEETGFVLE
			1	f		KDSEYCQKFLEEEEEVTINVTSKAGGIKKYQE
!	-		1		ŀ	YIPVQTGAHADLNPFYQKYSSRTQHAILYMN PHKINLDLILELLAYLDKSPQFRNIEGAVLIFL
[	· ·		[ [	ſ	ĺ	PGLAHIQQLYDLLSNDRRFYSERYKVIALHSI
				ŀ	ł	LSTQDQAAAFTLPPPGVRKIVLATNIAETGITI
				i		PDVVFVIDTGRTKENKYHESSQMSSLVETFVS
	1	[		[	ſ	KASALQRQGRAGRVRDGFCFRMYTRERFEG
		i				FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF
	ļ	ĺ		ļ	!	LSKALDPPQLQVISNAMNLLRKIGACELNEPK
	1	ſ		ſ	1	LTPLGQHLAALPVNVKIGKMLIFGAIFGCLDP
	1				1	VATLAAVMTEKSPFTTPIGRKDEADLAKSAL AMADSDHLTIYNAYLGWKKAROEGGYRSEI
J	J	J		)	)	TYCRRNFLNRTSLLTLEDVKQELIKLVKAAGF
1		l		1		SSSTTSTSWEGNRASQTLSFQEIALLKAVLVA
ļ		1				GLYDNVGKIIYTKSVDVTEKLACIVETAOGK
j	J	j	J	J	J	AQVHPSSVNRDLQTHGWLLYQEKIRYARVY
						LRETTLITPFPVLLFGGDIEVQHRERLLSIDGW
	1	ľ		i		IYFQAPVKIAVIFKQLRVLIDSVLRKKLENPK
431	1781	A	1474	,		MSLENDKILQIITELIKTENN
121	1/01	^	3474	1 (	441	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ
						PCPPAPAPSRPRSLGSLGQRVPAALATAAQEL
1	1	j	- 1	!	_ }	PATLGGDGGKPALTAGEAALPGLHRSGVPAA AARC*PCT/SRPT*STLSPTQAAWWCRPSRRQ
_		1				QRGEASTGGASGRRCGSCFQV
						,

SEQ   ID   SEQ   ID   Not   both	ero m	SEC ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
mucicotide sequence unce unce unce unce unce unce unce					1		
Sequence			nod	1			
	ľ		1	1			
1782   1782   A 3478   416   23   23   24   23   24   23   24   24	1			1			
### ### ### ### ### ### ### ### ### ##	seq-	uence				1	
Persidue of peptide   Sequence   Y=Tyrosine, X=Unknown, "=Stop codon,   Peposible nucleotide delicion,   Sequence   Seq	uence			914			
			1	•			
1782   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3478   A 3504   A 3		ŀ		i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
432				ł	peptide		/=possible nucleotide deletion, \=possible
1783   A   3504   1876   552   CLAPCSPOPERS   CLA		1	ŀ	İ	sequence	1	nucleotide insertion
1783   A   3504   1876   552   CLAPCSPOPENGMOPILLIPELTPULTYOLHES	432	1782	Α	3478	416	23	OLRRLTLPNFKTY/YSS*IIEIAWH**KNMOID
	1			İ			1 '
QKILKISKWIKDLNYECRITKILLDQEYPGDLGY	İ		Į			İ	
\$\$\text{SRAINSGSR}\$		ł	ł	ł	ł	1	
1783   A   3504   1876   552   CLAPCSPOPERNGMOPLILLIPPICLYOQLIUM	1				Ì	i	
SIGAPGESTILLVRTSKLLVGGLGULLVWILLL QTRSILAIQHLITSSAPLIAAPTAVCSCSRCS APRSIKCVARPAARTGLPTPAPASSPAPASPA APSPAPAESTAPPOHLITERPPAGSPPRPA GAPPRPAASPPAASPUTASPPUTASPPUTASPPUTASPPUTA ASPPAASPVITASPPUPAASPAJAPATASPVITASPPUPASPPAA ASPAPAASPVITASPPUPASPPUTASPPVITASPPUPASPPAA ASPAPAASPVITASPPUPASPPUTASPPVITA	433	1702		3604	1076		
GTRSLLALQHILTSSAPILLAPPTA/CSCSRCS APRSRCVARPARTIGI_TPTAPASSPAPASPA PASSPAASPARESTAPQPLILLPKPPPAGAPPRP GAPPRPAASPAPARESTAPQPLILLPKPPPAGAPPRP GAPPRPAASPSPAASPAPASPVLTASPPLPAASSPAA ASSPAASPAPAASPALAASPVHTASPPLYTASPPLPAASSPAA ASSPAPAASPALASPVLTASPPLYTASPPLYTASPPLY ASSPAVITASPPVHVASPPVHTASPPVHVASVLASPPVHASPPVHVASVLASPPVHASPPVHVASVLASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPAHVASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPPVHASPVHAS	433	1/83	A	3304	1870	332	, , , , , , , , , , , , , , , , , , , ,
APRSRCVAŘPAASICILEJTPAPASSPAPASSPA PAASPAPASSTAPOPCILLIJPKPPAPGAPPPRP GAPPPPAASPAPASSPAPAASPAPAASPVITASPPLP AASPSPAASPAPAASPAPAASPVITASPPLPAASPSPA ASPAPAASPVITASPPLPAASPALAASPVITI ASSPVAIVASPPVHTASPPVHVASPPVHTASPPVHVASPPVHVASPPV VHVASPPVHVASPPVHVASPPVHVASPPVHVASPPVHVASPPV VHVASPPVSCGGGTSPPP QFGAVPHSLAPSLAPSLAPSUS SPACE SPAC			l				7
PASSPAPAESTAIPOPLILLPKPPPAPGAPPRPR GAPPRPPAASPVLTASPPLASPSLTASPPLA ASSPSAASPASPASPVATASPPLASPSLTASPPLA ASSPSAASPAPARASPVLTASPPLASPSLASPALASPVHTI ASPPVHVASPPVHTASPPVHVASPPVHTASPPVHVASPPVHTASPPVHVASPPVHTASPPVHVASPVHVASPPVHVASPVHVASPPVHVASPVHVASPPVHVASPVHVASPVHVASPPVHVASPV		ł	ł	ł	1	i	1 7
GAPPRPAASPSPAASSPAPAASPUTTASPPLP AASPSPA ASPAPAASPUTTASPPLPAASPSPA ASPAPAASPVTTASPPLPAASPSPA ASPAPAASPVTTASPPLPAASPSPA ASPAPAASPVTTASPPLPAASPSPA ASPAPAASPVTTASPPLVASPPVTTASPPVVASPPVTTASPPVVASPPVTTASPPVVASPPVTTASPPVVASPPVTTASPPVVASPPVTASSPPVVASPPVTASSPPVASPPVTAS		Ì			1		
AASPSPAASPAUTASPPLPAASPALASPHTI ASPPVHVASPPVHTASPPLPAASPALASPHTI ASPPVHV		İ		1	ĺ		PAASPAPAESTA\PQPLILLPKP/PPAPGAPPPRP
ASPAPPAASPVLTASPPLPAASPVHTASPP ASPPVHNASPPVHTASPPVHNASPPVHTASPP ASPPVHNASPPVHTASPPVHNASPPVHNASPPVHNASPPVHVA		ļ		İ			GAPPPRPAASPSPAASPAPPAASPVLTASPPLP
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SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A-Alanine C-Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
437	1787	A	3554	5157	2939	PXSARSCWMRKG  AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG SASGCRYAAHPHWGLGGAAAAGGSWEPQPP RPVCEPAGRGKPHPPAAPRSPLLPGSRRRPHA AQPGARARTSPPPASARNMAARPAATLAWSL LLLSSALLREGCRARFVAERDSEDDGEEPVVF PESPLQSPTVLVAVLARNAAHTLPHFLGCLER LDYPKSRMAIWAATDHNVDNTTEIFREWLK NVQRLYHYVEWRPMDEPESYPDEIGPKHWP TSRFAHVMKLRQAALRTAREKWSDYILFIDV DNFLTNPQTLNLLIAENKTIVAPMLESRGLYS NFWCGITPKGFYKRTPDYVQIREWKRTGCFP VPMVHSTFLIDLRKEASDKLTFYPPHQDYTW TFDDIIVFAFSSRQAGIQMYLCNREHYGYLPIP LKPHQTLQEDIENLIHVQIEAMIDRPPMEPSQ YVSVVPKYPDKMGFDEIFMINLKRRKGQGGD RWLRTLYEQEIEVKIVEAVDGKALNTSQLKA LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK LMDNIDQAQLDWELIYIGRKRMQVKEPEKA VPNVANLVEADYSYWTLGYVISLEGAQKLV GANPFGKMLPVDEFLPVMYNKHPVAEYKEY YESRDLKAFSAEPLLIYPTHYTGQPGYLSDTE TSTIWDNETVATDWDRTHAWKSRKQSRIYSN AKNTEALPPPTSLDTVPSRDEL
438	1788	A	3563	130	527	IFFNSSSLFCRVFCLFLRWSFTLVAQARVQ*C NLSSLQPLPPGFK*FSCLSPPRS*DYRRPPPRPA NFLYF**RQGFTVLGQAGLELLT/S/GDPPTSA SQSAGITGVSHRAWPVHAISTHISLVKTRPSLT TLG
439	1789	Α	3565	446	1834	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSY GQPSLQDELKDNTTVFTRILDRLLDGYDNRL RPGLGERVTEVKTDIFVTSFGPVSDHDMEYTI DVFFRQSWKDERLKFKGPMTVLRLNNLMAS KIWTPDTFFHNGKKSVAHNMTMPNKLLRITE DGTLLYTMRLTVR\AECPMAFGRDFPM\D\AH ACPLKFGSYAYTRAEVVYEWTREPARSVVV AEDGSRLNQYDLLGQTVDSGIVQSSTGEYVV MTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSF WLNRESVPARTVFGVTTVLTMTTLSISARNSL PKVAYATAMDWFIAVCYAFVFSALIEFATVN YFTKRGYAWDGKSVVPEKPKKVKDPLIKKN NTYAPTATSYTPNLARGDPGLATIAKSATIEP KEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLL FGIFNLVYWATYLNREPOLKAPTPHQ
440	1790	A	3568	1	350	STSSCFPAAAAAIMREIVHLQAGQCGNQIĞAK FWEVISDEHGIDPTGTYHGDSDLQLERINVYY NEATGEAPVPSPTALRGPRGPCLG*RPPVPAG GKYVPRAVLVDMEPGTMDSV
441	1791	A	3569	2	1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDVS EEIIQYVLSIESAEEIREYVTDLLQGNEGKKGQ FIEELITKWQKNDQELISDPLQQCFKKDEILDG QKSGDHLKRGRKKGRNRQEVPAFTEPDTTAE VKTPFDLAKAQENSNSVKKKTKFVNLYTREG QDRLAVLLPGRHPCDCLGQKHKLINNCLICG RIVCEQEGSGPCLFCGTLVCTHEEQDILRGDS NKSQKLLKKLMSGVENSGKVDISTKDLLPH QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQVI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  DDESDYFASDSNQWLSKLERETLQKREEELR ELRHASRLSKKVTIDFAGRKILEEENSLAEYH SRLDETIQAIANGTLNQPLTKLDRSSEEPLGVL
						VNPNMYQSPPQWVDHTGAASQKKAFRSSGF GLEFNSFQHQLRIQDQEFQEGFDGGWCLSVH QPWASLLVRGIKRVEGRSWYTPHRGRLWIAA TAKKPSPQEVSELQATYRLLRGKDVEFPNDY PSGCLLGCVDLIDCLSQKQFKEQFPDISQESDS PFVFICKNPQEMVVKFPIKGNPKIWKLDSKIH QGAKKGLMKQNKAV
442	1792	A	3576		2019	MPRSHTGERLCEGKEGSQCAENFSPNLSVTK KTAGVKPYECTICGKAFMRLSSLTRHMRSHT AIRANEKPYKCKEC\GRAFSLSQILSK\HERSH TGEKPYKCKQCGKTFIYHOPFQRHERTHIGEK PYECKQCGKALSCSSSLRVHERIHTGEKPYEC KQCGKAFSCSSSIRVHERTHTGEKPYACK\EC GKAFIS\TTSVLTHMITHNGDRPYKCKECGKA FIFPSFLRVHERIHTGEKPYKCKQCGKAFRWS TSIQIHERIHTGEKPYKCKECGKAFSRISYFRIHERT HTGEKPYECKCGKTFNYPLDLKIHKRNHTG EKPYECKECAKTFISLENFRRHMITHTGDGPY KCRDCGKVFIFPSALRTHERTHTGEKPYECKQ CGKAFSCSSYIRIHKRTHTGEKPYECKECGK AFIYPTSFQGHMRMHTGEKPYKCKECGKAFS LHSSFR\RHTRIHNYEKPLEC*Q\CGKAFSVSTS LKKPMRNAQSDRKLY\KCEK*EKVFNSNRCF QSCENSH*REKSCQCK*YRKRDTR*FMYSQV PHNHVSVSNGPYR\CGSPIRLYNT*NISINRNL VAVVTP*CSTLFKCLWCWCKRAALSVV*/IVQ DSGRGWLTPVIPALWEAKAGGSRGQEIKTIL ANTVKPHLY
443	1793	A	3578	287	114	DFYERKFEQFIEGHKQIVNKWRDLLCSWKRK LSIIKKSVLQNNL*FSAASMRFQKVFF
444	1794	٨	3582	3335		HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT MTKVTLENFYSNLIAQHEEREMRQKKLEKV MEEEGLKDEEKRLRRSAHARKETEFLRLKRT RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH VYAMKILRKADMLEKEQVGHIRAERDILVEA DSLWVVKMFYSFQDKLNLYLIMEFLPGGDM MTLLMKKDTLTEEETQFYIAETVLAIDSIHQL GFIHRDIKPDNLLLDSKGHVKLSDFGLCTGLK KAHRTEFYRNLNHSLPSDFTFQNMNSKRKAE TWKRNRRQLAFSTVGTPDYIAPEVFMQTGYN KLCDWWSLGVIMYEMLIGYPPFCSETPQETY KKVMNWKETLTFPPEVPISEKAKDLILRFCCE WEHRIGAPGVEEIKSNSFFEGVDWEHIRERPA AISIEIKSIDDTSNFDEFPESDILKPTVATSNHPE TDYKNKDWVFINYTYKRFEGLTARGAIPSYM KAAK
445	1795	A	3584	1	6169	RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFD GGSRGKGEHFPYEQEIKFFAKVVLPLIDQYFK NHRLYFLSAASRPLCSGGHASNKEKEMVTSL FCKLGVLVRHRISLFGNDATSIVNCLHILGQT LDARTVMKTGLESVKSALRAFLDNAAEDLE KTMENLKQGGFTHTRNQPKGVTQIINYTTVA LLPMLSSLFEHIGQHQFGEDLILEDVQVSCYRI LTSLYALGTSKSIYVERQRSALGECLAAFAGA FPVAFLETHLDKHNIYSIYNTKSSRERAALSLP TNVEDVCPNIPSLEKLMEEIVELAESGIRYTQ

SEQ ID NO: of nucl- eotide seq- uence	SFQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \¬possible nucleotide insertion  MPHVMEVILPMLCSYMSRWWEHGPENNPER AEMCCTALNSEHMNTLLGNILKIIYNNLGIDE GAWMKRLAVFSQPIINKVKPQLLKTHFLPLM EKLKKKAATVVSEEDHLKAEARGDMSEAEL LILDEFTTLARDLYAFYPLLIRFGDYNRAKWL KEPNPEAEELFRMVAEVFIYWSKSHNFKREE QNFVVQNEINNMSFLITDTKSKMSKAAVSDQ ERKKMKRKGDRYSMQTSLIVAALKRLLPIGL NICAPGDQELIALAKNRFSLKDTEDEVRDIIRS NIHLQGKLEDPAIRWQMALYKDLPNRTDDTS DPEKTVERVLDIANVLFHLEQKSKRVGRRHY CLVEHPQRSKKAVWHKLLSKQRKRAVVACF RMAPLYNLPRHRAVNLFLQGYEKSWIETEEH YFEDKLIEDLAKPGAEPPEEDEGTKRVDPLHQ LILLFSRTALTEKCKLEEDFLYMAYADIMAKS CHDEEDDDGEEEVKSFEEKEMEKQKLLYQQ ARLHDRGAAEMVLQTISASKGETGPMVAAT LKLGIAILNGGNSTVQKMLDYLKEKKDVGF FQSLAGLMQSCSVLDLNAFERQNKAEGLGM VTEEGSGEKVLQDDEFTCDLFRFLQLLCEGH NSDFQNYLRTQTGNNTTVNIIISTVDYLLRVQ ESISDFY WYYSGKDVIDEQGQRNFSKAIQVA KQVFNTLTEYIQGPCTGNQQSLAHSRLWDAV VGFLHVFAHMQMKLSQDSSQIELLKELMDLQ KDMVVMLLSMLEGNVVNGTIGKQMVDMLV ESSNNVEMILKFFDMFLKLKDLTSSDTFKEYD PDGKGVIFKRDFHKAMESHKHYTQSETEFLL SCAETDENETLDYEEFVKRFHEPAKDIGFNVA VLLTNLSEHMPNDTRLQTFLELAESVLNYFQP FLGRIEIMGSAKRIERVYFEISESSRTQWEKPQ VKESKRQFIFDVVNEGGEKEKMELFVNFCED TIFEMQLAAQISESDLNERSANKEESEKERPEE GGPRMAFFSILTVRSALFALRYNILTLMRMLS LKSLKKQMKKVKKMTVKDMVTAFFSSYWSI FMTLHFVASVFRGFFRIICSLLLGGSLVEGA KKIKVAELLANMPDPTQDEVRGDGEEGERKP LEALLANMPDPTQDEVRGDGEEGERKP LEALLANMPDPTQDEVRGDGEEGERKP LEALLANMPDPTQDEVRGDGEEGERKP LEALLANMPDPTQDEVRGDGEEGERKP LEALLANMPDPTQDEVRGDGEEGERKP LEACLANSPDVPMPEVQE KFQEQYKLIPHNPNAGLSDLMSNPVPMPEVQE KFQEQYKLIPHNPNAGLSDLMSNPVPMPEVQE KFQEQYKLIPHNPNAGLSDLMSNPVPMPEVQE KFQEQXKLEEKEEKEEKEETKSEPEKAEGEGDGE
						VLLTNLSEHMPNDTRLQTFLELAESVLNYFQP FLGRIEIMGSAKRIERVYFEISESSRTQWEKPQ VKESKRQFIFDVVNEGGEKEKMELFVNFCED TIFEMQLAAQISESDLNERSANKEESEKERPEE QGPRMAFFSILTVRSALFALRYNILTLMRMLS LKSLKKQMKKVKKMTVKDMVTAFFSSYWSI FMTLLHFVASVFRGFFRIICSLLLGGSLVEGA KKIKVAELLANMPDPTQDEVRGDGEEGERKP LEAALPSEDLTDLKELTEESDLLSDIFGLDLKR EGGQYKLIPHNPNAGLSDLMSNPVPMPEVQE KFQEQKAKEEEKEEKEETKSEPEKAEGEDGE KEEKAKEDKGKQKLRQLHTHRYGEPEVPESA FWKKIIAYQQKLLNYFARNFYNMRMLALFV AFANFILLFYKVSTSSVVEGKELPTRSSSENA KVTSLDSSSHRIIAVHYVLEESSGYMEPTVRIL PILHTVISFFCIIGYYCLKVPLVIFKREKEVARK LEFDGLYITEQPSEDDIKGQWDRLVINTQSFP NNYWDKFVKRKVMDKYGEFYGRDRISELLG
446	1796	A	3592	1 3	355	MDKAALDFSDAREKKKPKKDSSLSAVLNSID VKYQMWKLGVVFTDNSFLYLAWYMTMSVL GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV RAGGGIGDEIEDPAGDEYEIYRIIFDTTFFFFVI VILLAIIQGLIIDAFGELRDQQEQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLF FLMYLINKDETEHTGQESYVWKMYQERCWE FFPAGDCFRKQYEDQLN AGLELLNSDDPPALASQSAGITGVTRTPSLFF* DTVLLCCSGWSAVAPSRLTAALFS*AQAVCL SLPRSWDYRRW/PPHPANFCIFCRDE/SLA/ML PRLVSNSWTQAILLPRPPKMLGLQV

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible mucleotide deletion, \=possible nucleotide insertion
447	1797	A	3598	1202	1070	LFVGGGPICPEGASGFAPGPAPAPRVGVDAEV GR*V*GAAASQGA/GSLRPRPTGPGHPGAWL QVWGAAAVCAGPAM*/AVRAKRGPRAG*EP NSPWRSGVLAA\RAVGAGPWP*P*PGCS*ARG PSSRSAPGLASGPAAPLLQGVHSSAGPLLCYI NGTLALGLKP**AWGWGEWRPKG
	1798	A	3604	3115	557	FRRKGGGFKDFGAGLKYNSRHEKVNGLEE GVEFLPVNNVKKVEKHGPGRWVVLAAVLIG LLLVLLGIGFLVWHLQYRDVRVQKVFNGYM RITNENFVDAYENSNSTEFVSLASKVKDALKL LYSGVPFLGPYHKESAVTAFSEGSVIAYYWSE FSIPQHLVEEAERVMAEERVVMLPFRARSLKS FVVTSVVAFPTDSKTVQRTQDNSCSFGLHAR GVELMRFTTPGFPDSPYPAHARCQWALRGD ADSVLSLTFRSFDLASCDERGRHLVITVYNTVL SPMEPHAVLVQLCGTYPPSYNLTFHSVQNVL LITLITNTERRHPGVFEATFFQLPRMSSCGGRL RKAQGTFNSPYYPGHYPPNIDCTWNIEVPNN QHVKVRFKFFYLLEPGVPAGTCPKDYVEING EKYCGERSQFVVTSNSNKITVRFHSDQSYTDT GFLAEYLSYDSSDPCPGQFTCRTGRCIRKELR CDGWADCTDHSDELNCSCDAGHQFTCKNKF CKPLFWVCDSLNDCGDNSDEQGCSCPAQTF RCSNGKCLSKSQQCNGKDDCGDGSDEASCP KVNVVTCTKHTYRCLNGLCLSKGNPECDGK EDCSDGSDEKDCDCGLRSFTRQARVVGGTD ADEGEWPWQVSLHALGQGHICGASLISPNWI. VSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPFFNDFTFDYDIALL ELEKPAEYSSMVRPICLPDASHVFPAGKAIWV TGWGHTQYGGTGALILQKGEIRVINQTTCEN LLPQQITPRMMCVGFLSGGVDSCQGDSGGPL SSVEADGRIFQAGVVSWGDGCAQRNKPGVY
449	1799	A	3618	2	613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQ EMTRRPSLMAGRQHGWSAQQSATVANPVPG ANPDLLPHFLGEPEDVYIVKNKPVLLVCKAV PATQIFFKCNGEWVRQVDHVIERSTDGSSGLP TMEVRINVSRQQVEKVFGLEEYWCQCVAWS SSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSL EQGIVLPCRPPEGIPPAE
450	1800	A	3620		2676	MEPSLGQGMDLTCPFGVSPACGAQASWSIFG ADAAEVPGTRGHSQQEAAMPHIPEDEEPPGE PQAAQSPAGQQGPPTAGVSCSPTPTIVLTGDA TSPEGETDKNLANRVHSPHKRLSHRHLKVST ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN LALLEEAKLVSERFLTRRGRKSRSSPGDSPSA VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPVEKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE HRETYQKLLEDIAVLHRLAARLSSRAEVVGA

					<del>, _ , _ , _ , _ , _ , _ , _ , _ , _ , _</del>	7
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P-Proline,
uence			914	ng to first	acid residue	Q-Glutamine, R-Arginine, S-Serine,
	1	ĺ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ .		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	i	1	peptide		/=possible nucleotide deletion, \=possible
		<u> </u>	l	sequence		nucleotide insertion
		Ī	1	_		VRQEKRMSKATEVMMQYVENLKRTYEKDH
		<b>!</b>	1			AELMEFKKLANQNSSRSCGPSEDGVLRTARS
		ĺ			•	MSLTLGKNMPRRRVSVAVVPKFNALNLPGQ
		1				TPSSSSIPSLPALSESPNGKGSLPVTSALPALLE
		1	I			NGKTNGDPDCEASAPALTLSCLEELSQETKA
		{		1		RMEEEAYSKGFQEGLKKTKELQDLKEEEEEQ
		ł	1			KSESPEEPEEVEETEEEEKDPRSSKLEELVHFL
		ł				QVMYPKLCQHWQVIWMMAAVMLVLTVVL
					]	GLYNSYNSCAEQADGPLGRSTCSAAQKDSW
	Į	ļ		1	1	WSSGLQHEQPTEQ
451	1801	A	3623	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI
	1007	1	1	1 ***		RHORIHTGEKPYECKVCGKAFRVSSQLKQHQ
	İ	1	•			RIHTGERPYOCKELKGRGAEMLAVLAVKEQ
						NRTPVNYGK
452	1802	Α.	3628	2	195	MTCLHSAKAFHY*SSCSFSCEEGFALIGPEVV
432	1802	1 ^	3020	-	''-	OCTALGVWTAPAPVCIAVOCOHLEALNEGT
		1			1	MG*DYPFTAFAYGSSCKYECHTVYRVRGLD
	ľ	1	1		ĺ	MLHSRGCYLWNGHFTT*EAISCEPLERPCH*S
	Į		1			V*CSFSCEEGFALIGPEVVQCTALGVWTAPAP
	1	1	1	}	}	VCIAVQCQHLEALNEGTMG
453	1803	A	3637	662	142	IQAKGLGIWHVPNKSPMQHWR\KGSLLRYRT
433	1803	] A	3037	002	142	DTGFLOTLGHNLLGIYOKYPVKYGEGKCWT
	ļ	J		ļ	ļ	DIGPLOTEDHINELOTTOKTTVKTGEGKCWT
		1	1			
	ľ				ŀ	AGFVQFRVFNNERAANALCAGMRVTGCNTE
		1			ĺ	HHCIGGGGYFPEASPQQCGDFSGFDWSGYGT
	1004	<del>  .                                     </del>	2641	ļ. <del></del>	-	\HVGYSSSREITE\AAVLLFYR
454	1804	A	3641	T	362	TQVHPAMLGLDELGRSGCGHCTQADLRFGD
	ļ				ļ	AAGRDPGQDNDRNTAEPAFPPPPRVMAAAA
	į	1			1	ALRAPAQSSVTFEDVAVNFSLEEWSLLNEAQ
	<u> </u>	<b></b>	<b></b>	<del> </del>		GCLYHDVMLETLTLISSLGKVLILNCDLS
455	1805	A	3646	2	414	AAAGRGASGALTGEGGGEQGRRVGLGSRAH
	1			İ		SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS
			i		i	RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR
		1				PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE
		<b>_</b>	<u> </u>	ļ <u></u>		SRVRAPSYDDIT
456	1806	A	3656	396	8	QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK
ì						LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW
	İ	1		1	ĺ	P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI
					1	SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
	1	<u></u>		L		F
457	1807	A	3660	14	1961	SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG
	ì	1			1	SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF
`	]	1	1	1	)	TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF
	1					YTRRNTQEWTQEWKECPDYVSAGENSCYFN
		1				SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ
	ł	1			1	PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN
		1			1	ADIQKGWMVLEYELQYKEVNETKWKMMDP
		1		]	1	ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY
	1	1				GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF
	1	1			1	GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI
1		1				KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS
	ļ					DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH
ľ	1	}		}	1	EKLHINLGVKDGDSGRTSCCEPDILETDFNAH
	1	1	1	1	l	DIHEGTSEVAQPORLKGEADLLCLDOKNONN
	1	1	1			
				İ	ì	
						SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE
1						SPYHDACPATÒQPSVIQAEKNKPQPLPTEĞAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS
						SPYHDACPATQQPSVIQAEKNKPQPLPTEĞAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPEMVSLCQENF
						SPYHDACPATÒQPSVIQAEKNKPQPLPTEĞAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS

660 ID	CEO IN	Met	1000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutarnine, R=Arginine, S=Serine,
		1	{	amino acid	of peptide	T-Threonine, V-Valine, W-Tryptophan,
	ł	1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì		1	peptide	1 -	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	1		<u> </u>			PVPDYTSIHIVQSPQGLILNATALPLPDKEFLS
	ſ	1	1	İ	Í	SCGYVSTDQLNKIMP
458	1808	A	3663	154	462	TRAPASGRSGAGLALSANAPDSGGHPGATEG
			1		<b>i</b>	PAGSLAHASGSARGTWRVRGRGSHGWERTV
			j			GAGGCANPVPALHSCASAPRGTGRVSALGPK
			}			TGSSPLSSPKG
459	1809	A	3664	902	135	LGKYNTSMALFDFVLHNSTGEIRYITEDDVIQ
		1				SQNALGKYNTSMALFESNSFEKTILESPYYVD
	)		ļ	1		LNQTLFVQVSLHTSDPNLVVFLDTCRASPTSD
			1			FASPTYDLIKSGCSRDETCK\VYPLFGHYGRF
	ŀ	1	[	1	1	QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRC
	<b>!</b>	1	(	1	1	\NQGCVSRSKRDISSYKWKTDSIIGPIRLKRDR
			i		İ	SAINGNSGFQHETHAEETPNQPFNSVHLFSFM
	•	1	j	ļ	[	VLALNVVTVATITVRHFVNQRADYQ\YQKLQ
	l .	<u> </u>	L		<u> </u>	NY
460	1810	Α	3670	850	557	LGILMSPQVEAGEI*ALLTPPPGCMQFSPLTL/P
		(		1		K*WVSPGLTP/PPPEVPSVFLVEPGLPHAGQA
			1		i	GLDLL\TSGDPPASTSQSARTTDVSHRAQPLAI
		<u> </u>		·		.S
461	1811	A	3671	2472	2099	IGVLAFETGSCSVTRLYCIGIIMPHCSLDLAGS\
	ŀ				1	TSAFRIAGTTSVHHHPQLTFFFFWIETGSHCV
	ļ	i	1			VQTGL*LLALSNPPALASQIAGISGMSHRAWP
	<u> </u>	ļ			l	GLVLYSLEFSLLCASQSLIMLFTCYNE
462	1812	Α	3672	394	110	VKPVNGESKRD*GADTQTCEGEADEQLQT\N
	ļ		}	1	<b>)</b>	CYYD/STKSFFYISCG*K\RKPTWAENRRLNA
		ĺ	1		1	KMFGIPLHSNSDPWGYEEREVIGFHRSRVSRG   HGS
1/2	1813	<del> </del>	3673	348	<del> </del>	ORNPFSAGHPORPPTSGSOSELLAOPRLRPGR
463	1813	Α	30/3	340	1	KSSFSRDQDVW*SQAVPKRQ*QRNPFSAGHP
	}	1	ł		1	QRPPTSGSQSELLAQPRLRPGRKSSFSRDQDV
	j	1	ļ	1	ļ	WPGQKPRPSQQQHQMCASPTLGQRSPFALEP
	ļ	i i	İ	1	<b>,</b>	VPAYHGGRDPFASARPSPVGIPKPRAAPAGG
	İ		1		İ	GWRRIRPKSSTK
464	1814	A	3676	2253	320	PVIORCSOPYGFSLLISFFLKCVSETSQOPPSR
707	1017	^	1 30,0	1 -2233	1 320	KVFOLLPSFPTLTRSKSHESQLGNRIDDVSSM
	•				<b>)</b>	RFDLSHGSPQMVRRDIGLSVTHRFSTKSWLS
		1	1	1	1	OVCHVCOKSMIFGVKCKHCRLKCHNKCTKE
	{	í	1			APACRISFLPLTRLRRTESVPSDINNPVDRAAE
	1	l .		1	İ	PHFGTLPKALTKKEHPPAMNHLDSSSNPSSTT
	1	1	1	i	ł	FSTPSSPAPFPTSSNPSSATTPP\NPSP\GQR\DSR
		1				FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE
	ì					AADGTRLDDQPKADVLEAHEAEAEEPEAGK
	ľ	i	İ	1		SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS
	ł	ì	1	1		VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR
		l	1	!	!	WHGEVAIRLLEMDGHNODHLKLFKKEVMN
		ì	1	1		YROTRHENVVLFMGACMNPPHLAIITSFCKG
				!	1	RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY
		ĺ	1	1	1	LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF
		ł	1	1	ì	\GISGVVP\EGRRENQLKLSHDWLCYLAPEIVR
			1	1	ŀ	EMTPGKDEDOLPFSKAADVYAFGTVWYELO
		Į	]	1	]	ARDWILKNOAAEASIWOIGSGEGMKRVLTS
			1	1		VSLGKEVSENLSACWAFDLQERPS\FSLLMD
		1	i		ŀ	MLEKLPKLNRRLSHPGHF*KSADINSSKVVPR
		1	1	1	ł	FERFGLGVLESSNPKM
465	1815	A	3679	8	803	IPSPAWWNSTWADTFSLLLALAVALYLGYY
.00	10.3	1 ''	1 33/7	۱	~~~	WACVLOTHRAFCASNTEDLETVVNHIKHRYP
			i	ĺ		QAPLLAVGISFGGILVLNHLAQARQAAGLVA
		1	Ì		i	ALTLSACWDSFETTRSLETPLNSLLFNOPLTA
		}	1	1	}	GLCQLVERLSY/E*DLQARTIRQFDERYTSVA
	<u> </u>	<del></del>	Ł	l	L	The state of the s

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- cotide	peptide seq-		USSN	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M-Methionine, N-Asparagine, P-Proline,
uence	derice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ŀ	}	/17	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		j	1	peptide	1 1 1	/-possible nucleotide deletion, \-possible
ļ	l	[	l .	sequence	ŀ	nucleotide insertion
		<b>†</b>				FGYODCVTYYKAASPRTKIDAIRIPVLYLSAA
}		]	J	]		DDPFSTVCALPKQAAQHSPYVALLITARGGHI
		1			\	GFLEGLLPWQHWYMSRLLHQYAKAIFQDPE
ł	ì	1		]		GLPDLRALLPSEDRNS
466	1816	A	3684	3	307	SSQYIVQSKTKIFL*AAREKQ/RHTCRRFSIRLS
į		ł				ANISSQTGEARGQWPSVFKVLKEKKLSTKKS
{		i	ł			FGQK*GR\RKTFPDKQK/LREFDTTRPTIQEML
1		1				TGVLQG
467	1817	A	3687	2465	837	ELPTPLIAAHQLYNYVADHASSYHMKPLRMA
j		ļ				RPGGPEHNEYALVSAWHSSGSYLDSEGLRHQ
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SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  GDDLRQDMLVLQLIQVMDNIWLQEGLDMQ
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PPVNESTKPSPSPWKLTPPMCSIPPVFPPKSGS PTTSWS/PSGHSKLEVERAQTGPFCLHIYCP*P GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY WTGHSFASQAWLRQVPEVSKHLQCPSAESLL TMEYHQPEDPAGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE	470	1929	-	2762	267	1240	
PTTSWS/PSGHSKLEVERAQTGPFCLHIYCP*P GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY WTGHSFASQAWLRQVPEVSKHLQCPSAESLL TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE	4/8	1078	^	3/03	20/	1240	
GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY WTGHSFASQAWLRQVPEVSKHLQCPSAESLL TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			ľ		]		
WTGHSFASQAWLRQVPEVSKHLQCPSAESLL TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPAESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			l				
TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPAESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			Ι .		]		
PDEHPQDTDARDADGEAREREP/RRPSFAA*P VWGQPAESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			l				
VWGQPESPLPEASSAPPGPTLGTLPEVETIRA CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			!				`
CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE			1				
	i		Ì	1	(	ľ	`
OTPLITOSTNGPLPSPCHHEHPLSSVEGEAPPA	ļ		l	1			
Q				<u></u>	L		QTPIITQSTNGPLPSPCHHEHPLSSVEGEAPPA

SEQ ID NO: of	SEQ ID	Met	SEQ	Predicted	Predicted end	
	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	,	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uenœ	LD <b></b>		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
,				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
!!!				peptide	•	/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
<u> </u>						EGSDHIG
479	1829	A	3766	2	2152	YSPIRLLEVCVPLPKIFIKRQAPLKVSLLQDLK
'''						DFFQKVSQVYVAIDERLASLKTDTFSKTREEK
1						MEDIFAOKEMEEGEFKNWIEKMOARLMSSS
1 [						VDTPQQLQSVFESLIAKKQSLCEVLQAWNNR
1 1				Į		LQDLFQQEKGRKRPSVPPSPGRLRQGEESKIS
ļ [						AMDASPRNISPGLONGEKEDRFLTTLSSQSST
		İ		ł		SSTHLOLPTPPEVMSEQSVGGPPELDTASSSE
1 1					i	DVFDGHLLGSTDSQVKEKSTMKAJFANLLPG
1 1						NSYNPIPFPFDPDKHYLMYEHERVPIAVCEKE
1 1					<b>!</b>	PSSIIAFALSCKEYRNALEELSKATQWNSAEE
1						GLPINSTSDSRPKSSSPIRLPEMSGGQTNRTTE
1 1		•		•		TEPQPTKKASGMLSFFRGTAGKSPDLSSQKRE
1				-	1	TLRGADSAYYQVGQTGKEGTENQGVEPQDE
1						VDGGDTQKKQLINPHVELQFSDANAKFYCRL
]		}	}			YYAGEFHKMREVILDSSEEDFIRSLSHSSPWQ
<b>i</b>					ļ	ARGGKSGAAFYATEDDRFILKQMPRLEVQSF
				1		LDFAPHYFNYITNAVQQKRPTALAKILGVYRI
						GYKNSQNNTEKKLDLLVMENLFYGRKMAQ
1		İ				VFDLKGSLRNRNVKTDTGKESCDVVLLDENL
1 1				İ		LKMVRDNPLYIRSHSKAVLRTSIHSDSHFLSS
						HLIIDYSLLVGRDDTSNELVVGIIDYIRTFTWD
1					•	KKLEMVVKSTGILGGQG*MPTVVSPELYRTR
						FCEAMDNYFLMVPDHCTGLGLNC
480	1830	A	3777	251	3	QGCGSAGTLIHY**ECKMVQLLWKTV*QFLI
						KLNIKDPAITLDVYPNEVKNYVRTKTYTQMF
<b>—</b>						I/ANFIMAKSWKQPTHPSVRT
481	1831	Α	3779	333	3	EAAIRQPEPNILDVNQIFKDLAMIIHDQGDLID
		[				SIEANAESSEVLVERAPGQLQRPA\YYQKKSR
1		-	l			KKMCLVVLVQTAIILICERIM*VVYTTKWSPPI VLPVSCFQGQKFN
482	1832	A	3780	2	371	TGGROGKNDHTSITEKPSRDFNRHLITONI*M
402	1032	^	3780	1 2	3/1	PNODMKSSSNSLIIRKVQIKPTILYHHIFTRKA
1 1		ĺ			ĺ	KMKTTDKTKYR*GFKAITTLIHCSQDCKLQ*S
						/L*ENHFMIFPKAEQHITYDTTIPFLR
483	1833	A	3787	43	448	LMKDLSPYVMETHYILNRLNER/RSMWRHIIG
105	.000	١.,	3,3,	1		KLPNTKDOEKILKAIRGRREVIQGS/RQQYRR
		l		1		PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK
i				1	]	LSFNIKGEMTFSDKTEFTTNRPSLKMLLKDRI
1				1		QEEGKMF*KEKCFKRKE
484	1834	A	3798	ī	727	FFFFETESRSVAQAGVQWCNLGSLQALPPGF\
				1		SHSPASASRVAGTTGTRH*ARLIFYIFSRDGVS
1		[	1	ĺ		PC*PGWS*SPDLVIRPP\RLPKCWDYRREPPRP
1				1		A*FFVFI.VE\QGFTMLARMVSIS*PQ/CDLPAS
						VSQNAGITGVSHCAWPCLHFCFFGFFFEMESC
1				ĺ	ĺ	SVAQAEVQWHDLRSLQAPPPGFTPFSCLSLPG
1						SWDYRRPPPRPANF\CIFSRDGVSPC*PGWSRS
L						PDLVIRPPRPPKVLGLQA
485	1835	Α	3802	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPPGF
		1		1		KQFSC\LSLPSSWD*R\PTSRPAKF/C\VIF*DG\V
1				L		SHCQPGWSAVVQPPLH
486	1836	À	3811	378	98	RYD*SSQSENIP\QKEFLLKYP*CTATLGMRN
1				1		MSIMKKKSIFSAEFYKVSLPSLLL\HLLAIEWG
				L		FHIEIQLTIHQHFLNYELESDFVHIVEYM
487	1837	Α	3814	771	320	FDPDWTRAAGIRHEKKPKALAYRRENSPGDL
				į .		PPPPLPPPEEEASWAL/GAEGSRQHVLPGAGA
1 1		-		ŀ		QWGEESGPGRAPGSPAGAPPR*RGLAP\NSRP
1		l				SFLSRGQGTSTCSTAGSNSSRGSSSSRGSRGPG RSRSRSQSRSQSQRPGQKRREEPR

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide scq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C-Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion  FRACLLELIPYAPTLSWTACPPAMAGPRGLLP LCLLAFCLAGFSFVRGQVLFKGCDVKTTFVT HVPCTSCAAIKKQTCPSGWLRELPDQITQDCR YEVQLGGSMVSMSGCRRKCRKQVVQKACCP GYWGSRCHECPGGAETPCNGHGTCLDGMDR NGTCVCQENFRGSACQECQDPNRFGPDCQSV CSCVHGVCNHGPRGDGSCLCFAGYTGPHCD QELPVWQELGFPQNNPRLRKAPNCKCLPG*H RNGLIATPNPCRP
489	1839	A	3822	934	669	FFFSEMESRSVTRLECSGAISAHLRLLGSSNSP ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLL/NLMIHPPRPPKVLGFQA
490	1840	A	3825	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA ASRPEASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQPPPP PPPPPPPQLPQPPPPQAQPLLPQPQPPPPPPPPPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	I Amino said source (A. Al. )
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A-Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
}	1	]	1 .	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ļ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	j	]	] [	peptide	`	/=possible nucleotide deletion, \=possible
<u> </u>	<del></del> -			sequence		nucleotide insertion
	ĺ					YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL
1	1					DSDQVFIGFVLKQFEYIEVGQFRESEAIIPNIFF
						FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR
[	[	1				KAVTHAIPALOPIVHDLFVLRGTNKADAGKE
	1	1	1		•	LETQKEVVVSMLLRLIQYHQVLEMFILVLOO
Ĭ.	ĺ	ŀ	1			CHKENEDKWKRLSRQIADIILPMLAKQOMHI
ŀ		1	Ì			DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF
1	1 1		- 1			VTPNTMASVSTVQLWISGILAILRVLISQSTED
		ļ				IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE
}	1 1	1	ł	}		EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT
}		ŀ				KQLKVEMSEQQHTFYCQELGTLLMCLIHIFKS
}	} <b>}</b>	1	- 1	}		GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR
ļ	i l					ARSMITTHPALVLLWCQILLLVNHTDYRWW
-	) <u> </u>	- 1				AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA
	]		Ì	Ť		AKLGMCNREIVRRGALILFCDYVCQNLHDSE
}	]		}	1		HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI
	ļ <u></u>	}	1	}		HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL
	J	- 1	j	j		ACRRVEMLLAANLQSSMAQLPMEELNRIQEY
	: 1	- 1				LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS
		- 1				PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK
1 1		- 1	[	[		SQCWTRSDSALLEGAELVNRIPAEDMNAFM
·			ŀ			MNSEFNLSLLAPCLSLGMSEISGGOKSALFEA
f [	ĺ	1	İ			AREVTLARVSGTVQQLPAVHHVFQPELPAFP
}						AAYWSKLNDLFGDAALYQSLPTLARALAOY
i i	- 1	į	1	- (	ĺ	LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL
1 !	i	ı	1	}		SWIILIHEQIPLSLDLQAGLDCCCLALQLPGL
1 1	ŀ	ľ	1	1	ľ	WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG
			1	į		EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI
1 1	ł		- 1	ł	ł	TAACEMVAEMVESLQSVLALGHKRNSGVPA
1			1			FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG
1 1	1	1		}	1	WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYR INTLGWTSRTQFEETWATLLGVLVTQPLVME
[		ŀ			į	QEESPPEEDTERTQINVLAVQAITSLVLSAMT
1 1	1	-	1		1	VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK
					1	LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD
}	1	- 1	1	1	1	PVPSLSPATIGALISHEKLLLQINPERELGSMS
1 1	1	- 1	1			YKLGQVSIHSVWLGNSITPLREEEWDEEEEEE
] ]	J	J	J	]	,	ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
] [				ŀ		LELYSRWILPSSSARRTPAILISEVVRSLLVVS
j f	J			J		DLFTERNQFELMYVTLTELRRVHPSEDEILAO
[ [		-	1	[		YLVPATCKAAAVLGMDKAVAEPVSRLLESTI
1 1		1		}		RSSHLPSRVGALHGVLYVLECDLLDDTAKOL
[ [	1	ſ	ĺ	-	1	IPVISDYLLSNLKGIAHCVNIHSOOHVLVMCA
	-	ļ				TAFYLIENYPLDVGPEFSASIIOMCGVMLSGS
[	1	ĺ	i		- 1	EESTPSIIYHCALRGLERLLLSEQLSRLDAESL
	l	- 1	- 1	1	1	VKLSVDRVNVHSPHRAMAALGLMLTCMYT
·	}	1	1	- 1	1	GKEKVSPGRTSDPNPAAPDSESVIVAMERVS
ļ [		-			1	VLFDRIRKGFPCEARVVARILPQFLDDFFPPQ
i /		}	1	1		DIMNKVIGEFLSNQQPYPQFMATVVYKVFQT
		]				LHSTGQSSMVRDWVMLSLSNFTQRAPVAMA
! !		I	}	}		TWSLSCFFVSASTSPWVAAILPHVISRMGKLE QVDVNLFCLVATDFYRHQIEEELDRRAFQSV
					[ ]	LEVVAAPGSPYHRLLTCLRNVHKVTTC
491	1841	3	826 4	69 3	02	SNPPASASRVAGITGVHQHAWLIFVFLVEMEF
				-	13	HHVGQAVLKLLISGDLPVSASQSA
492	1842	3	836 3	92 8	8	VAPSPMIMPOLYFYRDPEEIKEE*AAAEK\EE
1	İ		1	1	1 1	FQSEWTAVV/P/EFTATQSEVADWFKDMQVP
J		J		-	] :	SVPIQQFPTEDWST*PTMNDWSATSTAQTTE
						WVRITTEWP

SEQ ID	SEO ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
1		l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	1		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	į	09/496	correspondi		
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	Į.		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		J		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	L		L .	sequence	<u></u>	nucleotide insertion
493	1843	Α	3838	19	380	TPSDMNRAFETDTQSIGEKNRSPSEPDYFERK
ŀ		ł		Ì	ì	KFKRS*EKAHIRYKIDQPEDIPLK\EFLCKHSK
	•	i		1	!	CTATLSMRNMSLMKKKCSFSEEF\LAFFPSLL
i	ļ	l	1	1 _	i	VCHLLAIKLGFYIEIHLTTFNNTF
494	1844	Α	3845	2	352	FFFLRRSL/DSVAQAEAQWL\ELGLLQAPPPGF
ł	1	1		ł		KPISLP\GLPSSWDYGRPPPCPANFCIF/M*RRG
	ĺ	ļ	1			FTVLARMVLIS*PCDPPTLASQGTAITGMSYH
ŀ		ļ	i			ARPQDIDFLYAHQGRCWFRLL
495	1845	A	3847	1774	40	DIFFRRAKEGMGQDEAQFSVEMPLTGKAYL
1						WADKYRPRKPRFFNRVHTGFEWNKYNQTHY
ł	]					DFDNPPPKIVQGYKFNIFYPDLIDKRSTPEYFL
	1	i		Ì		EACADNKDFAILRFHAGPPYEDIAFKIVNREW
	-		1			EYSHRHGFRCQFANGIFQLWFHFKRYRYRR*
1	ļ	1	1			RPWGTAGRCPRGHSKGASVKLVVTPGPLSGL
	!	i				QGRGFTSHLRPHLSFARPQFPPI*KGGHH*AC
	i					HGELRRHWDRLA*GPDATEGALGASFEHEG
	1	ì			ì	GQQPPADLTVQADTLHRPSARLGGAHRACPK
	ì			ĺ		RRPHRVLWRWARGAWAWRCQAREKQETQG
	1	Į		Ì		QPCHITGHPLGREAEPAAAGAAPALAHRPPF
	ļ	1	•			ARTGSTE\PGPCWRPIRHCRRDPLWTPTLC\RD
	i					WPPTHPVLAGGVHFPAAG/IGGCVEVPVSVN
1	ļ			j	ļ	=
	ļ			1		VMGTKSH*AVLPPPPSTGPGGGGLPEGWGLE
1				į		KGEGLPPGIPPPGLLTGPW\SMRPVTPSFAHIR
				1	1	TVAPSHSPFSGQEGRGPHGCHSPGR\SGP\AGR
	ļ		1	1		LVLQHPTGTSPTEAKRKVPPGPPEGHPTSPVT
		ļ				SPRPPTAPPRHPASSGNSSVCFSKKTCRWEKK
	-	ļ				SFVLMELAYWQDRMFF
496	1846	Α	3849	830	442	AKSPLPLG*IQWR/NLGSLKLRLPGFK*FTCLG
1			İ	ĺ		LLSSWDYRSLPPRPVNFCILVELGFHHVDQAG
1						LKLLTSSALPALASQSAEITGMSHRIWPLPLLR
	ļ			l 		RPPVIRIRAPPQRLPFNLITSLKALSPNMATF
497	1847	Α	3859	2	393	ALRKTRRDGIARTGAQPAASWKGTNNYPWR
ł	1					LEMAGRPGSQEQSKDRGTGSLPPPSQRPLGPS
l	1	ŀ			}	PEGAGPSPPPPGIPRGGGSSSSEGP/PQLLFVPR
i				i		RFPAPKKGLPSDTPHSKAPPTPHLILGGEDSQ
					L	VPIL
498	1848	Α	3860	253	634	KNASTVYSSQGDPKSFFFLLRWSLALVAQAG
1	] .					EQ*RDLSSLQPPPPGFK*FSCLSLPSSWD\YRCP
	1	l		ĺ		LPCLANF\*FLVETGFHHVGQADLKLLTSGDP
[	1	[			1	PTSASESAGITGVSHRAWPRIHFLYWKTFFL
499	1849	A	3863	423	263	APSQISVAFLYAA/DKLFEKEI*KKIPFIIAS/DKI
		1				KIGINLTKEVKYLYTENYITLMKEIK/DTDKW
1						KDILY*WIGKINI*KMSTPPKAIYRFNAIPTKIP
1	1	ĺ	1			MTFFTEIEKSIIKFIWNHKKPPNTQSNIEQKE*S
	1	Į.	1		1	FCSILLWVFGGFLWPHMNFMIDFSISVKNVIGI
						LVGIALNL
500	1850	A	3865	2	15246	LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP
300	1030	^	3603	*	13240	DLRPWASDLDIMGDAEGEDEVQFLRTDDEV
]	]	}	1			VLQCSATVLKEQLKLCLAAEGFGNRLCFLEP
į	Ì	]	Į.		Ì	
1		1				TSNAQNVPPDLAICCFVLEQSLSVRALQEML
1		1	1	ļ		ANTVEAGVESSQGGGHRTLLYGHAILLRHAH
i	1	ł	1	į		SRMYLSCLTTSRSMTDKLAFDVGLQEDATGE
1	1	]	1			ACWWTMHPASKQRSEGEKVRVGDDIILVSVS
ĺ	1	1	1			SERYLHLSTASGELQVDASFMQTLWNMNPIC
1	1	1				SRCEEGFVTGGHVLRLFHGHMDECLTISPADS
1	ì	1	i			DDQRRLVYYEGGAVCTHARSLWRLEPLRIS
1						WSGSHLRWGQPLRVRHVTTGQYLALTEDQG
	1	1				LVVVDASKAHTKATSFCFRISKEKLDVAPKR
ļ	}	1	I		<b>J</b>	DVEGMGPPEIKYGESLCFVQHVASGLWLTYA
				· — — — — — — — — — — — — — — — — — — —		

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of		1100		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-					
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline, O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	, , , , ,
}		l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	!		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i				peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	Ĭ	1				APDPKALRLGVLKKKAMLHQEGHMDDALSL
	ļ					TRCQQEESQAARMIHSTNGLYNQFIKSLDSFS
1	ĺ	İ				GKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPS
1						EDLQHEEKQSKLRSLRNRQSLFQEEGMLSMV
1			ĺ			LNCIDRLNVYTTAAHFAEFAGEEAAESWKEI
1		ļ				VNLLYELLASLIRGNRSNCALFSTNLDWLVS
1			i			KLDRLEASSGILEVLYCVLIESPEVLNIIQENHI
1						KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV
	ł			Ì	'	RSNQDLITENLLPGRELLLQTNLINYVTSIRPN
1			l	l	:	IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ
]		1			,	ATHLRVGWALTEGYTPYPGAGEGWGGNGV
1			1			GDDLYSYGFDGLHLWTGHVARPVTSPGQHL
		<b>!</b>	}	j		LAPEDVISCCLDLSVPSISFRINGCPVQGVFESF
		•				NLDGLFFPVVSFSAGVKVRFLLGGRHGEFKF
		l		[		LPPPGYAPCHEAVLPRERLHLEPIKEYRREGP
		ļ	i	) :		RGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPH
i						LERIREKLAENIHELWALTRIEQGWTYGPVRD
						DNKRLHPCLVDFHSLPEPERNYNLQMSGETL
1	İ	1	[			KTLLALGCHVGMADEKAEDNLKKTKLPKTY
	l			ļ.		MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE
ł						NGHNVWARDRVGQGWSYSAVQDIPARRNPR
)	!	]	1	ļ		LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY
ļ	l		1			NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV
]			1	ļ		QSGRWYFEFEAVTTGEMRVGWARPELRPDV
				•		ELGADELAYVFNGHRGQRWHLGSEPFGRPW
1	1	1	l	Ì		QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS
]						ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD
[						VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS
1		Ì	ĺ	1		KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR
	İ					LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR
ł			1			CTAGATPLAPPGLQPPAEDEARAAEPDPDYE
1			j		·	NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ
ļ			1			AGGEAQPARAENEKDATTEKNKKKGFLFKA
ì		i				KKVAMMTQPPATPTLPRLPHDVVPADNRDD
!						PEIILNTTTYYYSVRVFAGQEPSCVWAGWVT
1	ļ		Į.	i		PDYHQHDMSFDLSKVRVVTVTMGDEQGNV
1			1	1		HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL
						VIGCLVDLATGLMTFTANGKESNTFFQVEPN
1			[	Ì		TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA
1		Į.		1		AMFQSERKNPAPQCPPRLEMQMLMPVSWSR
1	1	-	!	1		MPNHFLQVETRRAGERLGWAVQCQEPLTMM
						ALHIPEENRCMDILELSERLDLQRFHSHTLRL
1	1	1				YRAVCALGNNRVAHALCSHVDQAQLLHALE
1			1	1		DAHLPGPLRAGYYDLLISIHLESACRSRRSML
(	1	[	1	1		SEYIVPLTPETRATTLFPPGRSTENGHPRHGLP
1		1	!		_	GVGVTTSLRPPHHFSPPCFVAALPAAGAAEAP
	1		i		,	ARLSPAIPLEALRDKALRMLGEAVRDGGQHA
						RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE
	1					DVKQILKMIEPEVFTEEEEEEDEEEGEEEDEE
	1			1		EKEEDEEETAQEKEDEEKEEEEAAEGEKEEG
		1	1			LEEGLLQMKLPESVKLQMCHLLEYFCDQELQ
		1	l	Į.		HRVESLAAFAERYVDKLQANQRSRYGLLIKA
						FSMTAAETARRTREFRSPPQEQINMLLQFKDG
		1				TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD
				1		GEEEPEEETTLGSRLMSLLEKVRLVKKKEEK
1			1	ĺ		PEEERSAEESKPRSLQELVSHMVVRWAQEDF
1						VOSPELVRAMFSLLHRQYDGLGELLRALPRA
1						YTISPSSVEDTMSLLECLGOIRSLLIVOMGPOE
1			1	1		ENLMIQSIGNIMNNKVFYQHPNLMRALGMIE
1	1	ĺ	1		ľ	TVMEVMVNVLGGGESKEIRFPKMVTSCCRFL
L	L		L	L	L	I A IMPEA IM A LOCOLOGE SPETITLE LIMITAL SCCKUT

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C-Cysteine, D-Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion
						CYFCRISRQNQRSMFDHLSYLLENSGIGLGM QGSTPLDVAAASVIDNNELALALQEQDLEKV VSYLAGCGLQSCPMLVAKGYPDIGWKPCGG ERYLDFLRFAVFVNGESVEENANVVVRLLIR KPECFGPALRGEGGSGILLAAIEEAIRISEDPAR DGPGIRRDRRREHFGEEPPEENRVHLGHAIMS FYAALIDLLGRCAPEMHLIQAGKGEALRIRAI LRSLVPLEDLVGIISLPLQIPTLGKDGALVQPK MSASFVPDHKASMVLFLDRVYGIENQDFLLH VLDVGFLPDMRAAASLDTATFSTTEMALAV NRYLCLAVLPLITKCAPLFAGTEHRAIMVDS MLHTVYRLSRGRSLTKAQRDVIEDCLMSLCR
		•				YIRPSMLQHLLRRLVFDVPILNEFAKMPLKLL TNHYERCWKYYCLPTGWANFGVTSEEELHL TRKLFWGIFDSLAHKKYDPELYRMAMPCLC AIAGALPPDYVDASYSSKAEKKATVDAEGNF DPRPVETLNVIIPEKLDSFINKFAEYTHEKWAF DKIQNNWSYGENIDEELKTHPMLRPYKTFSE KDKEIYRWPIKESLKAMIAWEWTIEKAREGE EEKTEKKKTAKISQSAQTYDPREGYNPQPPDL SAVTLSRELQAMAEQLAENYHNTWGRKKKQ ELEAKGGGTHPLLVPYDTLTAKEKARDREKA QELLKFLQMNGYAVTRGLKDMELDSSSIEKR FAFGFLQQLLRWMDISQEFIAHLEAVVSSGRV
						EKSPHEQEIKFFAKILLPLINQYFTNHCLYFLS TPAKVLGSGGHASNKEKEMITSLFCKLAALV RHRVSLFGTDAPAVVNCLHILARSLDARTVM KSGPEIVKAGLRSFFESASEDIEKMVENLRLG KVSQARTQVKGVGQNLTYTTVALLPVLTTLF QHIAQHQFGDDVILDDVQVSCYRTLCSIYSLG TTKNTYVEKLRPALGECLARLAAAMPVAFLE PQLNEYNACSVYTTKSPRERAILGLPNSVEEM CPDIPVLERLMADIGGLAESGARYTEMPHVIE ITLPMLCSYLPRWWERGPEAPPSALPAGAPPP CTAVTSDHLNSLLGNILRIIVNNLGIDEASWM KRLAVFAQPIVSRARPELLQSHFIPTIGRLRKR
				10		AGKVVSEEEQLALEAKAEAQEGELLVRDEFS VLCRDLYALYPLLIRYVDNNRAQWLTEPNPS AEELFRMVGEIFIYWSKSHNFKREEQNFVVQ NEINNMSFLTADNKSKMAKAGDIQSGGSDQE RTKKKRRGDRYSVQTSLIVATLKKMLPIGLN MCAPTDQDLITLAKTRYALKDTDEEVREFLH NNLHLQGKVEGSPSLRWQMALYRGVPGREE DADDPEKIVRRVQEVSAVLYYLDQTEHPYKS KKAVWHKLLSKQRRRAVVACFRMTPLYNLP THRACNMFLESYKAAWILTEDHSFEDRMIDD LSKAGEQEEEEEEVEEKKPDPLHQLVLHFSRT
						ALTEKSKLDEDYLYMAYADIMAKSCHLEEG GENGEAEEEVEVSFEEKQMEKQRLLYQQARL HTRGAAEMVLQMISACKGETGAMVSSTLKL GISILNGGNAEVQQKMLDYLKDKKEVGFFQS IQALMQTCSVLDLNAFERQNKAEGLGMVNE DGTVINRQNGEKVMADDEFTQDLFRFLQLLC EGHNNDFQNYLRTQTGNTTTINIIICTVDYLL RLQESISDFYWYYSGKDVIEEQGKRNFSKAM SVAKQVFNSLTEYIQGPCTGNQQSLAHSRLW DAVVGFLHVFAHMMMKLAQDSSQIELLKEL LDLQKDMVVMLLSLLEGNVVNGMIARQMV DMLVESSSNVEMILKFFDMFLKLKDIVGSEAF QDYVTDPRGLISKKDFQKAMDSQKQFSGPEI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C-Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  QFLLSCSEADENEMINCEEFANRFQEPARDIG FNVAVLLTNLSEHVPHDPRLHINFLELAESILE YFRPYLGRIEIMGASRRIERIYFEISETNRAQW EMPQVKESKRQFIFDVVNEGGEAEKMELFVS FCEDTIFEMQIAAQISEPEGEPETDEGAGA AEAGAEGAEGAAGLEGTAATAAAGATARV VAAAGRALRGLSYRSLRRRVRRLRRLTAREA ATAVAALLWAAVTRAGAAGAGAAAGALGL LWGSLFGGGLVEGAKKVTVTELLAGMPDPT SDEVHGEQPAGPGGDADGEGASEGAGDAAE GAGDEEAVHEAGPGGADGAVAVTDGGFFR PEGAGGLGDMGDTTPAEPPTPEGSPILKRKLG VDGVEEELPPEPEPEPEPELEPEKADAENGEK EEVPEPTPEPPKKQAPPSPPPKKEEAGGEFWG ELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN FILLFYKVSDSPPGEDDMEGSAAGDVSGAGS GGSSGWGLGAGEEAEGDEDENMVYYFLEES TGYMEPALRCLSLLHTLVAFLCIGYNCLKVP LVIFKREKELARKLEFDGLYTTEQPEDDDVKG QWDRLVLNTPSFPSNYWDKFVKRKVLDKHG DIYGRERIAELLGMDLATLEITAHNERKPNPP PGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLG WYMVMSLLGHYNNFFFAAHLLDIAMGVKTL RTILSSVTHNGKQLVMTVGLLAVVVYLYTVV AFNFFRKFYNKSEDEDEPDMKCDDMMTCYL FHMYVGVRAGGGIGDEIEDPAGDEYELYRVV FDITFFFFVIVILLAIIQGLIIDAFGELRDQQEQV KEDMETKCFICGIGSDYFDTTPHGFETHTLEE HNLANYMFFLMYLINKDETEHTGQESYVWK
501	1851	A	3869	467	665	MYQERCWDFFPAGDCFRKQYEDQLS  VIVAIYCQLIFDKGAKTIQ*PFQQIAL/CKRMK LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV
						N
502	1852	A	3888	1042	724	SGMQWRDLTPLQPLPPRFKQFSCLSLPGSWD YRHAP\PLLTNF\*FLVEMGFCYVGQAGRKLL ASSDQSALASQSAGITGISTAPGPPFFFLNFEA GSCSVAQAGVQ
503	1853	A	3891	1773	1193	EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR QDYRSSLPHLASCCYYYYYYVVFL*RRGLTTL VQGGI.KLLPSSNPFASAP*TAGITGMSHCAGP HFNF*MFRKISCIRE*F*HTRIYDIPFLILFFKET WVLLCYPGWPQIPGLKPSSCLRLLSSWDHRC APPCPASFFIFHVDRVSPPCPGLVSITFKMLLL L
504	1854	В	3896	279	70	MVSKSKSILMSYNHVELTFSDMKKMPEAFRR TQKHTIYLIPYQVIFWSTGKDAMRSFMMPFY QKEYYENQ*
505	1855	A	3899	2	1396	EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG NENTKLELRKVPPELNNISKLNEHFSRFGTLV NLQVAYNGDPEGALIQFATYEEAKKAISSTEA VLNNRFIKVYWHREGSTQQLQTTSPKVMQPL VQQPILPVVKQSVKERLGPVPSSTIEPAEAQS ASSDLPQVLST\LLA*QKQCIIQLL/WKAAQKT LLVSTSAVDNNEAQKKKQEALKLQQDVRKR KQEILEKHIETQKMLISKLEKNKTMKSEDKAE IMKTLEVLTKNITKLKDEVKAASPGRCLPKSI KTKTQMQKELLDTELDLYKKMQAGEEVI'EL RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA VHGRGRGRGRGRGRGRGVPGHAVVDHRPRALEIS

nucleotide coride colded corresponding uence unce colded corresponding to first amino acid residue. Personal corresponding to first amino acid residue of peptide sequence peptide sequence sequence peptide sequence sequence peptide sequence sequence peptide sequenc	SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A-Alanine C=Cysteine, D-Aspartic Acid, E=Glutamic Acid,
Sequence	nucl-			in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
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Freiduc of	uence			914		l '	
		1					
						sequence	
AFTESDREDLLPHRQYGEEDCQIDDSSLHAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKLAWN   VITEKTRABEARAAWHARKEQOLKAWAWASSUBOCKOWO   SQRLLNEWMYEHFRQOMLDVAELCQES   GLSVDPSQKEPFVEINRILEALKVRVLRPALE   WAYSNREMIAQNSSLERKLHRYSLILMG   GTTNOREALQYARNFQPFALNHQKDIQVTM   GSLYVLRQGEERSPYVILLDANQWADICDIFT   RDACALLGLSVESPLSVSTSAGCVALPALININ   AVEQRCTIGVWHQKDELPEVDLG*KSAGY   HSFRACPILRQQTTDNNPPMKLVCGHISKDAL   NEMFNOSKLKCFVCPMEQSNDAKQIFF   SGROVILLCKAQAHLCRGEDSKDAKQIFT   RDACALLGLSVESPLSVSTSAGCVALPALININ   NEMFNOSKLKCFVCPMEQSNDAKQIFF   SGVTILLCKAQAHLCRGEDSKDAKQIFT   SGVTILLCKAQAHLCRGEDSKDAKGSTSTOQ   WPEG-GAWGMPCGPAUGSCFFOTTVQ   RPAKQRDKRRRHLGR   WCPAGTLDFPGPOPMYLLEEVMNQLNIRRIL   GULVAAIETPHEIVLI-MENYECPK*W*GLGGGFTTHAGASRGGVCAHSIEGGELFERVINGUNIRRIL   GULVAAIETPHEIVLI-MENYECPK*W*GLGGGTTHAGASRGGVCAHSIEGGELFERVINGUNIRRIL   FLY   STANGARGAWASTAGA   STANGARGAWASTAG				ł		1	
					sequence		
DIHSSYSRVGKADDKYPDOISSVGIGUCWQA							VITFKTRAEAEAAAVHGARFKGQDLKLAWN
DSORLINEWMYEHFROGMLDVAEELCOES   GLSVPDSOKEPFELRRILAYRVILRALE   WAYSINEMILAQNSSLEFKLHRILYFILLMG   GTTNOREALQYAKINGPPALBLMG   GTTNOREALQYAKINGPPALBLMG   GTTNOREALQYAKINGPPALBLMG   GTTNOREALQYAKINGPPALBLMG   GTTNOREALGYAKINGPALBLMG   GTTNOREALGYAKINGPALBLMG   GTTNOREALGYAKINGPALBLMG   GTTNOREALGYAKINGKALGHISDDALGHE   RDACALLGISSPST-VHLLDANQWADICDIFT   RDACALLGISSPST-VHLDANQWADICDIFT   RDACALLGISSPST-VHLDANGKAGHISRDAL   NKMFNOSKLKCPYCPMEOSRODAKQHF   HSFSCPLIRGOTDAPPPLFERSGGHISPTAGALPR   SHGVYLLCKAGAHLCRGEBSAGGHISGTGAGA   PGGGARCHPPSTCSPSWASPC*GAKASPALPR   SHGVYLLCKAGAHLCRGEBSAGSTSQA   WEPG*GAWGMPRCQGPALGSCFCPPGTTVQ   RPAKGRDIKRRHLGR   WCPAGTLDFFCPQEMYLLEREWMOLNHRNL   ICLVAALETPHEIVLFMCHYSCW*WGLGGGT   TRHGASRGGVCAHSIEGGELFERIVDEDYHLT   FV	506	1856	Α	3911	1952	919	DAELSGTLSLVLTQCCKRIKDTVQKLASDHK
GISYDPSQKEPPVELNRILEALKVRVLRPALE							1
WAVSNRÉMLIAQNSSLEFKLIRLYTISLLMG   GITTNQREALQYAKNEQPAHNQKDIQVLM   GSLVYLRQGIENSPYVHLLDANQWADICDIFT   RDACALLGLSVESPLSVESPAGCVALPALINIK   AVEGRQCTGVWNQKDELPIEVADICKSAGV   HSTRACPIL RQQTTDNNPPMKL VCGHIISRDAL   NKMFNGSKLKCPYCPMEQSRCDAKQIFF			Į.				, · · · · · · · · · · · · · · · · · · ·
GTTNQREALQYAKNFQPFALNHQKDIQVLM	İ				1		
GSL-YLRQGIENSPY-WILLDANQWADICDIFT	Ì	l	İ			ĺ	
RDACALLĞLSVEŞILSVŞSRAGCYALPALINIK			]				
HSFACPILRQQTTDNNPPMELVCHIISRDAL   NKMPNGSKLKCPVCPMEQSPGDAKQIF			]		ļ		
NKMPNGSKLKCPYCPMEGSPGDAKQIFF						,	• •
1857   A   3936   439   18	1	ì	ĺ				
PGGGARCHPPSTCSPSWASPG*GAKASPALDR   SHGVTILCKAQAHLCRGEDSKDASGSTSQA   WPGG*GAWGMPRGQGPALGSCFCPFGTTVQ   RPAKQRDKRNRHLGR     SHEVEN   WCPAGTLDPFGPGEMVLLEIEVMNQLNHRNL   IQLYAAIETPHEIVLFMEYECPK*W*GLGGGT   TRHGASRGGVCAHSIEGGEFERIVDEDYHLT   EV     SHEVEN   SHEV	507	1957	<b>-</b>	7026	420	10	
SHGVITLICKAQAHLICGGEDSKDASGSTSQA   WPG9GAWGMPG9GAWGAWGMPG9GAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGMPGGAWGWAWGWAWGWAWGWAWGWAWGWAWGWAWGWAWGWA	) JU /	1657	A	3930	439	10	
WEPG*GAWGMPRCQPALGSCFCPPGTTVQ   RPAKQRDKRNRHLGR		[					
1858							
IQLYAAIETPHEIVLFMEYECPK**W*GLGGTTTRHGASRGGVCAHSIEGGELFERIVDEDYHLT   FUND   1859   A						<u> </u>	
TRHGASRGGVCAHSIEGGELFERIVDEDYHLT EV	508	1858	A	3944	120	412	
S09		١.					
1859   A   3949   31   392	•		[				1
MVFFLQNFC/RIILNVA\WTGD*PNTL*KEQRG   ITFSDSKS*YKATKKTMWYCHKNRYID/ERN   RIEIPENPECDKIJFRKI.SMTTQ	509	1859	Α	3949	31	392	
RIEJEINPCICDKJIFRKLSMITQ	]					1.	l l
1860							ITFSDSKS*YKATKIKTMWYCHKNRYID/ERN
SASSVAATTG  SASSVAATTG  SASSVAATTG  PPAWAPRSPLIWAPTSGRHPCRAALPWSTSSV RWOPSEKOPPPAHRGPADSLSTAAGAAELS AEGAGKSRGSGEQDWVNRPKTVRDTLLALH QHGHSGPFESSFKKEPALTAVARTARKREPS PEPEGEVGPPK\TTERPSRGCPHPQRGSRSP*L LHPLLCRHHPLPHLPTGPHRLKRPRMP\SP MAALILVADNAGGSHASKDANQVHSTTRRN SNSPPSPSSMNQRRLGPREVGQGAGNTGGL EPVHPASLPDSSLATSAPLCCTLCHERLEDTH FVQCPSVPSHKFCFPCSRQSIKQQGASGEVYC PSGEKCPLVGSNVPWAFMQGEIATILAGDVK VKKERDS  512 1862 A 3957 1086 3 QDRARLDCSSATSAHCNLRLPGS*DSPASASR VAGTTDTHHHTWLILGSSVQTGFDHVGQAG LELLTSGDPPISASESAGIMGMSHCVWPYSWG LSHHMAPPQGDGGRARGTPGPEQSFWNLSC H*PRCQVPS*LMTQL/FWGRHQYNPTMKRGK LRHREACSLPLPGEGEPGLQPSS*SQ\PCSSPL FHHGL*AWLWCPELLLQGQARH*RSPPS/FK CPATLSLTAWSQTKRLRSQFLLLPWL*RAL*H PPCHWPSRSLSDFLPRSQG*RDGT*ASTFC SY**PTESHLVAQAGVQWRDLGSLQPPCPRL K\RFSRLSPPSSYTHRYVPSHLAESCISSRDRIP PSRPDRSRNSNSLSR  513 1863 A 3961 3038 476 VALTTSMCCNKQVIVIDKIKSASIADRCGALH VGDHILSIDGTSMEYCTLAEATQFLANTTDQ VKLEILPHHQTPLALKGPDHVKIQRSDRQLT WDSWASNHSSLHTNHYNTYHPDHCRVPAL TFPKAPPPNSPPALVSSSFPTSMSAYSLSSLN							
1861	510	1860	A	3954	1013	885	
AEGAGKSRGSEQDWVNRPKTVRDTLLALH QHGHSGPFESKPKKEPALTAVARTARKRKPS PEPEGEVGPPK\TTERPSRGCPHPQRGSRSP*L LHPLLCLRHHPLPHLPTGPHRLKRPRM\PSP MAALIL\VADNAGGSHASKDANQVHSTTRRN SNSPPSPSSMNQRRLGPREVGGQGAGNTGGL EPVHPASLPDSSLATSAPLCTLCHERLEDTH FVQCPSVPSHKFCFPCSRQSIKQQGASGEVYC PSGEKCPL\VGSNVPWAFMQGEIATILAGDVK VKKERDS  512 1862 A 3957 1086 3 QDRARLDCSSATSAHCNIRLPGS*DSPASASR VAGTTDTHHTWLILGSSVQTGFDHVGQAG LELLTSGDPFISASESAGIMGMSHCVWP*SWG LSHHMAPPQGDGRARGTPGPEQSFWNLSC H*PRCQVPS*LMTQL/FWGRHQYNPTMKRGK LRHREACSLPLPGEGEPGLQPSS\*SQNPCSSPL FHHGL*AWLWCPELLLQGQARRH*RSPPS/FK CPATLSLTAWSQTKRLRSQFLLLPWL*RAL*H PPCHWPSRRSLGDPLLPRSQG*RDGT*ASTFC SYF*DTESHLVAQAGVQWRDLGSLQPPCPRL K\RFSRLSPPSSYTHRYVPSHLAESCISSRDRIP PSRPDRSRNSNSLSR  513 1863 A 3961 3038 476 VALTTSMCCNKQVTVIDKIKSASIADRCGALH VGDHILSIGGTSMEYCTLAEATQFLANTTDQ VKLEILPHHQTRLALKGPDHVK\QRSDRQLT WDSWASNHSSLHTNHHYNTYHPDHCRVPAL TFPKAPPPNSPPALVSSSFSPTSMSAYSLSSLN	511	1861	A	3956	1	1054	
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DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL ARFYIAELTCAVESVHKMGFIHRDIKPDNILID RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL CDWWSVGVILFEMLVGQPPFLAQTPLETQM KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFP*NHTTPTDTSNFDPVDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHIPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMGIFLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF 519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV					!		
ARFYIAELTCAVESVHKMGFIHRDIKPDNILID RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL CDWWSVGVILFEMLVGQPPFLAQTPLETQM KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFP*NHTTPTDTSNFDPVVDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRDXSFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMGVFLH VGQAGLELLTSGDLPALASQSAGITGNSHRAR PENGFENIF  519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV				1	j	]	
RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL CDWWSVGVILFEMLVGQPPFLAQTPLETQM KVINWQTSLHIPPQAKLSPEASDLIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFF*NHTTPTDTSNFDPNVDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTFLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		i					ARFYIAELTCAVESVHKMGFIHRDIKPDNILID
RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL CDWWSVGVILFEMLVGQPPFLAQTPLETQM KVINWQTSLHIPPQAKLSPEASDLIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFF*NHTTPTDTSNFDPNVDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTFLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		1	Ì	1	! !	l	RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP
CDWWSVGVILFEMLVGQPPFLAQTPLETQM KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV				1		1	RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA
KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFP*NHTTPTDTSNFDM\DPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF 519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		1					
DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS AFKQFP*NHTTPTDTSNFDPNVDPDKL WSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV  517 1867 A 3980 1358 1022 FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD/SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF 519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		1	1	1	i (	ļ	CDWWSVGVILFEMLVGQPPFLAQTPLETQM
AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN EEENVNDTLNGWYKNGKHPEHAFYEFTFRF FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV QNTGSEIKNRDLVYV  FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		1					
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QNTGSEIKNRDLVYV				1			EEENVNDTLNGWYKNGKHPEHAFYEFTFRRF
S17		}	Į.	i	_	Į	FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD
VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD *RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518  1868  A 3986  974  666  SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519  1869  A 3994  751  126  NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		<u></u>	<u></u> _	L	L	L	
*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA QAIFQPQPPKVLGLQV  518 1868 A 3986 974 666 SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VQQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV	517	1867	A	3980	1358	1022	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
QAIFQPQPPKVLGLQV		)	1			}	VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD
1868   A   3986   974   666   SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF     519   1869   A   3994   751   126   NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV				1			
SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  519  1869  A 3994  751  126  NQGLRHVGLCRTCLVNQMFASSILGKSHIHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV						<u> </u>	L
VGQAGLELLTSGDLPALASQSAGITG\SHRAR PENGFENIF  1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHIS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV	518	1868	Α	3986	974	666	1
PENGFENIF  1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHIHIS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV							
519 1869 A 3994 751 126 NQGLRHVGLCRTCLVNQMFASSILGKSHHHS LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV		1	1	}		ļ	
LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV	_						1
DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV	519	1869	A	3994	751	126	NQGLRHVGLCRTCLVNQMFASSILGKSHHHS
QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV							LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC
		1					DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS
		}	Į	}			
		<u> </u>	<u>L</u>	<u> </u>			HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTP

		1 - 2 -	T'ono	T-5 - 1,-	- <del> </del>	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C-Cysteine, D-Aspartic Acid, E-Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	
nucl-	peptide	ľ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	<b>,</b>	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	İ	ĺ	Ī	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon.
				residue of	sequence	
		1	1	peptide		/=possible nucleotide deletion, \=possible
		ļ	<u> </u>	sequence		nucleotide insertion
			1		1	LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
	10.50	ļ.,	<u> </u>			AHV\FADLLLITLPSYYIPFC
520	1870	A	3999	882	698	QSFRLSLLSSWDYRHM*PRLANF*TVFFCRDR/
		L				SLALLPRLVSNSWPQAILPPRPPKVLGLQT
521	1871	Α	4011	1346	1178	FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
						PPTSASHVAGATGTHHHAWLLSV
522	1872	A	4015	2	377	QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
				1	ļ	IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
	1				1	EYGPVYSTWSALEGELAEPLEGVSACIGNCST
						AL*ELTDDMTEDFLFVLREYILYSDSMK
523	1873	Α	4018	341	19	ERVIHNQIQQAQRSPHIFNARRSS/PRPNIVELP
	!					KVKEVCKTSKS/GQVIYKGVSIRLRANFLAEP
	l	ſ	1	1		L*NRREWDEAIKVLKEKQ\FLSKMVYPANLSF
			•		ł	GNEGDITSFPAK
524	1874	Α .	4020	1067	743	FFLRWSL/DSVAQAGVKWCNLGSLQAPPPGF
						TPFSCLSLPSSWDYRHPPPRLAN*LTNFLCF**
		1		ł		RQGFTVLARMVLIS*PHDLPASASQSAGITGL
	1	1		1	ļ	SHCSWPTSSILS
525	1875	A	4021	781	351	QFRVIFFFLRRSHSVAQAGMQWHDHSLLQPL
						PPRLKQ/F/SHLSPPSIWDYRRVPPCLVNFSIFF
						VETGSCOPCLQLLGSSNPPASASQSAGIAGISH
		ł	i	1		QGQPE*SFDIRFACVIAALRETFQCLCSASRVN
			1			NKIINRPTHPVESSF
526	1876	Α	4024	80	341	TPSSTSRGTEEQQSSKMAWQRREEKEHLNVR
	1			1	1	RSSAEDGWKADKP/VDG*TPGEDHLPTPSPFQ
	]	İ		ł		LHIHSSESQLHHSVKSPPSLSFRLM
527	1877	A	4026	593	230	DFYLYPERKKRGQMMTAVSLTTRPQESVAFE
						DVAVYFTTKEWAIMG\PAERALYRDVMLEN
		1				YGGCGPL*CHPTSKPALVFS\LEQGKESCFSPA
		1	i			TGSSLSRNDWRAGWIGYLELRRYTYLS
528	1878	A	4028	1160	242	GTSELLCIQRWNWGPAFPPRPGLALAPTLQLL
		' '		1		VEMGSAKSVPVTPARPPPHNKHLARVADPRS
	l	1	1	ŀ	<b>;</b>	PSAGILRTPIQVESSPQPGLPAGEQLEGLKHAQ
						DSDPRSPTLGIARTPMKTSSGDPPSPLVKQLSE
						VFETEDSKSNLPPEPVLPPEAPLSSELDLPLGT
			1			QLSVEEQMPPWNQTEFPSKQVFSKEEARQPT
			1			ETPVASOSSDKPSRDPETPRSS\GSMRNRWKP\
	Į.	Į.	1	i		NSSKVL\GKSPLHPSCQDDNSPGTLTLRQGKA
			į			AFKPLSENVSELK\EGA\ILGTGR\LLKTEGRA
	1	1				WEQGQD\HDKENQHFPLVES
529	1879	A	4039	2	366	KDMVLIMEMOSMITMKCPQYL*E*RKIPDITK
	1	'-	,	1 -		CW*GCGSTGILIFC/WS*PL*KTI*QPR*FKQI*T
	j	J	}	J		ILTIIYSIM*EHTFHNAGV*LSDIYPRFMKGYV
	1			}		HTEICT*MFIAVLFVVVKTWKQF
530	1880	A	4057	358	3	LLEVNGNTIVTVFTKAQNKKNKGSRSILFKQL
	1000	'`	1057	330		RKYGSRINLLKSKHDKNICTENYKT*MKEIEA
	i	Į .		ļ	}	DTDKWKDILCSWIRRIHMKDILCSWIGRTHV
	1					VKISILPKVNYRFYLISIKIIMAI
531	1881	A	4061	50	278	TOGTEEIYKISSCEWVQASFSTPLITLHDFKIY
231	1001	^	1001	50	270	HKATVIKMVWYWHRO*KFSKN/RIESSEIEPH
	ŀ	1				IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNWIF
	1					T*KR
777	1000	<del></del>	4062		269	
532	1882	Α	4069	19	368	NDLLENFKFWE*FKE*LENINGTVTEKETGGV
		}				YKELSSPKYSGTRQFYGQTISNFPGKIISMVY
		1				KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIYL
		L	<b></b>	·		QIWMPVSLMNIVTLKCPT
533	1883	A	4076	1	355	PIRKFTKVAG*KSNTPK*LAFLHINNEQFENKI/
533	1883	A	4076	1	333	ITNI/PFILASKRIKYSGISLTKEMKDLYTETLLR KIKEDTNKWKDI/SCFWVGR/LNIVKMPK/VIC

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496 914	correspondi	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
				amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
		İ		peptide sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
	1					IFNAIPIKMPMMCMAKIEKNSS
534	1884	A	4088	3	1931	IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVL
						QTRLVDAAKALNLVHCHCLDIFINQAFDMQR DLQITPKRLEYTRKKENELYESLMNIANRKQE
		<u> </u>				EMKDMIVETLNTMKEELLDDATNMEFKDVI
	<u> </u>					VPENGEPVGTREIKCCIRQIQELIISRLNQAVA NKLISSVDYLRESFVGTLERCLQSLEKSQDVS
1		[				VHITSNYLKQILNAAYHVEVTFHSGSSVTRM LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
			•			ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ
	ļ	<u> </u>				LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS LESRSLODVLLHRKPKLGOELGRGQYGVVYL
						CDNWGGHFPCALKSVVPPDEKHWNDLALEF HYMRSLPKHERLVDLHGSVIDYNYGGGSSIA
					ļ	VLLIMERLHRDI.YTGLKAGLTLETRLQIALDV
						VEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKI TDLGFCKPEAMMSGSIVGTPIHMAPELFTGK
						YDNSVDVYAFGILFWYICSGSVKLPEAFERCA SKDHLWNNVRRGARPERLPVFDEECWQLME
ł					1	ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
535	1885	A	4090	2	417	NSEQPNRGLDDST ALMPHEANYEEIFLKTDKDMDGFESGLEVRE
						IFLKTR/GLPSTLLAHIWALCDSKDCGKLSKD HFALAFHLIT\QKLIKGIDPPLVLTPEKISPSNR
						ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
536	1886	A	4102	569	829	HNRKRIWLRA DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
					ļ	PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK EQNLEESHYLDFK*YYRAV
537	1887	Α	4104	54	281	SIDCEHLIRRMLVLDPSKRLTIAQIKEHKWML
						EVPVQRPVLYPQEQENEPSIGEFNEQVLRLM HSLGIDQQKTIE
538	1888	Α	4109	141	314	IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSQPL VPRENITAWMNAIGLIITALPVS
539	1889	A	4111	268	1	ASRPWGHSYP*FNQQEVDTLKRPIASSEI*MM
	1					I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW   PLFPKIYREGTLPHSFYEASITL
540	1890	Α	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE AALGDFLGLHRRTOOPAVDRLLSDASAOWR
		!				VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
	ł	}				GRWRREGCGAGGRGVCVAAWSQRSIAGNN DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH
						IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR CQYFRALLYGGMRESQPEAEIPLQDTTAEAFT
	ł		İ			MLLKYTYTGRATLTDEKEEVLLDFLSLAHKY
						GFPELEDSTSEYLCTILNIQNVCMTFDVASLY SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK
						TALLNIVLRDSFAAPEKDIFLALLNWCKHNSK
			1			ENHAEIMQAVRLPLMSLIELLNVVRPSGLLSP DAILDAIKVRSESRDMDLNYRGMLIPEENIAT
						MKYGAQVVKGELKSALLDGDTQNYDLDHG FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
			]			DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
						WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF ECMFTNKTFTLEKGLIVPMENVATIADCASVI
						EGVSRSRNALLNGDTKNYDWDSGYTCHQLG SGAIVVQLAQPYMIGSIRVLLWDCDDRSY
541	1891	Α	4146	282	778	GTLGYPNGARGQPQDNFFAHQ\VSHHPPISAC

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D-Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  HAESENFAFWQDMKWKNKFWGKSLEIVPVG TVNVSLPRFGDHFEWNKVTSCIHNVLSGQRW IEHYGEVLIRNTQDSSCHCKITFCKAKYWSSN
542	1892	A	4147	44	433	VHEVQGAVLSRSGRVLHRLFGKWHEGLYRG PTPGGQCIWKP SVDAYVCNDIVFSYRTTITLLEGA*LTHRYVA QDPKQGQLRSLHLTCDSAPAGSQGTWSTSCR INHLIFRGGAQITFLATFDDSPKAVLGDRLLLT ANVSSENNTPRTSKTTFQLELSVKDAVYTVV SSH
543	1893	A	4153	678	11	TISYPQCLTQMYFLISFANVDTFLLPIMALDH YVAICSALQ*CSIITP/ELCQGLPVLA*AGSSLIS PVHTVIMSRLAFCSSAQISHFYRDAYLLMKIA CSHT*\NQHVFLGAVVLFLAPCALILVSYIIA AAILRIPSPTRRRKACSICSSHLSLVTLFYGTV LGICI*PPDSFSAQDAIATIMYTVVTSMLNPFIY SLMNKEVQEAVRRLFSRGSHSSWCW
544	1894	A	4158	3	538	LLYAQAGVQ*LNLSSLQPQPAGLKQSSHPSLP SSWDYRYSTPHPANFFVEMEFHHVAQAGLEL LGSGDLPTSTSHSAGITGV\SHHAPPRLISSEGS LLGHLLCLPMVFPLLCVFVLISSSLAGEEAAG LRVQKLWFAVVLSHLPVCWFHCSGIWSEVIE LKVGREGHVLPWQAHVVEF
545	1895	A	4160	1	412	HPLGLGLVPSEIFSPQDKKAADGSILAPARGE DLEAGLKGSFMDGRLQASVSVFRIQRVGSAM QDTASAMPCLPYYPTSHCFMAGGKSRSQGW ELELSGEPAPGWQVLAGYTYTQARYLRDASE ANVGQPLRPVDPR
546	1896	A	4174	1252	1190	FFQVFIFLFLIFFKTEFHSCCPGAVQWHDLDSL QPPPPRFKGFSCLSLPSSWDYRHAPAHPANFV FLVETGFLHV\GQ\ASLELPTSGDTPAS\ASQSA GITGVSHHA*PRASGRRCW
547	1897	A	4176	3029		AGPDGLAAPASCQGARGQTRVPGAFSWLAP GSHHASEGLAPGVPPAGGVSAQELTAPPQEG WGLGAPPAAPRPESDEKRAGSDAVRSFSRGA RDSLGQRRLGGTRGAGPAGKGAQRTMGPAS GFHSFPPRPHQEPSPRSSCWQHLLWHCPWPQ PSRLPRLTPAQLLQGPGVLAAPPGP*HVPGFL AQSPWPLPSGPRSP*DPLHQGALVPLPQGGSP HTAPHCLPSVLSPAIQQPLLPTAST/SSRSPPAS TMAPIPSALAVWEPAGSSPQLSSAPADSSVPLP ALPKVLPPWTQKPLLGCLCQSPLPLLSPPDQI/ RCPPACSPAAASSFSFESQPCPSAPSKASPAPA ALIVGPHHPP*SQQPQSQSVHPHGPGGPQPPL AASSLFWMFCQPPPPHPQFLWHRPLPVTGKA LASYPLCFRPAPGSLRQTPLPPQFHIPRPGLSAP/ PPPASGTSDSSDSRSPSASAARVWPPANSPPPP AARHRPHPPEYFLSPCFFSCGFPRLLGRPRRPQ ALQTPRAWDLPPGSSPAPLCSGPELP*APPPLP PFPRVA*LGSGHPPSAQVPGLW*RCV*GHPIP RPVGHS*SGPPHSPPL*APPQAWPLELPPSRQC LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPGL PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL TTSRSASSLPEVVLASSLPKIPQSSGSPLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAQQHQPSPPSPHARSTLT PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPAH

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide	]	in USSN	nucleotide location		I≈Isoleucine, K≈Lysine, L=Leucine,
cotide	seq- uence		09/496	correspondi	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		}	) /14	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Ì			]	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i		1		peptide	Sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
			<del> </del>	Sequence		GTPASPGLGRSCLGKPQTLPWISFWPPSGRLA
		[	1		1	PGTWQPW/PVSPAPLSCLSAWDPWELPSPQPQ
ļ						VCSTAELPTSCLLSSPGP\PAFQPPRFGCL*GPP
į						GPPGLPPLOSSLSFPPPPPPVPOPPAPPALOWG
		1				LHLPGGRTK
548	1898	A	4180	2369	844	RIHREEDFOFILKGIARLLSNPLLQTYLPNSTK
2.0			1			KIQFHQELLVLFWKLCDFNKVGQPRGALQGD
ļ		ŀ				GEOLPO*PGGRDSVRLRGVGQSCPSLELSPLG
						PSPHP*KFLFFVLKSSDVLDILVPILFFLNDAR
		}	J			ADOSRVGLMHIGVFILLLLSGECNFGVRLNKP
			ļ		1	YSIRVPMDIPVFTGTHADLLIV\VFHKIITSGHQ
		1	ĺ			RLQPLFDCLLTIVVNVSPYLKSLSMVTANKLL
ļ		Į.	ļ	l		HLLEAFSTTWFLFSAAQNHHLVFFLLEVFNNI
1			i	1		IQYQFDGNSNLVYAIIRKRSIFHQLANLPTDPP
1			Í	ĺ	ĺ	TIHKALQRRRRTPEPLSRTGSQGGAPPWRAPA
ŀ			1			PLPLQSQAPSRPVWWLLQALTS*PRSPRCQR
		Ì				MAPCGPWNLSPSRAWRMAARLRGSPARHGG
			1	ļ	Ì	SSGDRP/HSSASGQWSPTPEWVLSWKSKLPLQ
i		1	1		ĺ	TIMRLLQVLVPQVEKICIDKGLTDESEILRFLQ
				ľ		HGTLVGLLPVPHPILIRKYQANSGTAMWFRT
		<u> </u>	<u> </u>			YMWGVIYLRNVDPPVWYDTDVKLFEIQRV
549	1899	A	4191	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKT
		l	ļ			ALLQDGRRKVHYLFPDGKEMAEEYDEKTSE
						LLVRKWRVKSALGAMGQWQLEVGDPAPLG
		1				AGNLGPELIKESNANPIFMRKDTKMSFQWRIR
				ŀ		NLPYPKDVYSVSVDQKERCIIVRTTNKKYYK
	1000	<del></del> _	1100			KFSIPDLDRHQLPLDDALLSFA\TPTAP
550	1900	Α	4192	1	1980	IRHTGSDIAGVCGWLLLSGPCGVGLDLDSRLL
		1		ľ		GASAMRRSEVLAEESIVCLQKALNHLREIWE LIGIPEDORLORTEVVKKHIKELLDMMIAEEE
		1	i			SLKERLIKSISVCQKELNTLCSELHVEPFQEEG
		l				ETTILQLEKDLRTQVELMRKQKKERKQE\LKL
ĺ		i	İ	İ		
1						I I DEODOEI CEIL CMPHADIDS VASABLEEL SO
1	}					LQEQDQELC\EILCMPHYDIDSASVPSLEELNQ
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATL
ļ						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATU QKLLRQVLEMQKSQNEAVCEGURTQIRELW
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQ\PEEEREAVATIMSGSKAKVRK\ALQ\LE
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQI\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQI\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK
						FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQLEMQKSQNEAVCEGURTQIRELW DRLQIPEEEREAVATIMSGSKAKVRKALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQLEMQKSQNEAVCEGURTQIRELW DRLQIPEEEREAVATIMSGSKAKVRKALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATL QKLLRQ\LEMQKSQNEAVCEG\LTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLVICITVCLSYLPE
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLICITVCLSYLPE AG\QYSSFFLYLR\QVIGFG\TVKIAAFIAMVGI
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLVICITVCLSYLPE
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQ\RELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLICITVCLSYLPE AG\QYSSFFLYLR\QVIGFG\TVKIAAFIAMVGI
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQLEMQKSQNEAVCEGURTQIRELW DRLQIPEEEREAVATIMSGSKAKVRKALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLICITVCLSYLPE AGQYSSFFLYLR\QVIGFG\TVKIAAFIAMVGI LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQLEMQKSQNEAVCEGURTQIRELW DRLQIPEEEREAVATIMSGSKAKVRKALQULE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLUCITVCLSYLPE AGQYSSFFLYLRIQVIGFGYTVKIAAFIAMVGI LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML QLAWYGFGSQAWMMWAAGTVAAMSSITFP
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATUL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIELWEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLVICITVCLSYLPE AG\QYSSFF\LYLR\QVIGFG\TVKIAAFIAMVGI LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML QLAWYGFGSQAWMMWAAGTVAAMSSITFP AISALVSRNAESDQQGVAQGIITGIRGLCNGL GPALYGFIFYMFHVELTELGPKLNSNNVPLQ GAVIPGPPFLFGACIVLMSFLVALFIPEYSKAS
551	1901	A	4194	3	1008	FRQHVTTLRETKASRREEF/VSSIKRQIILCME ELDHTPDTSFERDVVCEDEDAFCLSLENIATL QKLLRQ\LEMQKSQNEAVCEG\LRTQIRELW DRLQIPEEEREAVATIMSGSKAKVRK\ALQ\LE VDRLEELEKCKTMKKVIEAIRVELVQYWDQC FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP KLEEELKARIEL WEQEHSKAFMVNGQKFME YVAEQWEMHRLEKERAKQERQLKNKKQTET EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK PVAASTCSGKKTPRTGRHGANKENLELNGSI LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS DSSTVGLQRELSKASKSDATSGILNSTNIQS AWHEGLVSSPAIGAYLSASYGDSLVVLVATV VALLDICFILVAVPESLPEKMRPVSWGAQISW KQADPFASLKKVGKDSTVLLVICITVCLSYLPE AGQYSSFFLYLRIQVIGFGTVKIAAFIAMVGI LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML QLAWYGFGSQAWMMWAAGTVAAMSSITFP AISALVSRNAESDQQGVAQGIITGIRGLCNGL GPALYGFIFYMFHVELTELGPKLNSNNVPLQ

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
552	1902	A	4197	2	14302	ARPPPAPGSRQOKQKAAPGAAAAAELRGAR EPAPARRGTMADGGEGEDEIQFLRTDDEVV LQCTATIHKEQQKLCLAAEGFGRRLCFLESTS NSKNVPPDLSICTFYLEQSLSVRALQEMLANT VEKSEGQVDVEKWKFMMKTAQGGGHRILL YGHAILLRHSYSGMYLCCLSTSRSSTDKLAFD VGLQEDTTGEACWWTIHPASKQRSEGEKVR VGDDLILVSVSSERYLHLSYGNGSLHVDAAF QQTLWSVAPISSGSEAAQGYLIGGDVLRLH GHMDECLTVPSGEHGEEQRRTVHYEGGAVS VHARSLWRLETLRVAWSGSHIRWGQPFRLR HVTTGKYI.SI.MEDKNLLLMDKEKADVKSTA FTFRSSKEKLDVGVRKEVDGMGTSEIKYGDS VCYJQHVDTGLWLTYQSVDVKSVRMGSIQR KAIMHHEGHMDDGISLSRSQHEESRTARVIRS TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR QNLFQEEGMINLVLECIDRLHVYSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIIKEGHIKSIISLLDKHGRNHKVLD VLCSLCVCHGVAVRSNOHLICDNLLPGRDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEPFVTAFATHLRVGWASTEGYSP YPGGGEEWGGNGVGDDLFSYGFDGLHLWSG CLARTVSSPNQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL KVEHSREYKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENIHELWMN KIELGWQYGFVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCOPDQELGSDERAFAPDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSSSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPOFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRYDKDKEATKPETNNHKDYAQEKPSRLKQ RFLLRRTKPPYSTSHSARLTEDVLADDRDY DFLMQTSTYYYSVRIFPGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLLGBEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDLSTYYYSVRIFPGQEPANWWGWITS DFHQYDTGFDLDRVRTVTVTLLGDEKGKVHE SIKRSNCYMVCAGESMSPGGRRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDUSTISERQGWLVQCLDPLQFMSTHLIPEN RSVDILETTEGEELLKFHYHTILRLYSAVCALG NIRVAHALCSHVDEPQLLYAIENKYMPGLLR AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLLI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	<b>j</b>			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1			l .	peptide		/-possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						MGIFHNEDLKHILQLIEPSVFKEAATPEEESDT
						LEKELSVDDAKLQGAGEEEAKGGKRPKEGLL
1	1		İ			QMKLPEPVKLQMCLLLQYLCDCQVRHRIEAI
ì						VAFSDDFVAKLQDNQRFRYNEVMQALNMSA
						ALTARKTKEFRSPPQEQINMLLNFKDDKSECP
1						CPEEIRDQLLDFHEDLMTHCGIELDEDGSLDG
}						NSDLTIRGRLLSLVEKVTYLKKKQAEKPVES
						DSKKSSTLQQLISETMVRWAQESVIEDPELVR
1	}		<b>!</b>			AMFVLLHRQYDGIGGLVRALPKTYTINGVSV
						EDTINLLASLGQIRSLLSVRMGKEEEKLMIRG
			ļ			LGDIMNNKVFYQHPNLMRALGMHETVMEV
1			1	'		MVNVLGGGESKEITFPKMVANCCRFLCYFCR
1 .						ISRQNQKAMFDHLSYLLENSSVGLASPAMRG
ì	! .		<b>!</b>			STPLDVAAASVMDNNELALALREPDLEKVVR
						YLAGCGLQSCQMLVSKGYPDIGWNPVEGER
ł						YLDFLRFAVFCNGESVEENANVVVRLLIRRPE
1	!					CFGPALRGEGGNGLLAAMEEAIKIAEDPSRD
1						GPSPNSGSSKTLDTEEEEDDTIHMGNAIMTFY
1	İ					SALIDLLGRCAPEMHLIHAGKGEAIRIRSILRS
			1			LIPLGDLVGVISIAFQMPTIAKDGNVVEPDMS
						AGFCPDHKAAMVLFLDRVYGIEVQDFLLHLL
1						EVGFLPDLRAAASLDTAALSATDMALALNRY LCTAVLPLLTRCAPLFAGTEHHASLIDSLLHT
						VYRLSKGCSLTKAQRDSIEVCLLSICGQLRPS
	· ·					MMQHLLRRLVFDVPLLNEHAKMPLKLLTNH
			}			YERCWKYYCLPGGWGNFGAASEEELHLSRK
			ŀ			LFWGIFDALSQKKYEQELFKLALPCLSAVAG
	ļ.					ALPPDYMESNYVSMMEKQSSMDSEGNFNPQ
1			1			PVDTSNITIPEKLEYFINKYAEHSHDKWSMDK
						LANGWIYGEIYSDSSKVQPLMKPYKLLSEKE
	Ì		i			KEIYRWPIKESLKTMLARTMRTERTREGDSM
						ALYNRTRRISQTSQVSVDAAHGYSPRAIDMS
1						NVTLSRDLHAMAEMMAENYHNIWAKKKKM
						ELESKGGGNHPLLVPYDTLTAKEKAKDREKA
						QDILKFLQINGYAVSRGFKDLELDTPSIEKRFA
1						YSFLQQLIRYVDEAHQYILEFDGGSRGKGEHF
						PYEQEIKFFAKVVLPLIDQYFKNHRLYFLSAA
	j					SRPLCSGGHASNKEKEMVTSLFCKLGVLVRH
						RISLFGNDATSIVNCLHILGQTLDARTVMKTG
1						LESVKSALRAFLDNAAEDLEKTMENLKQGQF
						THTRNQPKGVTQIINYTTVALLPMLSSLFEHI
1						GQHQFGEDLILEDVQVSCYRILTSLYALGTSK
1						SIYVERQRSALGECLAAFAGAFPVAFLETHLD
					ĺ	KHNIYSIYNTKSSRERAALSLPTNVEDVCPNIP SLEKLMEEIVELAESGIRYTOMPHVMEVILPM
1						LCSYMSRWWEHGPENNPERAEMCCTALNSE
1						HMNTLLGNILKIIYNNLGIDEGAWMKRLAVF
1						SQPIINKVKPQLLKTHFLPLMEKLKKKAATVV
1						SEEDHLKAEARGDMSEAELLILDEFTTLARDL
						YAFYPLLIRFVDYNRAKWLKEPNPEAEELFR
1				1		MVAEVFIYWSKSHNFKREEONFVVONEINN
1			}			MSFLITDTKSKMSKAAVSDQERKKMKRKGD
1				į	l	RYSMOTSLIVAALKRLLPIGLNICAPGDQELIA
		!				LAKNRFSLKDTEDEVRDIRSNIHLQGKLEDP
						AIRWQMALYKDLPNRTDDTSDPEKTVERVL
						DIANVLFHLEOKSKRVGRRHYCLVEHPORSK
] .		,				KAVWHKLLSKQRKRAVVACFRMAPLYNLPR
						HRAVNLFLQGYEKSWIETEEHYFEDKLIEDLA
						KPGAEPPEEDEGTKRVDPLHQLILLFSRTALT
]						EKCKLEEDFLYMAYADIMAKSCHDEEDDDG

NO. of No. of a double bediefe estide estide sequence per publication (continuous) proposed in the continuous proposed in the con	िट के के कि	SEO ID	Met	T SEC	Predicted	Dredicted and	Amino acid sequence (A=Alanine C=Cysteine,
nucheotide sequence unnec unnec desired sequence services of sequence services of peptide sequence seq	SEQ ID	SEQ ID	Met	SEQ ID NO:		Predicted end	
sequence seq	4		100				
uence  ue							
uence    914   anino first anino icd of peptide peptide peptide peptide peptide peptide sequence   Peptide pep		1 '		[			
amino acid residue of septide residue of sequence peptide sequence	1 -	uciice					
residue of peptide sequence   Y-Tyrosine, X-Unknown, **siog codon,	uence	]	ĺ	314			
Poptide   /-possible nucleotide deletion, \( \)	1	1	ł	1			
Sequence   nucleotide insertion			Ī			sequence	
EEEVKSPEKEMBKOKLLYQQARLHDRAGA  EMVLQTISASKGETGPMVAATLKLGIAILNOG NSTVQQKMLDYLKEKKDVGFFQSLAGLMOG CSVLDLNAFERGKOKLLYQQARLHDRAGA NSTVQQKMLDYLKEKKDVGFFQSLAGLMOG CSVLDLNAFERGKOKAFGLGMVYTEGESGEKV LQDDEFTCDLFRFLQLLCEGINSDFONYTT QGCTONQSLAHSLWDAVQKYFNILTE QGCTONQSLAHSLWDAVQKYFNILTE QGCTONQSLAHSLWDAVQKYFNILTE QGCTONQSLAHSLWDAVQKYFNILTE MLSQSSQLELLKELMDLQKDMVVMLIS MLEGNVNNGTIGGKOWDMLVESSNNVEMIL KFFDMFLKUDITSSDTFKEYDPDGKGVISK RPHKAMESHKHYTQSETBFLLSSSNNVEMIL KFFDMFLKUDITSSDTFKEYDPDGKGVISK RPHKAMESHKHYTQSETBFLLGSSNIVAKGATISM FDMFURLOFFLLASSVLNYEPGLRIEMG SAKRIERVYFEISESSRTQWEKPQVKESKGTENE TLDYEEFSKRHEFPAKDIGFROWAVLLTDLSEH MPNDTRLQTFLLEASSVLNYEPGLRIEMG SAKRIERVYFEISESSRTQWEKPQVKESKGTENE TLDYEEGSEKKEMELFVNTECDTREMQLAA QISESDLNERSANKEESSKERFEEQGFRMAFILL FPVVNSGGEKEKMELFVNTECDTREMQLAA QISESDLNERSANKEESSKERFEEQGFRMAFILL ANMPDFTQDEVKGGGEKEKKLYMELL ANMPDTTQDEVKGGGEKKKLYMELL ANMPDTTQDEVKGGGEKKKLYMELL ANMPDTTQDEVKGGGEKKKLYBEL ANMPDTTADEVKYFTENGEGGGVYKLIP HNRNAGLSDIMSNPVRMFEVQEKREGGGVYKLIP HNRNAGLSDIMSNPVRMFEVQEKREGGGVYKLIP HNRNAGLSDIMSNPVRMFEVQEKREGGGVYKLIP HNRNAGLSDIMSNPVRMFEVQEKREGGGVYKLIP HNRNAGLSDIMSNPVRMFEVQEKREGGGVYKLIP FYKVSTSSVVECKELPTRSSSNAAKVTSLDSS SSRIPLASTON FOR FOR FOR FOR FOR FOR FOR FOR FOR FOR	i	i	ľ				
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SAKRIERVÝFEISESSRTQWEKPQVKESKROFI FDVNNEGGEREKHEPVNFCEDTIFEMOLAA QISESDLNERSANKEESEKERPEGOPRMAFF SILTVRSALFALRYNILTIMRMI.SLKSLKKOM KKVKKMTVKDMYTAFFSSYWSIFMTLLHEV ASVFROFFRICSLLLGGSLVEGAKKIKVAELL ANMPDFPIQEVRGDGEGEGERFLEAALPSED LTDLKELTEESDLJSDIFGLDLKREGGQYKLIP HNPNAGLSDLMSNPMEVQEKPGQKAK EEEKEEKETKSEPEKAEGEDGEKEEKAKED KGKQK, RQH.HTM-GPEPVPSSAFWKLIAV QQKLLNYFARSYFWMRM.ALFVAFANFILL FYKVSTSSVVEGKEPTRSSSENAKVISLDSS SHRIIAVHYVLEESSGYMEPTVRILPILHTVISF FCIIGTYCLKVPLVIFKREEKVARKLEFDGLYI TEQPSEDDIKGQWDRLVNITQSEPNYWDKF VKKKVMDKYGEFYGRORISELLGMDKAALD FSDAREKKPKKNSSLSAVLNSIDVKYQMW KLGVVFIDNSFLYLAWYMT  553 1903 A 4199 31 767 LPELNGRGAGLRRAEPSERGGGAERTQQVAA LPI.SHGRGAGLRRAEPSERGGGAERTQQVAA LPI.SHGRGAGLRRAEPSERGGGAERTQQVAA LPI.SHGRGAGLRRAEPSERGGGAERTQQVAA LPI.SHGRGAGLRRAEPSERGGGAERTQDYAL ERADDRSKPVESDADELLFNIPFTGHVKLK GIIMGEDDDSHPSEMRLYKNIPQMSFDDTER EPDQTFSLNRDL.IGELEVATKISRFSNVYHLSI HISKNFGADTTKVFYIGLRGEWTELRHEVTI CNYEASANPADHRVHQVTPQTHETS  554 1904 A 4200 1 961 GIPCTEMGRFDNANVTGEWEFAIHVCFKTHSL EICKACKNILAYGEWTELRHEVTI CNYEASANPADHRVHQVTPQTHETS GIPCTEMGRFDNANVTGEWEFAIHVCFKTHSL EICKACKNILAYGEWTELRHEVTI CNYEASANPADHRVHQVTPQTHETS ONGELTVRAKLVLPSRTRKLQEACPGWKHSFVPSGV TPAQLROSKLELTVNQALFGMNDRILLGGT RIGGSKGDTAVGGARCSKLQWQKVLSSPN LWTDMTLVLH  555 1905 A 4211 331 2419 KENKKARNIVANGGACCSQKLQWQKVLSSPN LWTDMTLVLH WITHERTGNATRSGQNONQTWRAVSRTNP NNGEFRFSLEHVNNENRGFEHGEDYTDDHLS SNROPHTANRQQRSTLSPVARRTRSQJSNNFH NNGEFRFSLEHVNNENRGFHGEDYTDIPLS SNROPHTANRQQRSTSSPVARRTRSQJSNNFH NNGEFRFSLEHVNNENRGFEHGEDYTDIPLS						1	
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SEQ ID NO: of nucl- ectide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion GGAAGIPRANASRTNFSSHTNQSGGSELRQRE GQRFGAAHVWENGARSNVTVRNTNQRLEPI RLRSTSNSRSRSPIQRQSGTVYIINSQRESRPV QQTTRRSVRRRGRTRVFLEQDRERERRGTAY TPFSNSRI.VSRITVFEGEESSRSTAVRRHPTIT LDLQVR\RIRPGENRDRDSIANRTRSRVGLAE NTVTIESNSGGFRRTISRLERSGIRTYVSTITVP LRRISENELVEPSSVALRSILRQIMTGFGELSSL MEADSESELQRNGQHLPDMHSELSNLGTDN NRSQHREGSSQDRQAQGDSTEMHGENETTQP HTRNSDSRGGRQLRNPNNLVETGTLPILRLAH FFLLNESDDDDRIRGLTKEQIDNLSTRHYEHN SIDSELGKICSVCISDYVTGNKLRQLPCMHEF HIHCIDRWLSENCTCPICRQPVLGSNIANNG
556	1906	A	4212	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKR KSPENTEGKDGSKVTKQEPTRRSARLSAKPA PPKPEPKPRKTSAKKEPGAKISRGAKGKKEEK QEAGKEGTAPSENGETKAEEIHISRSTVNVST SRGTPPSTLSVKGQIETVRVKGTEN
557	1907	A	4213	774	507	ARRFSCLTLQTSWGHRH\GPPRP\ANFVFLVET GFLHIGQAGHKLPTSGDPPASASQSARITGMS HRTWFLASFLIDSCKNFIVYKIMYTL
558	1908	A	4225	3	1253	TYRHAEREHPETSSATKVSYDYRHKRPKLLD GDQDFSDGRTQKYCKEEDRKYSFQKGPLNRE LDCFNTGRGRETQDGQVKEPFKPSKKDSIAC TYSNKNDVDLRSSNDKWKEKKKKEGDCRKE SNSSSNQLDKSQKLPDVKPSPINLRKKSLTVK VDVKKTVDTFRVASSYSTERQMSHDLVAVG RKSENFHPVFEHLDSTQNTENKPTGEFAQEIIT IIHQVKANYFPSPGITLHERFSVKMADIHKADV NEIPLNSDPEIHRRIDMSLAELQSKQAVIYESE QTLIKIIDPNDLRHDIERRKERLQNEDEHIFHI ASAAERDDQNSSFSKNYTTQRKDIITHKPFEV EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVQ KSLYIQAKYQRLRFTGPRGFITHKFRERLMRK KKVP
559	1909	Α	4235	i i	323	KFSIPFFLRWSFTLV\PRLEGNDMISVHCNLGL LGLSHSPASASQVGGITGTQHHTGLIFGFLIET EFHHVGQAGLELLTSGDPPALAFQSAGITGVS HHAWLQVLNS
560	1910	A	4246		1569	TLSLLERVLMKDIVTPVPQEEVKTVIRKCLEQ AALVNYSRLSEYAKIEGKKREMYELPVFCLA SQVMDLTIQNQKDAENVGRLITPAKKLEDTIR LAELVIEVLQQNEEHHAEAFAWWSDLMVEH AETFLSLFAVDMDAALEVQPPDTWDSFPLFQ LL'NDFLRTGLLICGNGK\FHKHLQDLFAPLVV R/YMWDLDGSSPIAQSIHRGLLSRESWEPVNN GSGTSEDLFWKLDALQTFIRDLHWPEEFGK HLEQRLKLMASDMIESCVKRTR\LAFEVKLQK TSSIQQIFRVPQFNMAPCFNVMGLMAKGSIQP KL\CSMEMGQEFAKMWHQYHSKIDELIEETV KEMITLLVAKFVTILEGVLAKLSRYDEGTLFS SFLSFTVKAASKYVDVPKPGMDVADAYVTF VRHSQDVLRDKVNEEMYIERLFDQWYNSSM NVICTWLTDRMDLQLHIYQLKTLIRMVKKTY RDFRLQGVLDSTLNSKTYETIRNRLTVEEATA SVSEGGGLQGISMKDSDEEDEEDD
561	1911	Α	4257	1300	654	SELVQFLLIKDQKKIPIKRADILKHVIGDYKDI FPDLFKRAAERLQYVFGYKLVELEPKSNTYIL

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-			in USSN	location	corresponding	I≈Isoleucine, K=Lysine, L=Leucine,
cotide	seq- uence		09/496	correspondi	to last amino	M-Methionine, N=Asparagine, P=Proline,
seq-	delice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
delice			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/-possible nucleotide deletion, \-possible
j		1		sequence		nucleotide insertion
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564	1914	A	4270	3	368	ILKRKLSSLNSEVSTIQNTRMLAFKATAQLFIL
						GCTWCLGLLQVGPAAQVMAYLFTIINSLQGF
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565	1915	Α	4288	83	406	RNSRPLWCSPPASQPRQAPVSQSCCCPLPSSSS
	ļ	l		}	1	PPSALLAPTKPRALGTLRLYECSPELCTTMLP
						PAWLLMLCQAPRPQDPDPRLTQPEKSLQEAP
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566	1916	Α	4298	1041	229	LNSSQKLACLIGVEGGHSLDSSLSVLRSFYVL
ĺ			1			GVRYLTLTFTCSTPWAESSTKFRHHMYTNVS
				1		GLTSFGEKVVEELNRLGMMIDLSYASDTLIRR
			1	1		VLEVSQAPVIFSHSAARAVCDNLLNVPDDILQ
						LLKKNGGIVMVTLSMGVLQCNLLANVSTVA
		1		1		DHFDHIRAVIGSEFIGIGGNYDGTGRFPQGL\E
1		-		Į.		DVSTYPVLIEELLSRSWSEEELQGVLRGNLLR VFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
		ĺ	1	1		FHLGASEWTPRLLIWR
567	1917	A	4299	1	1106	GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
307	1917	^	4277	1 1	1100	DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
						WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ
						MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
	1				l	VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ
	+				1	WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD
		1	1	1	1	NTVVMEEIRRLCRTSVPCAGATAFPADSDRH
				1		CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD
						INEAYVETLKHCFMMPQSLGVIGGKPNSAHY
						FIGYVGEELIYLDPHTTQPAVEPTDGCFIPDES
	ļ	}		1	]	FHCOHPPCRMSIAELDPSIAVVRGGHLSTQAF
		1				GAECCLGMTRKTFGFLRFFFSMLG
568	1918	A	4300	2012	1843	SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS
		1				LMSVLIPKLPQLHGVRIFGINKY
569	1919	Ā	4302	186	531	WTFCLFL/WWVPESARWLLTQGHVKEAHRY
307	1,717	<u></u>	1 .5 42	<u> </u>		1 The same of the same of

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	i=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ŀ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	ł	Į	amino acid	of peptide	7—Theorem N. M. W. S. Serine,
	1	1	· ·	residue of	sequence	T=Threonine, V=Valine, W=Tryptophan,
	ļ	}	į	peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	1	į	sequence	1	/=possible nucleotide deletion, \-possible
		<del> </del>	+	Soquenoc	<del></del>	nucleotide insertion
	ĺ	1	1	1	1	LLHCARLNGRPVCEDSFSQEVRVNVCVSM
	1			İ		CVWWGVGCVKCLPPRAHHIWQEKPLGPH
570	1920	<del> </del>	1222	<u> </u>		VTESKLEAEGKTKEKAREKERKKKS
370	1920	Α	4308	3	869	RSGQGKVYGLIGRRRFOOMDVLFGLNLLT
	1	j		ł		GKRNKLRVYYLSWI.RNKILHNDPEVEKKO
	1	1	[	ſ	ĺ	WTTVGDMEGCGHYRVVKYERIKFLVIALK
						VEVYAWAPKPYHKFMAFKSFADLPHRPLL
	1	ſ	ſ	ĺ	[	DLTVEEGQRLKVIYGSSAGFHAVDVDSGN
	1					DIVIDUALOS OFFICIALIES DATE OF THE CONTROL OF THE C
	1	}	1	1	j	DIYIPVHIQSQITPHAIIFLPNTDGMEMLLCY
	1	i		ł.		DEGVYVNTYGRIIKDVVLQWGEMPTSVAY
	1	ł	i	1	ì	SNQIMGWGEKAIEIRSVETGHLDGVFMHKI
						QRLKFLCERNDKVFFASVRSGGSSQVYFM
571	1921	+ A	4309	J- <u>-</u>	<del> </del>	NKNCIMNW
,,,	1921	^	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEA
	1	]	j ,	ļ		KEHREFRAKTNRDLEIKDOEIEKLRIELDES
	i	1	1 1			QHLEQEOOKAALAREECLRITELLGESPHO
		ł	1			HLTRQEKDSIQQSFSKEAKAQALQAQQREQ
	ĺ	ĺ	í i			LTQKIQQMEAQHDKTENEQYLLLTSQNTFL
	L		}			KLKEECCTLAKKLEQISQ
72	1922	A	4318	i	1119	CATPL COVCORTOYOUR
			10.10	•	1117	GATPLGSVGGRTGKMDAATLTYDTLRFAEI
	}	1 .	1 1			DFPETSEPVWILGRKYSIFTEKDEILSDVASR
	I		[			WFTYRKNFPAIGGTGPTSDTGWGCMLRCG
	1	1 :	i i			MIFAQALVCRHLGRDWRWTQRKRQPDSYF
						VLNAFIDRKDSYYSIHOIAOMGVGFGKSIGC
						WYGPNTVAOVLKKI.AVFDTWSSI AVIIIANA
	[	<b>[</b> [	[			NTVVMEEIRRLCRTSVPCAGATAFPADSDRI
		1		1		CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLY
			1	1		DINEAYVETIAKHCFHGWPQFPG/VVHREGE
		1		!		PNSAHYFIGYVGEELIYLDPHTTQPAVEPTD
	·	1	1	1	ı	CFIPDESFHCQHPPCRMSIAELDPSIAVVRGG
		1				I STOAEGAEGGI CATTRICTION TO THE
73	1923	A	4333	363	1066	LSTQAFGAECCLGMTRKTFGFLRFFFSMLG
i			.555	100	1000	GOVPVGLASKPFQILYGHTNEVLSVGISTELI
- 1	]	ļ	ļ	ļ	1	MAVSGSRDGTVIIHTIQKGQYMRTLRPPCES
						LFLTIPNLAISWEGHIVVYSSTEEKTTLK\ERM
ļ	j	J	j	J	J	HYICFSINGKYLGSOILKEOVSDICIGEHIVTO
1	- 1	- 1	ļ	J	J	SIQGFLSIRDLHSLNLSINPLAMRI.PIHCVCVT
						KEYSHILVGLEDGKLIVVGVGKPAEVKPSISN
- 1	ſ	Ì	ſ	ĺ	1	FISHAVGDYFGSPSFQLIEKSPLGINKLKAKFI
1						FSKGSK
4	1924	A	4346	359	1234	MDTLEEVTWANGSTALPPPLAPNISVPHRCL
Ì	1	- 1	1	- 1		LLYEDIGTSRVRYWDLLLLIPNVLFLIFLLWK
ŧ	- 1	- 1	1	ŀ	}	I PSAD AVIDITOCORDITORIA A PROPERTIE LINE
1	- 1	+				LPSARAKIRITSSPIFITFYILVFVVALVGIARA
- 1	1	1		J	ļ	VVSMTVSTSNAATVADKILWEITRFFLLAIEL
- 1	1	1	İ			SVIILULAFGHLESKSSIKRVLAITTVI SI AYS
- 1	- 1	j	j	1	1	TQGTLEILYPDAHLSAEDFNIYGHGGRQFWL
- 1	l		1	1		VSSCFFFLVYSLVVILPKTPLKERISLPSRRSEN
- 1						VYAGILALLNLLOGLGSVLLCFDIIEGI CCVD
		<del></del>			[	ATTFLYFSFFAPLIYVAFLRGFFGSEPKILF
5	1925	A	4360	2038	1512	<b>GCWWRHPWLASQRDCLDCRIQLAEKFVKAY</b>
1	- 1	- 1	1	ľ		SKPSRPDMNPIRVKEVYRLEEMEKIFVRLEM
	1	- 1		ļ		KIIK GSSGTDKI SALCH I KTEEWEVILAKI AKTEM
-	1	1	1	ł	1.	KIIKGSSGTPKLSYTGRDDRHFVPMGLYIVRT
	1	- 1			į	VNEPWTMGFSKSFKKKFFYNKKTKDSTFDLP
1	J	- 1		J	]	ADSIAPFHICYYGRLFWEWGDGIRVHDSQKP
3	1926	A -	1265	<del>-</del>	{ '	QDQDKLSKEDVLSFIQMHRA
ĭ J	. 720	^ ]'	4365 76	59 :	500	<b>QVEGRQGREVKRTAWRISPVWRPARCRRRST</b>
			İ	[	[ ]	PQP/PE/PGAQOQERHROGEAPMOAL DPRAED
					1	GPQAQSHAACOPEPEPPRVLLDPTAARGGVO
	- 1	1	i	ſ	1 4	GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS
- 1	1	1				OKT/OLSKAPGEAPHPOTHTPWPAGCET BAKE

SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	1	in	nucleotide	Iocation	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Į.	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ł				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
l				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	]	1		peptide sequence		nucleotide insertion
577	1927	A	4366	: 785	502	SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
1 377	1,727	l ^	4500	703	302	ASSNSRASTPKVAGITGARPHARIIFVFLIEMG
				į		FHNVGQAGL/DTLTLVICPPQPPKLLGLQM
578	1928	A	4367	1	221	FFFFLKKSRCVTQAGVQG\PISLHPPPPGFKRF
		1		-		SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
		i				SGWSRTPDLR
579	1929	Ā	4383	1	224	FETESHSVTQAGMQWHNLGSLQPMP/PGLKR
		1				FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
	•					CWPGWSSTPDLK
580	1930	Α	4397	410	94	SRLKPYSTNVTAKKLPATNIPNLDCFTAKLYQ
	i	1				\VFKKGI\IHILHELFQNKEEGAFPNS/FYEASFT
ļ	1	1	1			LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK
	1001	ļ				QLKSSDL
581	1931	Α	4414	670	3	VLVHRQCGGILRLRRKEAVSVLDSADIEVTDS
į.		1				RLPHATIVDHRPQHRWLETCNAPPQLIQGKA
ŀ	}	1	1		]	RSAPKPSQASGHFSVELVRGYAGFGLTLGGG RDVAGDTPLAVRGLLKDGP\AQRCGRLEVGD
}				i		LVLHINGESTQGLT\HAQAVERIRAGGPQLHL
	1	ŀ				VIRRPLETHPGKPRGVGEPRKGVVPSWPDRSP
	1				ì	DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG
				ļ	l	SPE
582	1932	Α	4424	194	449	VLYIRKKKRLEKLRHQLMPMYNFDPTEEQDE
	1					LEQELLEHGRDAASVQAATSVQAMQGKTTL
ł	}					PS\QGPLQRPSRLVFT\DVANAIHV
583	1933	Α	4435	1	166	APGPPVPPPGSPPEQMPGPCPASMPP/DPPPGS
						PPEQMPGPCPVSAPP/GPPPGSPPEQMPGPCPV
504	1004	ļ.,	1420			SAPPALLQDTSV
584	1934	Λ	4439	1	628	SÄTPQQPSAPQHQGTLNQPPVPGMDESMSYQ
			1			APPQQLPSAQPPQPSNPPHGAHTLNSGPQPGT APATQHSQAGPATGQAYGPHTYTEPAKPKK
ĺ	1					GQQLWNRMKPAPGT\EVSSSTSRSDPLLLPPR
	1					ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR
İ	1					GNLSGKPDDWP/LGHERVCGALLHRL*VGGG
	1	ł				QGPHGKAAQGGAAGAAAGRLGLYH
585	1935	Α	4463	10	144	HKPVTNSRDTQEVPLEKAKQVLKIIATFKHTT
						SIFDDFAHYEKRQ
586	1936	Α	4464	1309	103	LNAESYVSFTTKLDIPTAAKYEYGVPLQTSDS
						FLRFPSSLTSSLCTDNNPAAFLVNQAVKCTRK
						INLEQCEEIEALSMAFYSSPEILRVPDSRKKVPI
						TVQSIVIQSLNKTLTRREDIDVLQPTLVNAGH
						FSLCVNVVLEVKYSLTYTDAGEVTKADLSFV
	]	J	] .			LGTVSSVVVPLQQKFEIHFLQENTQPVPLSGN PGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLT
		1				ILHSTTEQDCLALEGVRTPVLFGYTMQSGCK
	ľ					LRLTGALPCQLVAQKVKSLLWGQGFPDYVA
						PFGNSQGP/ADMLDWVPIHFITQSFNRKDSCQ
						LPGALVIEVKWTKYGSLLNPQAKIVNVTANLI
	1				ļ	SSSFPEANSGNERTILISTAVTFVDVSAPAEAG
		<u> </u>				FRAPPAINARLPFNFFFFFV
587	1937	A	4471	614	387	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVF
	1					CKDR/SFTWLPRLVLNSWLQVILLPWPPTGCD
	1000	Ļ.,	<u> </u>			NKHEPPCPATKRRHSGSI
588	1938	A	4480	1720	1458	HDLGSLQPPPPGFKRFSCLSLPSSWDYRLMPP
						CPANFCIII/DFLVETGFHHVGQASHELLTSGD
500	1020	<del> </del>	4407	022	333	PPTSASQSAGITGMSYHTWFGES
589	1939	A	4487	922	332	APVTTSPRVGQPW/RTALALRSLYRARPSLRC PPVELPWAPRRGHRLSPADDELYORTRISLLO
			[ i			REAAQAMYIDSYNSRGFMINGNRVLGPCALL
						PHSVVQWNVGSHQDITEDSFSLFWLLEPRIEI
	L	L	L		L	THE THE THE THE THE THE THE THE THE THE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of nucl-	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
eotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			]	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide	,	/=possible nucleotide deletion, \=possible
			ļ	sequence		nucleotide insertion
			1			VVVGTGDRTERLQSQVLQAMRQRGIAVEVQ DTPNACATFNFLCHEGRVTGAALIPPPGGTSL
		l		1		TSLGQAAQ
590	1940	A	4492	1	472	FFFFETESRSVAOAGVOWRDLGSLOAPPPGFT
3,70	1	1.	1172	*	''-	PFSCLSLPSSWDYRRPPLRPANFFVFLVETGFP
ľ		ľ	Ì		1	RFSRDGLDLLT/S/GDPPTSASQSAGITGVSHR
				İ		ARPKRIGEPRRKCGNAVVWPSTSLGDHRVTS
					j	VPHQGGLPGPIRVAPSSAGQREASQGPPGR
591	1941	A	4495	1444	1116	IAARFTLAKTWNQLKRP\TMIDSIKKTR\YIYT
Į						MEYYADTERNEIMSF\AGTWVELEAIILSKLM
						LKDNWVEDTIPQGAVPCTATAEGMKRLLFAL
	L	1	L			EPWDSSCFPHPSSGV
592	1942	Α	4496	2	919	RTRPLFSGRPTRPVCTMSDERRLPGSAVGWL
			-			VCGGLSLLANAWGILSVGAKQKKWKPLEFL
						LCTLAATHMLNVAVPIATYSVVQLRRQRPDF EWNEGLCKVFVSTFYTLTLATCFSVTSLSYHR
						MWMVCWPVNYRLSNAKKQAGHTVMGIWM
1	Į.			į		GSFILSALPAVGWHDTSERFYTHGCRFIVAEI
	Ì			•		GLGFGVCFLLLVGGSVAMGVICTAIALFQTL
	i		İ			AVQVGRQADHRAFTVPTIVVEDAQGKRRSSI
1	1	ſ	1	1	ĺ	DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL
		Į	1			GPFSLADTHLSDLPYTWGDRDSGGACVM
593	1943	Α	4506	2	193	FFFEAESCSVPQAGVQRPDLGWLHAPPP\GSC
						HFPASASQVAGTTHARHHTQLIF\AFLVENGL
594	1944	A	4507	1327	647	KMAGGVRPLRGLRALCRVLLFLSOFCILSGG
324	1,744	l .,	1307	132,	1 0 17	ESTEIPPYVMKCPSNGLCSRLPADCIDCTTNFS
1			1			CTYGKPVTFDCAVKPSVTCVDQDFKSQKNFII
	ł		}			NMTCRFCWQLPETDYECTNSTSCMTVSCPRQ
						RYPANCTVR\DHVHCLGNRTFPKMLYCNWT
			1			GGYKWVYGLWLLRHHPRWGLGADRF\YLGP
		1				VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG
595	1945	A	4512	533	264	PADGSLYI FFFKMESYSVARLECSGAISAPCNLHLLGSNN
293	1945	A	4512	333	204	SPASASRV/AGNIGARHHTQQIFVLLVQMRVH
1					i	YVGODGLDLL/NLMIHPPRSPKVLGLQA
596	1946	A	4513	3	1674	HASDHLYPNFI.VNELILKQKQRFEEKRFKLD
	•••			ا آ		HSVSSTNGHRWQIFQDWLGTDQDNLDLANV
				Į.	<b>‡</b>	NLMLELLVQKKKQLEAESHAAQLQILMEFLK
		}		1		VARRNKREQLEQIQKELSVLEEDIKRVEEMS
				l .		GLYSPVSEDSTVPQFEAPSPSHSSIIDSTEYSQP
						PGFSGSSQTKKQPWYNSTLASRRKRLTAHFE
				ŀ		DLEQCYFSTRMSRISDDSRTASQLDEFQECLS
			[	1		KF\TRYNSVRPL\ATLSYASDLYNGSQYKSLV
		İ	[	Ì		FEFDRDCDYFAIAGVTKKIKVYEYDTVIQDA
						VDIHYPENEMTCNSKISCISWSSYHKNLLASS   DYEGTVILWDGFTGQRSKVYQEHEKRCWSV
						DFNLMDPKLLASGSDDAKVKLWSTNLDNSV
ļ		!				ASIEAKANVCCVKFSPSSRYHLAFGCADHCV
		1				HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG
	1					EEIVSASTDSQLKLWNVGKP\YCLRSFKGHIN
						EKNFV\GLASNGDYIACGSENNSLYLYYKGLS
	Į.	]		ļ		KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV
		<u> </u>				CWRALPDGESNVLIAANS\QGTI\KVLELV
597	1947	Α	4518	536	824	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS
	ł	I		}		ASQVAEITSVRHHTWLIFCILGQMGFHHVGE
600	1040	<u> </u>	4504	ļ.,	204	QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP
598	1948	A	4524	1	384	FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF TLGKLPRKTLSVKLMKNRDEVQAMIYDDGSS
L	<u> </u>	L	L	L	<u> </u>	I TOWN TO A WITHWARDE A CWAILLING 29

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  RRREMQSQSVMLALRRGDAVWLLSHDHDG YGAYSNHGKYTIFSGFLVYPDLAPAAPPGLG ASELL
599	1949	A	4526	366	776	MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP NPFAVCEAGTPAMFQTAWRQMESCSI/AQAG VQWRDPGSLHPPPLGFKRFSCLSLPSSWDYK HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI PPPWLPKVLGLQA
600	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS DPPASASRVAGTTGARHHTQLIFVFLVETGFH \MLARDGLKLLTSSDPPASASQSSWDYRREPP RLANFFVFLVETGSRYVAQAGVQWLFTGAIP LLISTGVLTCSVSDLGRFTPP
601	1951	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS VGSPKAKEALNMLTWRAEQEGGMQFWVSSE SKLSDSWQPRSLDIEVAAYALLSHFLQFQTSE GIPIMRWLSRQRNSLGGFASTQDTTVALKALS EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT HNRLLLQTAELADGTANGSV/SISANGFGFAI CQLNVVYNVKASGSSRRRRSIQNQEAFDLDV AVKENKDDLNHVDLNVCTSFSGPGRSGMAL MEVNLLSGFMVPSEAISLSETVKKVEYDHGK LNLYLDSVNETQFCVNIPAVRNFKVSNTQDA SVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSD VQRLPSL
602	1952	A	4540	1963	295	MRAPGRPALRPLPPLLLLLLSSPWGRAVPC VSGGLPKPANITFLSINMKNVLQWTPPEGLQG VKVTYTVQYFIYGQKK WLNKSECRNINRTYC DLSAETSDYEHQYYAKVKAIWGTKCSKWAE SGRFYPFLETQIGPPEVALTTDEKSISVVLTAP EK WKRNPEDLPVSMQQIYSNLKYNVSVLNT KSNRTWSQCVTNHTLVLTW\LEPNTLYCVHV ESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK IIFWYVLPISITVFLFSVMGYSIYRYIHVG\KEK HP\ANLILIYG\NEFDKRFFVPA\EKIV\INF\ITL NISDDSKISHQDMSLLGKSSDVSSLNDPQPSG NLRPPQEEEEVKHLGYASHLMEIFCDSEENT\ EGTSFTQQESLSRTIPPDKTVIEYEYDVRTTDI CAGPEEQELSLQEEVSTQGTLLESQAALAVL GPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEE EPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCE PSEGDGLGEEGLLSRLYEEPAPDRPPGENETY LMQFMEEWGLYVQMEN
603	1953	A	4543	3	600	YSAVEFVEQASGISDWWNPALRKRMLSDSGL GMIAPYYEDSDLKDLSHSRVLQSPVSSEDHAI LQAVIAGDLMKLIESYKNGGSLLIQGPDHCSL LHYAAETGNGEIVKYILDHGPSELLDMADSE TGETALHKAACQRNRAVCQLLVDAGASLRK\ TDSKGKTPQERAQQA\GDPDLAA/YTIESRQN YKVIGHEDLETAV
604	1954	A	4548	3	938	QDNKVQNGSLHQKDTVHDNDFEPYLTGQAN QSNSYPSMSDPYLSSYYPPSIGFPYSLNEAPW STAGDPPIPYLTTYGQLSNGDHHFMHDAVFG QPGGLGNNIYQHRFNFFPENPAFSAWGTSGS QGQQTQSSAYGSSYTYPPSSLGGTVVDGQPG FHSDTLSKAPGMNSLEQGMVGLKIGDVSSSA VKTVGSVVSSVALTGVLSGNGGTNVNMPVS KPTSWAAIASKPAKPQPKMKTKSGPVMGGG LPPPPIKHNMDIGTWDNKGPVPKAPVPQQAP

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, [= soleucine, K=Lysine, L=Leucine.
seq- uence	uence		09/496 914	correspondi ng to first amino acid residue of	to last amino acid residue of peptide sequence	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide sequence	sequence	/=possible nucleotide deletion, \=possible nucleotide insertion
					ł	SPQAAPQPQQVAQPLPAQPPALAQPQYQSPQ QPPQ
605	1955	A	4553	2	2304	ILLQEKRNCLLMQLEEATRLTSYLQSQLKSLC ASTLTVSSGSSRGSLASSRGSLASSRGSLSSVS FTDIYGLPQYEKPDAEGSQLLRFDLIPFDSLGR DAPFSEPPGPSGFHKQRRSLDTPQSLASLSSRS SLSSLSPPSSPLDTPFLPASRDSPLAQLADSCE GPGLGALDRLRAHASAMGDEDLPGMAALQP HGVPGDGEGPHERGPPPASAPVGGTVTLRED SAKRLERRARRISACLSDYSLASDSGVFEPLT KRNEDAEEPAYGDTASNGDPQIHVGLLRDSG SECLLVHVLQLKNPAGLAVKEDCKVHIRVYL PPLDSGTPNTYCSKALEFQVPLVFNEVFRIPV HSSALTLKSLQLYVCSVTPQLQEELLGIAQIN LADYDSLSEMQLRWHSVQVFTS\LNHQGRGR LGVQERAPPGTLHTPSPSPASTDAVTVLLAR TTAQLQAVERELAEERAKLEYTEEEVLEMER KEEQAEAISERSWQADSVDSGCSNCTQTSPPY PEPCCMGIDSILGHPFAAQAGPYSPEKFQPSPL KVDKETNTEDLFLEEAASLVKERPSRRARGSP FVRSGTIVRSQTFSPGARSQYVCRLYRSDSDS STLPRKSPFVRNTLERRTLRYKQSCRSSLAEL MARTSLDLELDLQASRTRQRQLNEELCALRE LRQRLEDAQLRGQTDLPPWVLRDERLRGLLR EAERQTRQTKLDYRHEQAAEKMLKKASKEI YQLRGQSHKEPIQVQTFREKIAFFTRPKNIPPL
606	1956	A	4555	3429	776	PADDV PGSGPGPAPFLAPVAAPVGGISFHLQIGLSREP VLLLQDSSGDYSLAHVREMACSIVDQKFPEC GFYGMYDKILLFRHDPTSENILQLVKAASDIQ EGDLIEVVLSASATFEDFQIRPHALFVHSYRA PAFCDHCGEMLWGLVRQGLKCEGCGLNYH KRCAFKIPNNCSGVRRRILSNVSLTGVSTIRT SSAELSTSAPDEPLLQKSPSESFIGREKRSNSQ SYIGRPIHLDKILMSKVKVPHTFVIHSYTRPTV CQYCKKLLKGLFRQGLQCKDCRFNCHKRCA PKVPNNCLGEVTINGDLLSPGAESDVVMEEG SDDNDSERNSGLMDDMEEAMVQDAEMAMA ECQNDSGEMQDPDPDHEDANRTISPSTSNNIP LMRVVQSVKHTKRKSSTVMKEGWMVHYTS KDTLRKRHYWRLDSKCITLFQNDTGSRYYKE IPLSEILSLEPVKTSALIPNGANPHCFEITTANV VYYVGENVVNPSSPSPNNSVLTSGVGADVAR MWEIAIQHALMPVIPKGSSVGTGTNLHRDISV SISVSNCQIQENVDISTVYQIFPDEVLGSQQFGI VYGGKHRKTGRDVAIKIIDKLRFPTKQESQLR NEVAILQNLHIPGVVNLECMFETPERVFVVM EKLHGDMLEMILSSEKGRLPEHITKFLITQILV ALRHLHFKNIVHCDLKPENVLLASADPFPQV KLCDFGFARIIGEKSFRRSVVGTPAYLAPEVL RNKGYNRSLDMWSVGVIIVYSLSGTFPFNED EDIHDQIQNAAFMYPPNPWKEISHEAIDLINN LLQVKMRKRYSVDKTLSHPWLQDYQTWLDL RELECKIGERYITHESDDLRWEKYAGEQGLQ
607	1957	A	4563	1	4499	SRPWWLRASERPSAPSAMAKRSRGPGRRCLL ALVLFCAWGTLAVVAQKPGAGCPSRCLCFRT TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI QPGAFRRLRNLNTLLLNNNQIKRIPSGAFEDL ENLKYLYLYKNFIQSIDRQAFKGLASLEQLYL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  HFNQIETLDPDSFQHLPKLERLFLHNNRITHL VPGTFNHLESMKRLRLDSNTLHCDCEILWLA DLLKTYAESGNAQAAAICEYPRRIQGRSVATI TPEELNCERPRITSEPQDADVTSGNTVYFTCR AEGNPKPEIIWLRNNNELSMKTDSRLNLDD GTLMIQNTQETDQGIYQCMAKNVAGEVKTQ EVTLRYFGSPARPTTVIQPQNTEVLVGESVTL ECSATGHPPPRISWTRGDRTPLPVDPRVNITPS GGLYIQNVVQGDSGEYACSATNNIDSVHATA FIIVQALPQFTVTPQDRVVIEGQTVDFQCEAK GNPPPVIAWTKGGSQLSVDRRHLVLSSGTLRI SGVALHDQGQYECQAVNIIGSQKVVAHLTVQ PRVTPVFASIPSDTTVEVGANVQLPCSSQGEP EPAITWNKDGVQVTESGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMVLSVNVPD VSRNGDPFVATSIVEAIATVDRAINSTRTHLF DSRPRSPNDLLALFRYPRDPYTVEQARAGEIF ERTLQLIQEHVQHGLMVDLNGTSYHYNDLVS PQYLNLIANLSGCTAHRRVNNCSDMCFHQKY RTHDGTCNNLQHPMWGASLTAFERLLKSVY ENGFNTPRGINPHRLYNGHALPMPRLVSTTLI GTETVTPDEQFTHMLMQWGQFLDIBDLDSTV VALSQARFSDQHCSNVCSNDPPCFSVMIPPN DSRARSGARCMFFVRSSPVCGSGMTSLLMNS VYPREQINQLTSYIDASNVYGSTEHEARSIRD LASHRGLLRQGIVQRSGKPLLPFATGPPTECM RDENESPIPCFLAGDHRANEQLGLTSMHTLW FREHNRIATELLKLNPHWDGDTTYYETRKIVG AEIQHITYQHWLPKILGEVGMRTLGEYHGYD PGINAGIFNAFATAAAFRFGHTLVNPLLLPGLD ENFQPIAQDHLPLHKAFFSPFRIVNEGGIDPLL RGLFGVAGKMRVPSQLLNTELTERLFSMAHT VALDLAANIQRGRDHGIPPYHDYRVYCNLS AAHTFEDLKNEIKNPEIREKLKRLYGSTLNID LFPALVVEDLVPGSRLGPTLMCLLSTOFKRLR DGDRLWYENPGVFSPAQLTOIKQTSLARILCD NADNITRVQSDVFRVAEFPHGYGSCDEIPRVD LRVWQDCCEDCRTRGQFNAFSYHFRGRRSLE FSYQEDKPTKKTRPKIPSVGRQGEHLSNSTS A/FSTRSDASGATNDFQRVCSWEMQKTITDLR TQIKKLESRUSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVEACPPATCAVPVNI PGACCPVCLQKRAEEKP
608	1958	Ā	4566		1135	FSFLC/GVSGRLGLDSEEDYYTPQKVDVPKAL IIVAVQCGCDGTFLLTQSGKVLACGLNEFNKL GLNQCMSGIINHEAYHEVPYTTSFTLAKQLSF YKIRTIAPGKTHTAAIDERGRLLTFGCNKCGQ LGVGNYKKRLGINLLGGPLGGKQVIRVSCGD EFTIAATDDNHIFAWGNGGNGRLAMIPTERP HGSDICTSWPRPIFGSLHHVPDLSCRGWHTILI VEKVLNSKTIRSNSSGLSIGTVFQSSSPGGGE GGPDAW
609	1959	A	4567	1	412	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH RARPRINLRNVIYSFAVTYCLNYISLAMSSTL KLSFHVLSGS
610	1960	A	4570	697	467	ECRGVISAH\CCTLCLPSSSDSASAF\RVARTT GTCDYAQLIFAFLVEMGFHHVGQDGLHLL/N LVIRPPRPPKVLGLQA

SEO ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ĺ		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide		/=possible nucleotide deletion, \=possible
	l	1	1	sequence		nucleotide insertion
611	1961	A	4571	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
1					İ	WNPNVPESPRIPAPRLPKRMSGAPTAGAALM
]	J		1	1	į	LCAATAVLLSAQGGPVQSKSPRFASWDEMN
	ŀ	İ	1			VLAHGLLQLGQG\CANT\GAHPQSAERAGA\R
	į	1				LSACGSACQGTEGSTDI.PLAPESRVDPEVLHS
		ļ		ļ	ļ	LQTQLKAQNSRIQQLFHKVAQQQRHLEKQHL
l	1		1	+	1	RIQHLQSQFGLLDHKHLDHEVAKPARRKRLP
						EMAQPVDPAHNVSRLHRLPRDCQELFQVGER
1					i	QSGLFEIQPQGSPPFLVNCKMTSDGGWTVIQR
1		ļ	1	ĺ		RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL
ļ		]	}	J	]	EKVHSITGDRNSRLAVQLRDWDGNAELLQFS
1						VHLGGEDTAYSLQLTAPVAGQLGATTVPPSG
				<b>!</b>		LSVPFSTWDQDHDLRRDKNCAKSLSGGWWF
			1			GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT
İ		1	i .			WRGRYYPLQATTMLIQPMAAEAAS
612	1962	Α	4575	162	3	FFFETESRSVAQAGVQWRDLSSLQPPPPG\SR
			1			GSPASASPVAGITGTRHHRTRG
613	1963	A	4584	687	321	PLAQRRPFLWVTVKTNGHIWGSSTYPHFWGS
		}		1		SNS/PASASQVAGIPNARHQARIIFVFLVEPRF
	Ī	1	1		ĺ	HHVGRAGLGFL/NLAICLPQHPKVLGLQACN
Ĺ		1	I			LNIKPHPAHKYISMIQFNVHFMCMSVHIYI
614	1964	A	4589	727	299	PGSAQSAQRGRGRRRARAGSATQITMYSFMG
ł		ł	i .		l .	GGLFCAWVGTILLVVAMATDHWMQYRLSGS
					ł	FAHQGLWRYCLGNKCYLQTDSIAYWNATRA
	1			ĺ	<u> </u>	FMILSALCAISGIMGIMAF/GWVAVLMTFFA
<u> </u>			ļ.,		<u> </u>	GIFYMCAYRVHECRRLSTPR
615	1965	A	4590	2	414	TILPEKIQAWAQKQCPQSGEEAVALVVHLEK
		{	f	•	ĺ	ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ
		1			1	PEQVETQPRAVSREEPGSLHSGHQEQLNRKR
	1	1	1	i	1	ERRPLPKNARPSPWVPALADEWNTLHQEVTT
<u></u>	1000	-	1.722	773	100	TRLPAGSQEPVKD DFALVAQAGVQWHNLGSPQPLPPGFKRFSCL
616	1966	A	4592	//3	488	SLPSSWEYRCVPP/RLANFVFLVEMGFLHVGO
		1				AGLELPTSGDPPALASQSAGITGVTTVPSGPG
617	1967	В	4595	84	478	XRHGLREPLLERRCAAASSFQHSSSLGRELPY
01/	1967	В	4393	°4	4/0	DPVDTEGFGEGGDMQERFLFPEYILDPEPQPT
ļ	Į.					REKQLQELQQQEEEERQRQQRREERRQQNL
į	1			1		RARSREHPVVGHPDPALPPSGVNCSGCGAEL
[		1		1	!	HCQDAR*
618	1968	1	4596	2945	1188	ARSRNSARGVYGMCVDTLFLCFLEDLERNDG
""	1300	^	4390	2343	1100	SAERPYFMCSTLKKPLARRCFPAIHAYKGVL
1	1	]	1	1		MVGNETTYEDGHGSRKNITDLVEGAKKANG
ł		l	1	}	1	VLEARQLAMRIFEDYTVSWYWIIGLVIAMA
			1	1	!	MSLLSIILLHLLAGIMGWVMIIMENSELGYRIF
						HCYMEYSRLRGEAGSDVSLVDLGFQTDFRV
1				[		YLHLROTWLAFMIILSILEVIIILLLIFLRKRILI
1					i	AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI
!	}	1	1	}	ł	AYWASTAVFLSTSNEAVYKIFDDSPCPFTAKT
1	1				Ì	CNPETFPSSNESRQCPNARCQFAFYGGESGYH
1		1			ì	RALLGLOIFNAFMFFWLANFVLALGQVTLAG
1	ļ					AFASYYWALRKPDDLPAFPLFSAFGRALRYH
						TGSLAFGALILAIVQIIRVILEYLDQRLKAAEN
					}	KFAKCLMTCLKCCFWCLEKFIKFLNRNAYIM
1		1	1		1	IAIYGTNFCTSARNAFFLLMRNIIRVAVLDKV
	}		1		1	TDFLFLLGKLLIVGSVGILAFFFFTHRIRIVQDT
	1		1		l	APPLNYYWVPILTVIVGSYLIAHGFFSVYGMC
						VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL
						LNKTNKKAAES
619	1969	A	4601	2	357	RTSVEPYILGEF/RKLSNNTKVVKTEYKATEY
			1		<u> </u>	

(DEC 10)	1.000.70	T-5-7-4	Lego	T 50 - 11 - 1	<del></del>	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	1 * *	ļ	in		location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first amino acid		Q=Glutamine, R=Arginine, S=Serine,
1	1		1	residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
İ					sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	<b>J</b>		J	peptide		/=possible nucleotide deletion, \=possible
	ļ	ļ	<u>-</u>	sequence		nucleotide insertion
			1			GLAYGHFSYEFSNHRDVVVDLQGWVTGNGK
İ		Í			1	GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN
			İ			NQHVECNEICHRLSLTRPSMEKPCKS
620	1970	Α	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQRVEGPR
	Ì	i				KGHLEEEEEDGEEGAETLAHFCPMELRGPEP
	ļ	l	1	Į.	1	LGSRPRQPNLIPWAAAGRRAAPYLVLTALLIF
					}	TGAFLLGYVAFRGSCQACGDSVLVVSEDVN
		)	}		)	YEPDLDFHQGRLYWSDLQAMFLQFLGEGRL
		1	ĺ			EDTIRQTSLRERVAGSAGMAALTQDIRAALS
		1	l .			RQKLDHVWTDTHYVGLQFPDPAHPNTLHWV
	Ì	i	Ī	ľ	ĺ	DEAGKVGEQLPLEDPDVYCPYSAIGNVTGEL
						VYAHYGRPEDLQDLRARGVDPVGRLLLVRV
	ł	ŀ		}	ł	GVISFAQKVTNAQDFGAQGVLIYPEPADFSQ
				ì	{	DPPKPSLSSQQAVYGHVHLGTGDPYTPGFPSF
		]		ļ	Ì	NQTQFPPVASSGLPSIPAQPISADIASRLLRKL
		l	1			KGPVAPQEWQGSLLGSPYHLGPGPRLRLVVN
					]	NHRTSTPINNIFGCIEGRSEPDHYVVIGAORDA
	i	1		ŀ		WGPGAAKSAVGTAILLELVRTFSSMVSNGFR
			Į	l	1	PRRSLLFISWDGGDFGSVGSTEWLEGYLSVL
					ĺ	HLKAVVYVSLDNAVLGDDKFHAKTSPLLTSL
				i		IESVLKQVDSPNHSGQTLYEQVVFTN\PSWD\
	!	l	1	İ		AEVIRPLPM\DSSAY\SFTAFVGVPAVEFSFME\
	i					DDQ\AYPFLHTKEDTYENLHKVLQGRLPAVA
	1	ļ		1		QAVAQLAGQLLIRLSHDRLLPLDFGRYGDVV
						' '
					ļ	LRHIGNLNEFSGDLKARGLTLQWVYSARGDY
	[	1		•		IRAAEKLRQEIYSSEERDERLTRMYNVRIMRV
	ł	ļ				EFYFLSQYVSPADSPFRHIFMGRGDHTLGALL
l	ĺ	1	ľ	İ		DHLRLLRSNSSGTPGATSSTGFQ\ESRFRRQL\
621	1971	A -	4610	702	224	ALL\TWDACKGAANALSGDVWNIDNNF
021	19/1	I A	4010	793	334	ISRVDDFVGSGIANVIIAVAIFSIPAFARLVRG\
			1			NTLVLKQQTFIESARSIGASDMTVLLRHILPGT
	ļ	ļ	1			GSSIVVFFTMRIGTSIISAASLSFLGLGAQPPTP
:		1	Į.			EWGAMLNEARADMVIAPHVAVFPALAIFLTV
		<u></u>	\	ļ. <u>.</u>		LAFNLLGDGLRDALDPKIKG
622	1972	A	4614	2	820	LVYVMIAIFCIASAMSLYNCLAALIHKIPYGQ
		1				CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF
	l	1		1		RNEDRWAWILQDILGIAFCLNLIKTLKLPNFK
		1			!	SCVILLGLLLLYDVFFVFITPFITKNGESIMVEL
		ļ	[			AAGPFGNNEKNDGNLVEATGQPSAPHEKLPV
		1		!		VIRVPKLIYFSVMSVCLMPVSILGFGDITVPGL
		j	)	J		LIAYCRRFDVQTGSSYIYYVSV\TVAYAIGMIL
						TFVVLG\LMKKGQPALLYLVPCTLITA/CQFV
			1			AWETVREMKKFWERVTS
623	1973	Α	4619	17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF
						GGCCESGLPNTMPSAFSVSSFPVSIPAVLTQT
	ļ l		[			DWTEPWLMGLATFHALCVLLTCLSSRSYRLO
		j		]	J	IGHFLCLVILVYCAEYINEAAAMNWRLFSKY
						OYFDSRGMFISIVFSAPLLVNAMIIVVMWVW
		1		İ		KTLNVMTDLKNAQERRKEKKRRRKED*GAA
			[	į i		AAWSLRPSRPPSAAPSAAVCVAWASFOLTHG
						LKNRCFI
624	1974	Α	4622	164	668	VSCYTALQSIMNQPESANDPEPLCAVCGQAH
U44	17/4	^	4022	104	000	
J			1	]	J	SLEENHFYSYPEEVDDDLICHICLQALLDPLD
į						TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVL
ì						QHCKKSSILVNKLLNKLLVTCPFREHCTQVL QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED
						CHAIDLEHHEATSOAWGTHT *SOLLGDIDOED
			[	l	I	CICEDEDITII GIOGNA OTTIE OGEROICENCED
<u> </u>						CLSPGVHHCSEV
625	1975	A	4625	474	473	CLSPGVHHCSEV CFLSPSPLLPPLILSSSSSPSFPLPPPPTLLPSTLP PPLLIPSS*LSP

<u> </u>	1 000 ID	1 1 1 - 4	1 800	h - 1: 1	1 D	(A-A)
SEQ ID NO: of	SEQ ID	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
	NO: of	hod	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-		Ì	1	location		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	i	USSN		corresponding to last amino	
seq-	uence	•	09/496	correspondi	acid residue	M=Methionine, N=Asparagine, P=Proline, O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid		
		1	į.		of peptide	T=Threonine, V=Valine, W=Tryptophan,
			I	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
	1054	<u> </u>	1.00	sequence	<u> </u>	nucleotide insertion
626	1976	A	4629	249	3	KLKGNECFCYHCNVCIFLMIKK*GLFLC*IYFI
	•	1	1		1	LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP
	ļ <u></u>		<u> </u>			ASASQVAGIAGTHH
627	1977	A	4635	1	301	FFFFETKPFFAPQAGGQGPSRGSLNPLPTGLK
	l			ļ	1	QFSGLTT.SRSGNNGPRPPPRVNFGILRGNGVP
				ĺ		PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
			1_			ARAYL
628	1978	A	4648	1357	782	KLFSSQRLFGPHIQAINPSFLLLSFFPS*LLAMR
		1	1	}		TVGNNAFILVFLVYRIVLLLF*HV*PAYFQPSK
						NKTAKINCN*RPFLFLVCYLL*AELHIGIFIANF
						YDCIPNKLNEHLWPKLLQSLIFHVDFCGFLHK
		ļ				VFYICFTEFLLFLYFL*LFIIKVSCSII*CSTICVF
		ł	1		ì	SYKSFAVIIFFVDNTRFFSFGF
629	1979	Α	4660	18	999	HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV
		ĺ				KVKTVCQIPLMKEMLKRFQVAVNLAEDTAH
		Ì		·		PKLVFSQEGRYVKNTASASSWPVFSSAWNYF
		ŀ	1			AGWRNPQKTAFVERFQHLSCVLGKNVFTSG
!	j	j		<b>!</b>		KHYWEVESRDSLEVAVGVCREDVMGITDRS
	l .				1	KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ
	i					EPALHRVGVYLDRGTGNVSFYSAVDGVHLH
		ļ			-	TFSCSSVSRLRPFFWLSPLASLVIPPVTORK*G
	1	1		i	1	FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
		ļ				WSIFWVSLTVPFGICPLCASOEAVPWEVGLA
ı	1			!	ļ	NGDGTGNFPRRFWEIFL
630	1980	Α	4669	2	358	FFFFFETESHSVAQAGMQWRNLGSLPAPPPGF
	.,,,,,	1	1005	_	***	TPFFCLSLLNGWDYRRPPPHLANFFVLLVETG
						FHDVGQDGLDLLTS*STPSASQSAEITGVSHC
ı	ĺ	İ			ĺ	TRLKKIRFAKGHVEFFFESHVE
631	1981	A	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV
05.	1301	1 **	1071	,,,,	***	AHTCNPCTLGGRGRWIT*GSGVQDQPGPTWQ
	i				1	NPVFLERRPRALHSSPGLTTQRILWAQGLWV
		1		:		GAGSTGCSRGPRGEGVFREG
632	1982	A	4678	1 34	314	RSTHASGMISPSFGFMGHLLRLEFEILPSTPNP
032	1302	^	4076	34	317	*LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFP
		1			1	ASGLAPVPTHWTVSELSRSPVATATFC
633	1983	A	4696	1	1365	RTLGMEGERRASQAPSSGLPAGGANGESPGG
000	1903	l ^•	4070	*	1.303	GAPFPGSSGSSALLQAEVLDLDEDEDDLEVFS
	J	1			J	KDASLMDMNSFSPMMPTSPLSMINQIKFEDEP
		1				DLKDLFITVDEPESHVTTIETFITYRITKTSRG
		}				EFDSSEFEVRRRYQDFLWLKGKLEEAHPTLII
			i	1		PPLPEKFIVKGMVERFNDDFIETRRKALHKFL
	1	1			1	
1		1				NRIADHPTLTFNEDFKIFLTAQAWELSSHKKQ
i :	ľ	1	1		ì	GPGLLSRMGQTVRAVASSMRGVKNRPEEFM
	1	1				EMNNFIELFSQKINLIDKISQRIYKEEREYFDE
	1	1				MKEYGPIHILWSASEEDLVDTLKDVASCIDRC
	1	1			<b>]</b> .	CKATEKRMSGLSEALLPVVHEYVLYSEMLM
l		1	i	1		GVMKRRDQIQAELDSKVEVLTYKKADTDLL
			1			PEEIGKLEDKVECANNALKADWERWKQNM
			1			QNDIKLAFTDMAEENIHYYEQCLATWESFLT
		L	<u> </u>			SQTNLHLEEASEDKP
634	1984	A	4708	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTQ
ı		ļ	1	]	ļ	WISKAVYKHREMCGLTSTGRKSHGLEKDRM
		1	L			FPHAIGGSCRAA*RRKTLQFPCYH
635	1985	Α	4709	42	341	YIKQPDAKERRRTVHWKKETESEASEITIPPST
						PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVL
		1	1		[	WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT
					1	
					i .	SED
636	1986	A	4721	2	351	SED  EKPDHFFPEGTSFIHEPRRPN*GDLVHCLGGIS

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide seq-	seq- uence		USSN 09/496	location correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uenœ	}	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK
		<u> </u>	1			MYFTTPSNHNAYQVDSVQST
637	1987	A	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLLQDH LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
		1	ļ			DSSASSSRAAGITGVHHHAWLIFFFLVETGFL
			i			HAG*AGLELLTSGDPPASASRSAGITGVSHHA
		l <u></u> .	<u> </u>	L		RPRETRFL
638	1988	A	4734	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG
			1			TLERGHWNNKMEFVLSVAGEIIGLGNVWRFP VLCYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
						GOYTSOGGVTAWRKICPIFEGIGYASOMIVIL
						LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE
	}		<u>L</u>		<u> </u>	WNTEHCMEFQKTNGSLNGTSENATSPVIEFW
639	1989	A	4743	1040	699	QGLTLLPRMECSATITAHCSLELPGSIDLPTSA
						S*VARTTGTHHHPWLILVLLL*TWGSYYVAQ AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
	1	1		İ	1	TSNHVLYTQEGLRRGKEG
640	1990	A	4771	527	2	GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN
						WIRRRPCLPSGCLKMNREIGPLQHSLCCPGWS
				}		QTPGLKAILLRQPPK*LGLQMESHSCPPAWSA
	1	[				MARSRLTATSASQVQAILLPQPPGTTDSCSPS PDHEQQPLSWVLPPPQKDMNPREQQVALGP
		ł				QAAALPWAVWRNDCFPR
641	1991	Λ	4780	16	473	RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
	J	ļ	1	}	ļ	LQLAASPYFSPSWAECPQPVPAGTHATWCLA
	]	}			İ	RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP
						FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP QRDTDTGVHTGSGTHTHAHTPPEK
642	1992	A	4798	1	487	GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
			1	} -		FIELLDTIFFVLRKKNSQVTFLHVFHHTIMPW
	}	1	1			TWWFGVKFAAGGLGTFHALLNTAVHVVMY
		İ				SYYGLSALGPAYQKYLWWKKYLTSLQLVQF VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
						FLLLFLH
643	1993	A	4799	2	391	LMAFIEMHISGSLVYLKIKTKIYSYFSMLNFLL
		i	1			QEIPLSEILRISSPRDFTNISQGSNPHCFEIITDT
		1	1			MVYFVGENNGDSSHNPVLAATGVGLDVAQS
	-					WEKAIRQALMPVTPQASVCTSPGQGKDHSK O*ASVCTSPGQGKDHSKQ
644	1994	A	4800	488	101	AYPLFAVHPVHTECVAGVVGRAYLLCALFFL
	1	]		1		LSFLGYCKAFRESNKEGAHSSTFWVLLSIFLG
	ļ	1	1	1		AVAMLCKEQGITVLVRAATWLGPAFSVCPFP
645	1005	↓	4005	150	100	SYKDIWGWPCLCGVLHAYIPLLV
645	1995	A	4805	458	126	LLWTTVLCQTPARPQSTMIHLGHILFLLLLPV AAAOTTPGERSSLPAFYPGTSGSCSGCGSLSL
		1	1			PLLAGLVAADAVASLLIVGAVFLCARPRRSP
					İ	AQEDGKVYINMPGRG
646	1996	A	4817	47	1033	LQGDTWHLSFLSHFSRLHGGVPGRGLLEGNI.
		1			1	LQPQAPGHDMTSIPFPGDRLLQVDGVILCGLT
			1	1	ĺ	HKQAVQCLKGPGQVARLVLERRVPRSTQQC PSANDSMGDERTAVSLVTALPGRPSSCVSVT
				Į.		DGPKF*SSN*KRIANGLGFSFVQMEKESCSHL
		1	1	1		KSDLVRIKRLFPGHPAEENGALAAGDIILGRE
			1		]	WEGPRKASSSRCRGSWAMQLSVQAGPSFAS
						YYPAAVEVLHLLRGAPQEVTLLLCRPPPGAL BELFORWOTBELSADVEETBATCTDSCTSBIL
						PELEQEWQTPELSADKEFTRATCTDSCTSPIL GSRGQLGGTVPPQMQGKAWGLRPESSQKAIR
		1				EGTMGAKTERDLGPVP
647	1997	A	4854	1044	335	PRVRGDWPLEKKKSNSNIHPIFSWCGSTDSKD

SÉQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				amino acid residue of	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Sequence	/-possible nucleotide deletion, \-possible
		ļ		sequence		nucleotide insertion
	-	┼	<del></del>	sequence	<del> </del>	IVMPTYDLTDSVLETMGRVSLDMMSVQANT
	1			1	ļ	GPPWESKNSTAVWRGRDSRKERLELVKLSRK
					İ	HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
	l					FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
		ĺ		ł		QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
	1	1	ļ	ł	1	LKWAKDHDEEAKKIAKAGQEFARNNLMGD
						DIFCYYFQTFPRNMPIYK
648	1998	A	4867	2030	837	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
						SEEEEKSGLGAKIPVTIITGYLGAGKTTLLNYI
	Į.			1		LTEQHSKRVAVILNEFGEGSALEKSLAVSQG
				}		GELYEEWLELRNGCLCCSVKDNGLRAIENLM
				İ	ļ	QKKGKFDYILLETTGLADPGAVASMFWVDA
	į					ELGSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
	İ				l	NEATRQVALADAILINKTDLVPEEDVKKLRT
			j			TIRSINGLGQILETQRSRVDLSNVLDLHAFDSL SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
		1		1		NAKEEHLNMFIONLLWEKNVRNKDNHCMEV
						IRLKGLVSIKDKSQQVIVQGVHELYDLEETPV
		{				SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
		]	ļ	i	1	VTETEKOWTTHFKEDOVCT
649	1999	Α	4873	226	189	DGVSLLLPKLGVQWAQYWAHWQPPLPGFKR
		1				FSCLSLRSSWD*KCAPPHPAFVFLVEMGFHRV
					1	GQAGLELRTSGDPPASASQSAGITGVSHI.A*P
	<u></u>	<u> </u>				TSMPLLPFQRLCVYI
650	2000	A	4874	2	437	FFFLRRSFAFVAQAGVQWCDLGSPQPLPPGF
		[		[	1	K*FSCLSLPSSWDYRHAPPPCPS*FLYF**RQG
		1				FTMLARLVLNS*PHDLPTSPSQSAEIKGVSHR
	1	ŀ				CPASFYLFLKYYLEAKFCA*GECAPSAGVGA
651	2001	A	4898	1701	771	GYKRGHKSCLLINCVVQI DAWGPETRLARILNPDSFIEPRPGRLPELEATR
031	2001	1	4070	1701	) '' <sup>1</sup>	PHMEPKASCPAAAPLMERKFHVLVGVTGSV
		1	1	ļ		AALKLPLLVSKLLDIPGLEVAVVTTERAKHFY
• 0						SPODIPVTLYSDADEWEMWKSRSDPVLHIDL
						RRWADLLLVAPLDANTLGKVASGICDNLLTC
	]	J		]		VMRAWDRSKPLLFCPAMNTAMWEHPITAQQ
			1			VDQLKAFGYVEIPCVAKKLVCGDEGLGAMA
						EVGTIVDKVKEVLFQHSGFQQS*PGISVMGVP
						LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA
	100-	Ļ. —	4005			LSLPRGQACSRLNWTEGPGLSFFQPGEAAA
652	2002	Α	4927	1	611	FRGRQTSRPARGFSPWRPPGTMQEPSSGECPA
				1	1	SP*LPCASNRLAFGGLIFPCAPLVPYPAPFSPLL
					1	PAFSCAPRPRAHTHSRTHPSAPLVPKPSSRAR
	1		1	1	1	GQSPIPSRASSPSCSWAQVPGVALARCAGVC   KPGDSWRVAACISGRCCSRGRRRGSGPRNPE
						QSFRGAWGPSFWGSWKSQRELSAGGAQAWP
					}	LLGSAGSGLRGEA
653	2003	A	4965	2	283	FFFFI*DGVSLCHPGWNAVARSWLTATSASR
				-		VQAVSCFRLPSSWDYRHATMPG*FF*YF**R
	1	J	J	I		WGFTILAILVLNS*PQVICPPWPPKVLTLQA
654	2004	Α	4968	3 .	437	RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGD
		İ		i		IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW
				}	}	DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP
	1	1		1	<b>i</b> .	PPCLTHLAAASCVVVWCGRWKRDSAECQCD
		<u> </u>				HSCSAVSQQEDRCRSSSCS
655	2005	Α	4983	201	397	MNNNTTCIQPSMISSMALPHYILLCIVGVFGN
						TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
656	2006	Α	4988	332	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLVI
657	2007	<del>-</del> -	7000	120	165	REVHIKTMR*HFLPIRLEKNKNNIKD
		В	5008	129	465	MAGMKTASGDYIDSSWELRVFVGEEDPEAES

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	]	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
[			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1	1.	peptide	1	/=possible nucleotide deletion, \=possible
L	<u></u>	L		sequence		nucleotide insertion
						VTLRVTGESHIGGVLLKIVEQINRKQDWSDH
					J	AIWWEQKRQWLLQTHWTLDKYGILADARLF
<u> </u>		L				FGPQHRPVILRLPNRRALRLX*
658	2008	Α	5017	1	292	FFFFKETESHSVTQAGVQWHDLGSLQPPPPGF
	1					KRFSCLSLLSSWDYRCAPPHPANFVFLVETGF
						HHVAQAGLKLLTL*SANLGLSTSLPIPLFILLS
659	2009	Α	5018	17	338	RGHGGKSLTGGTPGNWGDGLLVSEDWSHLIF
{						T*NSLVSPVLGKWSPCLQGPGLSAVHTWPWL
Ì	1	J	]	į	J	MAACWAVHVKTHMRPGLAVLPRLVLNSWS
	-	<b> </b>	****			*AIILLWPPKALGLQA
660	2010	Α	5028	2	310	SRVDDFVGERRGGCDECLCGHRGLRAVPLG
	İ	1			}	HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST
	1	1			Ì	AGSCPRQKKTTPGPTVLCVCSFWIYQRGEPH
777	2011	<u> </u>	5050	750	423	HRTGARWNH
661	2011	Α	5050	752	431	RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ
						LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS
	1					LELLGSSHPPTSASQSARITGVSHRAWPLK*F
662	2012	-	5054	40	103	NLNQYQTLTMN   ELNNGPFQMPLCNGGNLAVTGSWADRSPLH
662	2012	Α	5054	48	103	EAASQGRLLALRTLLSQGYNVNAVTLDHVTP
						LHEACLGDHVACARTLLEAGANVNAITIDGV
}					Į	TPLFNACSQGSPSCAELLLEYGAQAQLESCLP
	ļ					SPTHEGASKGHHECLDILISWGIDVDQEIPHSG
	[	ļ				TPLYVACMAQQFHCIWNLIYAGAGVRKGKY
	ļ	1			}	WDTPLPGAGHQSTQKLE*LFAMVEIWQ
663	2013	A	5066	951	580	VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK
		l				ADLPEGVAVSGPSPAEFCRKHRLPAPVPFSCA
			ļ			GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF
}	l	1	1		i	WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ
664	2014	Α	5071	550	1	LSFIEVLSMEQVNKTVVREFVVLGFSSLARLQ
	1					QLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTP
					J	MYFFLAILSCSEICYTFVIVPKMLVDLLSQKK
						TISFLGCAIQMFSFLFFGSSHSFLLAAMGYDR
						YMAICNPLRYSVLMGHGVCMGLMAAAWAC
	<u> </u>		<u> </u>			GFTVSLVTTSLVFHLPFHSSNQHE
665	2015	Α	5074	496	692	QQYHNTGSAGHHAHCQVGHSPHVHYPSGCG
		į				PL*IQRGLPSFNSLEGHSLKDSGHEESVQLDSE
	}					HDVQRSLYCDTAVNDVLNTSVTSMGSQMPD
						HDQNEGFHCREECRILGHSDRCWMPRNPMPI
						RSKSPEHVRNIIALSIEATAADVEAYDDCGPT
	ĺ	1	[			KRTFATFGKDVSDHPAEERPTLKGKRTVDVT
						ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL
111	2016	<b> -</b>	6000	400	249	PTKPSVSYEIVDPGITARRC
666	2016	A	5080	408	248	IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPL
(/2	0017	<del> </del>	700:	100	047	VGPKAQLSGLQLQPCLYKRR
667	2017	A	5081	129	247	DLTNSHFFLFDFQKTGPPLGGPKAQFSSLQLQ
	0010	<u> </u>	7001		622	PCVY*RR
668	2018	A	5086	852	233	NIKSNDRWVQIKTAYKYFF*KNGDNYNWVF
		1				RALPTTFADIENLKYLLFTRDASQPFYLGHTV
		1				IFGDLEYVTVEGGIVLSRELMKRLNRLLDNSE
	}	Į	]			TCADQSVIWKLSEDKQLAICLKYAGVHAENA
		1				EDYEGRDVFNTKPIAQLIEEALSNNPQQVVEG
						CCSDMAITFNGLTPQKMEVMMYGLYRLRAF
220	2010	<b>_</b>	5101	1	220	GHYFNDTLVFLPPVGSEND
669	2019	A	5101	1	329	PGRPTRPPLLTLLAHVSPEPAGPSCDSLAQPG
						ASGV*VQHDSHPPLLCGSQCLSEPVPGSHGPP RGCQHEAAPCPRGPGSDGLHHASAACASLPP
						SPILPVLLPELGPL
670	2020	Ā	5102	3	547	DAWGNRCAVGAAPRLIHLHLCCTPADPSRKP
370	2020	<u> </u>	7104	,	J4/	DA WONKCA YOAAFREITERECCITADTSKAP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DEL*NMNGRVDYLVTEEEINLTRGPSGLGFNI VGGTDQQYVSNDSGIYVSRIKENGAAALDGR LQEGDKILSVNGQDLKNLLHQDAVDLFRNA GYAVSLRVQHRLQVQNGPIGHRGEGDPSGIPI FMVLVPYFALTMVAAWAFMRYRQQL
	2021	A				RDGREELCLQQEPTLPSRICSSAPLLYFLFICPF VLLLLLLISLLCLYWKARKLSTLRSNTRKEKA LWVDLKEAGGVTTNRMED*EEDECN
672	2022	A	5148	72	314	IIYFSYNIFLKITELLNDVERLKQALNGLSQLT YTSGNPTKRQSQLIDTLQHQVKSLEQQLAVS NQAHGALQEYVLAPCS
673	2023	A	5152	210	335	REILCSRIGRLNIV+MSLFPNLTCRLNAIPIKIPA NHFVEVT
674	2024	A	5153	3	2953	LTEDQPFDILQKSLQEANITEQTLAEEAYLDA SIGSSQQFAQAQLHPSSSASFTQASNVSNYSG QTLQPIGVTHVPVGASFASNTVGVQHGFMQH VGISVPSQHLSNSSQISGSGQIQLIGSFGNHPS MMTINNLDGSQIILKGSGQQAPSNVSGGLLV HRQTPNGNSLFGNSSSSPVAQPVTVPFNSTNF QTSLPVHNIIIQRGLAPNSNKVPINIQPKPIQM GQQNTYNVNNLGIQQHHVQQGISFASASSPQ GSVVGPHMSVNIVNQQNTRKPVTSQAVSSTG GSIVIHSPMGQPHAPQSQFLIPTSLSVSSNSVH HVQTINGQLLQTQPSQLISGQVASEHVMLNR NSSNMLRTNQPYTGPMLNNQNTAVHLVSGQ TFAASGSPVIANHASPQLVGGQMPLQQASPT VLHLSPGQSSVSQGRPGFATMPSVTSMSGPSR FPAVSSASTAHPSLGSAVQSGSSGSNFTGDQL TQPNRTPVPVSVSHRLPVSSSKSTSTFSNTPGT GTQQQFFCQAQKKCLNQTSPISAPKTTDGLR QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ QEKVVGSSPGHPAVQVESHSGGQKRPAAKQ LTKGAFILQQLQRDQAHTVTPDKSHFRSLSD AVQRLLSYHVCQGSMPTEEDLRKVDNEFETV ATQLLKRTQAMLNKYRCLLLEDAMRINPPAE MVMIDRMFNQEERASLSRDKRLALVDPEGFQ ADPCCSFKLDKAAHETQFGRSDQHGSKASSS LQPPAKAQGRDRAKTGVTEPMNHDQFHLVP NHIVVSAEGNISKKTECLGRALKFDKVGLVQ YQSTSEEKASRREPLKASQCSPGPEGHRKTSS RSDHGTESKLSSILADSHLEMTCNNSFQDKSL RNSPKNEVLHTDIMKGSGEPQPDLQLTKSLET TFKNILELKKAGRQPQSDPTVSGSVELDFPNF SPMASQENCLEKFIPDHSEGVVETDSILEAAV NSILEC
675	2025		5154	599	1880	LKKMEPFSCDTFVALPPATVDNRIIFGKNSDR LYDEVQEVVYFPAVVHDNLGERLKCTYIEID QVPETYAVVLSRPAWLWGAEMGANEHGVCI GNEAVWGREEVCDEEALLGMDLVRLGLERA DTAEKALNVIVDLLEKYGQGGNCTEGRMVF SYHNSFLIADRNEAWILETAGKYWAAEKVQE GVRNISNQLSITTKIAREHPDMRNYAKRKGW WDGKKEFDFAAAYSYLDTAKMMTSSGRYCE GYKLLNKHKGNITFETMMEILRDKPSGINME GEFLTTASMVFILPQDSSLPCIHFFTGTPDPER SVFKPFIFVPHISQLLDTSSPTFELEDLVKKKS HFKPDRRHPLYQKHQQALEVVNNNEEKAKI MLDNMRKLEKELFREMESILQNKHLDVEKIV NLFPQCTKDEIQIYQSNLSVKVSS

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	ľ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	)	1	peptide	,	/=possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
676	2026	A	5155	2	306	FFFLRRSLALSPRPDCGLQWRNLGSLQAPPPG
		1	-100	-	***	FTPFSCLSLPSSWDYRRPPPRPANFLYF**RRG
						FTLLARMVSIS*PHDPPASASQSAGITGVSHRA
			1			RPT
677	2027	A	5167	97	740	FFHSVDLLALEQSKTFYKPDWFDIVESEVKCC
0,,	2027	^	3107	*'	/40	KEAVCVIDMSSFTEFEITSTGDQALEVLQYLF
	i	ĺ		<b>!</b>		SNDLDVPVGHIVHTGMLNEGGGYENDCSIAR
	1		1	<u> </u>		
						LNKRSFFMISPTDQQVHCWAWLKKHMPKDS
	Ī	ſ	(	{	ĺ	NLLLEDVTWKYTALNLIGPRAVDVLSELSYA
i	l	1				PMTPDHFPSLFCKEMSVGYANGIRVMSMTHT
	<u> </u>	L	<del></del>			GEPGFMLYIPIEYRWGFTMLSTLVSNS
678	2028	Α	5183	1919	2018	PALCRLRDDMTVCVADFGLSKKIYSGDYYRQ
	ì				1	GRIAKMPVKWIAIESLADRVYTSKSDVWAFG
	l	l	1		i	VTMWEIATRGMTPYPGVQNHEMYDYLLHG
	!	ĺ	1	<u>.</u>		HRLKQPEDCLDELCKI**SPQSP
679	2029	Α	5190	39	499	RESQVKHFKMRKIDLCLSSEGSEVILATSSDE
		į				KHPPENIIDGNPETFWTITGMFPQEFIICFHKH
	1	1	}			VRIERLVIQSYFVQTLKIEKSTSKEPVDFEQWI
			į.	ŀ		EKDLVHTEGQLQNEEIVAHDGSATYLRFIIVS
	1		1		İ	AFDHFASVHSVSAEGTVVSNLSS
680	2030	ÍΑ	5204	541	92	EILAVLKLACGDISLNALALMVATAVLTLAPL
						LLICLSYLFILSAILRVPSAAGRCKAFSTCSAH
		1			1	RTVVVVFYGTISFMYFKPKAKDPNVDKTVAL
		}		ļ		FYGVVTPSLNPIIYSLRNAEVKAAVLTLLRGG
	1		1		ŀ	LLSRKASHCYCCPLPLSAGIG
681	2031	A	5207	10	247	VPDNGDVTKLPVCSTLVEETSLTVSEAMEQSI
	1 2031	1	1 220.	. "	1	KNESPLPGTLAHTCNTSTLGGRGRWIT*GREF
		ŀ				DTSMANMVKPCLYRK
682	2032	A	5210	2	231	FFFETESYSITQAGVQWPNLSSLKTLPPGFK*F
002	2032	^	3210	~	1 -3.	SCLSLPSSWDYRCLPPCPANFCIFSRNGVLPC
	1	ĺ	1			WPGWSRTPDLS
683	2033	A	5218	85	402	CPSVSGLIKSDLRRHNINIGITNVDVKAVSNIF
06.7	2033	^	3216	53	702	MILLRSMYRINVKPYFFI*LFFSRVNC*SVIIG
		l				YARCYTFLIF*LFL*IPADSPTDQEPKTVMLSK
	1					OSESAI
684	2034	A	5220	1	194	NLMKEMONLNSENHKTWEEYKDTK*IMSYF
064	2034	^	3220	1	134	YG*ALNVIKMAVLPKLMYRFSATLVKIPQHL
		ļ		1		TDS
106	2025	<del> </del>	5000	260	440	
685	2035	A	5228	260	440	LHSQDGNSDPRKPQGEMSAHAFPVQTCGEED
	0000	<del>  , -</del>	5000		500	QKKTPQVPINFTELSKCS*S*KIMSGERE
686	2036	A.	5239	79	508	GGEAAARAKLSSPRPHRVGRRERGVGGMS
		1			İ	AFSEAALEKKLSELSNSQQSVQTLSLWLIHHR
	1	1			[	KHSRPIVTVWERELRKAKPNRKLTFLYLAND
	i	1				VIQNSKRKGPEFTKDFAPVIVEAFKHVSSETD
	<u>L</u> .	<u></u>	<u> </u>	<u> </u>	1	ESCKKHLGRVLSIWEERS
687	2037	Α	5244	1	428	MAAVVAATALKGRGARNARVLRGILAGATA
						NKASHNRTRALQSHSSPEGKEEPEPLSPELEYI
	1					PRKRGKNPMKAVGLAWAIGFPCGILLFILTKR
		1				EVDKDRVKQMKARQNMRLSNTGEYESQRFR
				l		ASSQSAPSPDVGSGVQT
688	2038	A	5249	1	1407	LQQTEDKSLLNQGSSSEEVAGSSQKMGQPGP
	1			1		SGDSDLATALHRLSLRRQNYLSEKQFFAEEW
			1	<u> </u>		QRKIQVLADQKEGVSGCVTPTESLASLCTTQS
	1	1		1		EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY
	1	1	1	1	1	HWOOLAOPNLGTILDPRPGVITKGFTQLPGD
			1			AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS
	1	1	1	i		KPVTGIFLPPITSAGGPVTVATANPGKCLSCT
	1					NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS
						GSSSNTAVNSPALAYRLSIGESIINRRDSTTT
	1	1	L	L	L	OSSISTATION ALA I RESIDESTITATED STIT

SEQ	ID   SEQ I	D T Me	t SEO	Predicted	Predicted end	1 Aming gold
NO:		f ho	1		nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	) F - F	c	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine
seq-	e seq- uence		USSN		correspondin	g   I=Isoleucine, K=Lysine, L=Leucine
uence			09/496 914	-011 00 p 011 01		M=Methionine, N=Asparagine, P=Proline
1	·		714	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine,
-		1	- }	residue of	sequence	T=Threonine, V=Valine, W=Tryptophan,
- )	,	J		peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
<u> </u>		L	_	sequence		nucleotide insertion
1					<u> </u>	FSSTMSLAKLLQERGISAKVYHSPISENPLQPL
ĺ	1	i		1	1	PKSLAIPSTPPNSPSHSPCPSPLPFEPRVHLSEN
}	1		ł	1		FLASRPAETFLQEMYGLRPSRNPPDVGOLKM
				ŀ	1	NLVDRLKRLGIARVVKNPGAOENGRCOEAEL
	j					GPQKPDSAVYLNSGSSLLGGLRRNOSI PVIM
689	2039	A	5254	1 2	2621	GSFAAPVCTSSPKMGVLKED
	1	'	3234	1	2021	LSLFGSRALGRSGARAMAKAKKVGARRKAS
1	ì		ĺ		1	GAPAGARGGPAKANSNPFEVKVNRQKFQILG RKTRHDVGLPGVSRARALRKRTQTLLKEYKE
1	- 1	- }	- }	1	1	RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA
ļ		1		)		LEQQRHHEKKSIYNLNEDEELTHYGQSLADIE
	ļ			}		KHNDIVDSDSDAEDRGTLSGELTAAHFGGGG
4	ł	1	l l	1	1	GLLHKKTQQEGEEREKPKSRKELIEELIAKSK
1		1				QEKRERQAQREDALELTEKLDODWKFIOTTI
1	ł	ł	- }	1	ł	SHK1PKSENRDKKEKPKPDAYDMMVRELGE
ł	- 1	-	i	l	}	EMKAQPSNRMKTEAELAKEEQEHLRKLEAE
ļ						RLRRMLGKDEDENVKKPKHMSADDLNDGFV LDKDDRRLLSYKDGKMNVEEDVQEEQSKEA
1						SDPESNEEEGDSSGGEDTEESDSPDSHLDLES
	l l	1	1	1	(	NVESEEENEKPAKEQRQTPGKGLISGKERAG
	f	1		1	1	KATRDELPYTFAAPESYEELRSLLLGRSMEFO
						LLVVERIQKCNHPSLAEGNKAKLEKLEGELLE
	ł				İ	Y VGDLA IDDPPDLTVIDKLVVHLYHLCOMEP
1	j		}			ESASDAIKFVLRDAMHEMEEMIETKGRAALP
1				1	İ	GLDVLIYLKITGLLFPTSDFWHPVVTPALVCL
İ	ı	1	1		ľ	SQLLTKCPILSLQDVVKGLFVCCLFLEYVALS QRFIPELINFLLGILYIATPNKASQGSTLVIIPFR
ļ	i	i	i			ALGKNSELLVVSAREDVATWQQSSLSLRWA
	1	1	1			SRLRAPISTEANHIRLSCLAVGLALLKRCVLM
l	1	ĺ	1			YGSLPSFHAIMGPLRALLTDHLADCSHPOPLO
		1	1	1		ELCOSTLTEMESOKOLCRPLTCEKSKPVPI K1
			1			FTPRLVKVLEFGRKOGSSKEEOERKRLIHKHK
	ľ	1	l	1 1		KEFKGAVREIRKDNOFLARMOLSEIMERDAE
690	2040	A	5261	1	304	RKRKVKQLFNSLATQEGEWKALKRKKFKK
	1	1	1	] -	304	FFFFVFLVETGFHHVGQAGLELLTSGDPPTW ASQSAGITGVSHCSWPVIYVLSTLLHAVRNVL
	1	1	<b>1</b>	[		FKRTFPLKSSSFLSYDKEIFPILIVLKFYLVTLT
(0)		<u> </u>				SFVK
691	2041	A	5270	3	158	NCHTTHCTANWVHLPGTPPGWKIDGPAAAL
692	2042	<del> </del>	+			EVLSSFFFFFLKFSYKPONIV
072	2042	A	5282	56	1268	GMEPVGCCGECRGSSVDPRSTFVLSNI.AEVV
		}	]			ERVLTFLPAKALLRVACVCRLWRECVRRVLR
	1	[		ſ		THRSVTWISAGLAEAGHLEGHCLVRVVAEEL
				ľ		ENVRILPHTVLYMADSETFISLEECRGHKRAR
		[			ľ	KRTSMETALALEKLFPKQCQVLGIVTPGIVVT PMGSGSNRPQEIEIGESGFALLFPQIEGIKIQPF
		ĺ	1 1	1		HFIKDPKNLTLERHQLTEVGLLDNPELRVVLV
		Į	}	- 1		FGYNCCKVGASNYLQQVVSTFSDMNIILAGG
				1		QVDNLSSLTSEKNPLDIDASGVVGLSESGHRI
		ſ		ĺ	[	QSATVLLNEDVSDEKTAEAAMORLKAANIPE
				ł		IINTIGEMEACYGRGEOYYRAKGNYEADAED
		l	}		-	KFFPSVPLFGFFGNGEIGCDRIVTGNFILRKCN
693	2043	A	5301	363	607	EVKDDDLFHSYTTIMALIHLGSSK
	~~~	^	3301	362	507	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
694	2044	Ā	5310	1	204	ACFPTNIVTLCHSIA
				- 1	204	RVLTAINHTLKENLRKFYKGKKDKPLDLRPK
	<u>                                      </u>			-		KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA
695	2045	Ā	5315	125	1596	ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP
						- COURTEDICTIVITATALP

SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I-Isoleucine, K-Lysine, L-Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ		ĺ	peptide		/-possible nucleotide deletion, \-possible
_	1		l	sequence	<u> </u>	nucleotide insertion
						TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
			1			SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
	j					LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
	i				İ	CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR
			1			ATIQFHQPQRFKDELWRIQEKLECYFGSLVGS
		İ	ŀ			NVYITPAGSQGLPPHYDDVEVFILQLEGEKH
	ľ		1	ì	1	WRLYHPTVPLAREYSVEAEERIGRPVHEFML
						KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
			1			YQNNSWGDFLLDTISGLVFDTAKEDVELRTG
			1	1	ļ	IPRQLLLQVESTTVATRRLSGFLRTLADRLEG
			]			TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
l	1	j	]	1		GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
						GLRFPLSHLDALKQIWNSPAISVKDLKLTTDE
		i				EKESLVLSLWTECLIQVV
696	2046	A	5318	1476	742	LMKXYLEAAELGEISDIHTKLLRLSSSOGTIET
0,0	2040	^	3310	1470	/ · · ·	SLODIDSRLSPGGSLADAWAHOEGTHPKDRN
	1		1			VEKLOVLLNCMTEIYYOFKKDKAERRLAYN
Ì	i	1	i	1	1	EEQIHKFDKQKLYYHATKAMTHFTDECVKK
						YEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDI
		ł			]	EEEVSKYQEYTNELQETLPQKMFTASSGIKHT
	i		1	)	į	MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
					1	LAENNHILESGGSLTMDGGLRNVDCL
697	2047	A	5320	244	478	LDYNFFLFEMTFGLVSQAGVQWHDLGSLQPP
			1			PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
	l	[			l	VSPSWPGWSRTPDFR
698	2048	Α	5324	266	714	LPIRKSLRSVRSGFPTSQSPITRNLDGTASGSC
						LAKTVTGSLFRINVGLRGLVAGGIIGALLGTP
			i		1	VGGLLMAFQKYSGETVQERKQKDRKALHEL
						KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
700	2049	A	5224	699	277	KKIEALLNLPRNPSVIDKQDKD
699	2049	A	5334	099	211	RPHGHLVCISSSAGLSGVNGLADYCASKFAA
						FGFAESVFVETFVQKQKGIKTTIVCPFPIKTGM FEGCTTGCPSLLPILEPKYAVEKIVEAILQEKM
						YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
		ļ				LHAMDGFADQKK
700	2050	A	5344	3	614	PTAEEMSSLTPESSPELAKRSWFGNFISLDKEE
700	2030	l ( )		ا آ	***	OIFLVLKDKPLSSIKADIVHAFLSIPSLSHSVLS
				1		QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG
		1				PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV
						VETIQAQLLSTHDQPSVQALADEKNGAQTRP
		}				AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
						LLATNGTPL
701	2051	A	5346	3	1383	HASVLFCRVMAASKTQGAVARMQEDRDGSC
		ŀ	1			STVGGVGYGDSKDCILEPLSLPESPGGTTTLE
		1				GSPSVPCIFCEEHFPVAEQDKLLKHMIIEHKIV
			1			IADVKLVADFQRYILYWRKRFTEQPITDFCSV
	1	}	1		1	IRINSTAPFEEQENYFLLCDVLPEDRILREELQ
	1	1	1		İ	KQRLREILEQQQQERNDTNFHGVCMFCNEEF
	[	1				LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL
	1	ł				CTLQKKLDNLQCLYCEKTFRDKNTLKDHMR
						KKQHRKINPKNREYDRFYVINYLELGKSWEE
		1	1			VQLEDDRELLDHQEDDWSDWEEHPASAVCL
		[				FCEKQAETIEKLYVHMEDAHEFDLLKIKSELG
			1			LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS
	]	j	l			KADLRTHMEETKHTSLLPDRKTWDQLEYYFP
		1	1			TYENDTLLWTLSDSESDLTAQEQNENVPIISE
		L <u>.                                    </u>	60.00		1.5.60	DTSKLYALKQSSILNQLLL
702	2052	<u>A</u>	5356	2502	1540	MAAATRGCRPWGSLLGLLGLVSAAAAAWD

			1	,	- <del> </del>	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	-		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide		/=possible nucleotide deletion, \=possible
	ļ. <u>.</u>	L		sequence		nucleotide insertion
					}	LASLRCTLGAFCECDFRPDLPGLECDLAQHL
	1	ĺ	Ϊ	ĺ	İ	AGQHLAKALVVKALKAFVRDPAPTKPLVLSL
		1		1		HGWTGTGKSYVSSLLAHYLFQGGLRSPRVH
	1	ľ				HFSPVLHFPHPSHIERYKKDLKSWVQGNLTA
	ļ		ł			CGRSLFLFDEMDKMPPGLMEVLRPFLGSSWV
		1	i	1	ĺ	VYGTNYRKAIFIFISNTGGEQINQVALEAWRS
		1	ļ	1	}	RRDREEILLQELEPVISRAVLDNPHHGFSNSGI
		Ì	ŀ			MEERLLDAVVPFLPLQRHHVRHCVLNELAQL
	ļ					GLEPRDEVVQAVLDSTTFFPEDEQLFSSNGCK
	}		ł			TVASRIAFFL
703	2053	A	5380	278	657	LFLQKLRMKTEEEARTHTEIEMFLRKEQQKL
		i				EERLEFWMEKYDKDTEMKQNELNALKATKA
		1	[			SDLAHLQDLAKMIREYEQVIIEDRIEKERSKK
					1	KVKQDLLELKSVIKLQAWWRGTMIRREIGGF
	ŀ		1			KM
704	2054	Α	5381	1	1003	FRGRAVKMAAVVEVEVGGGAAGERELDEV
	ļ					DMSDLSPEEQWRVEHARMHAKHRGHEAMH
				1	}	AEMVLILIATLVVAQLLLVQWKQRHPRSYN
			l		1	MVTLFQMWVVPLYFTVKLHWWRFLVIWILF
	1	1	ł		}	SAVTAFVTFRATRKPLVQTTPRLVYKWFLLIY
						KISYATGIVGYMAVMFTLFGLNLLFKIKPEDA
			Ĭ.			MDFGISLLFYGLYYGVLERDFAEMCADYMA
					ł	STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV
						SEEGIIENTYRLSCNHVFHEFCIRGWCIVGKK
	1	į.	1			QTCPYCKEKVDLKRMFSNPWERPHVMYGQL
	ĺ		í		1	LDWLRYLVAWQPVIIGVVQGINYILGLE
705	2055	A	5396	3	675	IYDRDPLQLATRAGQPLDINMAGEPKPYRPKP
						GNKRPLSALYRLESKEPFLSVGGYVFDYDYY
						RDDFYNRLFDYHGRVPPPPRAVIPLKRPRVA
	•	1	Ī		[	VTTTRRGKGVFSMKGGSRSTASGSTGSKLKS
		1	1			DELQTIKKELTQIKTKIDSVLGRLDKIEKQQK
			1			AEAEAQKKLLEESLVLIQEECVSEIADHSTEEP
		i			1	AEGGPDADGEEMTDGIEEAFDEDGGHELFLQ
					1	IK
706	2056	A	5410	2	98	GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI
	i					S
707	2057	A	5415	6	287	PFKLTPSFLSHAFSSGQERKVFIELNHIKKCNT
		1	]	ļ -	i	VRGVFVLEEFGNYTILLLGLDSHGSNSNLGAP
	]	İ	1		1	EEGLGAGRKRTSVEKSGGAGVTRKKRDP
708	2058	A	5423	3	291	SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS
		1		-		TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS
					1	GCTIFKTVTLTARSTASLLKSVRPRTHQKE
709	2059	A	5424	679	347	RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG
	-327	[	1	1	1	SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ
	1	1				VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK
	1	1			1	GKWFCPRCVQEKRKKK
710	2060	A	5442	1073	559	QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS
710	2000	^		1075	1 337	GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY
	Į	1	1		1	EESDSDESWTTESAISSEAILSSMCMNGGEEK
	}				1	PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI
		1			1	RVRKPFKCRCGKSYKTAOGLRHHTINFHPPV
	1	1		ł	_	SAEIIRKMOO
711	2063	<del> </del>	6440	<del> </del>	210	GDSLCVPQYNKYREERVILFLKMASGHAFQP
711	2061	Α	5449	1	319	
					1	DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL
		1	1		1	NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD
	20.52	<b>⊢.</b> —	5455	<u> </u>	<del></del>	LYRDIPELQGF
717	2062	Α	5499	T 91	749	RPTPGHGDFWMOPLTKDAGMSLSSVTLASAL
712	2002	^	3477		1	
/12	2002	^	3477	-	]	QVRGEALSEEEIWSLLFLAAEQLLEDLRNDSS DYVVCPWSALLSAAGSLSFQGRVSHIEAAPF

nucleotide seq- unce colde seq- unce colde seq- unce colde seq- unce colde seq- unce colde seq- unce colde seq- unce colde sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Design   Seq	NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide	D-Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine
194							
1914			i				
mino acid residue of sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence			1	l .			
Page		İ	ſ				
		1			residue of		
		]			peptide		/=possible nucleotide deletion, \=possible
			1		sequence		nucleotide insertion
RRCTLOSVLEACRYMEKEVSVYPAPAGILHR							KAPELLQGQSEDEQPDASQMHVYSLGMTLY
RIVGLVICHTSEVSREPCESSSCWCVCVAIKI   2063   A   5506   22   478   VEELLVSRLOPHLHTPMYFELAHLST,DLSTT   TSSIPQLI,YNLNGCDKTISYMGCAJQLFLEIGL   GGVECLLLAWAYDRCVALCHLFIGH   GGVECLLLAWAYDRCVALCHLFIGH   GGVECLLLAWAYDRCVALCHLPMAYINN   PRICRGI,VSVTWGCGVANSILAMSPVTUR.PR   COHHEVDHELCEMPALIRMACISTV     2064   A   5514   25   220   ARPYWCENNIGIGKLSTADGKAFADPEVUR   RITSSVSCALDEAAAALTMRAESTANAGQ	ł	Ì	ſ				WSAGFHVPPHQPLQLCEPLHSILLTMCEDQPH
13	1				1		RRCTLQSVLEACRVHEKEVSVYPAPAGLHIR
TSSIPQLLYNLINGCDKTISYMGCAJQLELEJGL				1			RLVGLVLGTISEVSREPCFSSSSCWSCVAIKI
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721 2071 A 5632 146 536 MSALIVRKLRSAELTLFSELPTVLGANVNAA KLHETALHHAAKVKNVDLIEMLIEFGGNIYA RDNRGKKPSDYTWSSSAPAKCFEYYEKTPLT LSQLCRVNLRKATGVRGLEKIAKLNIPPRLID YLSYN  722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVR VEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCPC HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT	l	1	ĺ	ł			
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RDNRGKKPSDYTWSSSAPAKCFEYYEKTPLT LSQLCRVNLRKATGVRGLEKIAKLNIPPRLID YLSYN  722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT	121	20/1	^	7032	140	230	
LSQLCRVNLRKATGVRGLEKIAKLNIPPRLID YLSYN  722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT			l				
722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT			1				
722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGHLQILLMF TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT	}	1	l	l	1		
TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVR VEKNQELCHLSTIDW GLLQPAGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT	722	2072	A	5638	3	3806	
LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAPGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT	'		l **	~~~	~	2000	
VALPALGAVLRGAVRVEKNQELCHLSTIDW GLLQPAGANHIVGNKLGEECADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT							
GLLQPAPGANHIVGNKLGEEČADVCPGVLGA AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT				}	}		
AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT			l				·
HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT							
ACRHLYFQGACLWACPPGTYQYESWRCVTA ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT			,				
ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT			]				
	1		1				
	1	}	İ		1		RNSSSIFCHKCEGLCPKECKVGTKTIDSIQAA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QDLVGCTHVEGSLILNLRQGYNLEPQLQHSL GLVETITGFLKIKHSFALVSLGFFKNLKLIRGD AMVDGNYTLYVLDNQNLQQLGSWVAAGLTI PVGKIYFAFNPRLCLEHIYRLEEVTGTRGRQN KAEINPRTNGDRAACQTRTLRFVSNVTEADRI LLRWERYEPLEARDLLSFIVYYKESPFQNATE HVGPDACGTQSWNLLDVELPLSRTQEPGVTL ASLKPWTQYAVFVRAITLTTEEDSPHQGAQS PIVYLRTLPAAPTVPQDVISTSNSSSHLLVRW KPPTQRNGNLTYYLVLWQRLAEDGDLYLND YCHRGLRLPTSNNDPRFDGEDGDPEAEMESD CCPCQHPPPGQVLPPLEAQEASFQKKFENFLH NAITIPISPWKVTSINKSPQRDSGRHRRAAGPL RLGGNSSDFEIQEDKVPRERAVLSGLRHFTEY RIDIHACNHAAHTVGCSAATFVFARTMPHRE ADGIPGKVAWEASSKNSVLLRWLEPPDPNGL ILKYEIKYRRLGEEATVLCVSRLRYAKFGGV HLALLPPGNYSARVRATSLAGNGSWTDSVAF YILGPEEEDAGGLHVLLTATPVGLTLLIVLAA LGFFYGKKRNRTLYASVNPEYFSASDMYVPD EWEVPREQISIRELGQGSFGMVYEGLARGLE AGEESTPVALKTVNELASPRECIEFLKEASVM KAFKCHHVVRLLGVVSQGQPTLVIMELMTR GDLKSHLRSLRPEAENNPGLPQPALGEMIQM ACEIADGMAYLAANKFVHRDLAARNCMVSQ DFTVKIGDFGMTRDVYETDYYRKGGKGLLP VRWMAPESLKDGIFTTHSDVWSFGVVLWEIV TLAEQPYQGLSNEQVLKFVMDGGVLEELEGC PLQLQELMSRCWQPNPRLRPSFTHILDSIQEEL RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSP TPRDCSPQNGGPGH
723	2073	A	5672	1	216	LAWIDNILPEKEKKETDKKRKRKKGAHEDCD EEPQFPPPSVIKIPMESVQSDPQNGIHCIARKR SSSWSYSL
724	2074	A	5704	4235	940	ARGRRSRPVWAASWGGRGRPAARRPRGLA ATMGFELDRFDGDVDPDLKCALCHKVLEDP LTTPCGHVFCAGCVLPWVVQEGSCPARCRGR LSAKELNHVLPLKRLILKLDIKCAYATRGCGR VVKLQQLPEHLERCDFAPARCRHAGCGQVLL RRDVEAHMRDACDARPVGRCQEGCGLPLTH GEQRAGGHCCARALRAHNGALQARLGALHK ALKEALRAGKREKSLVAQLAAAQLELQMT ALRYQKKFTEYSARLDSLSRCVAAPPGGKGE ETKSLTLVLHRDSGSLGFNIIGGRPSVDNHDG SSSEGIFVSKIVDSGPAAKEGGLQHDRIIEVN GRDLSRATHDQAVEAFKTAKEPIVVQVLRRT PRTKMFTPPSESQLVDTGTQTDITFEHIMALT KMSSPSPPVLDPYLLPEEHPSAHEYYDPNDYI GDIHQEMDREELELEEVDLYRMNSQDKLGLT VCYRTDDEDDIGIYISEIDPNSIAAKDGRIREG DRIIQINGIEVQNREEAVALLTSEENKNFSLLI ARAELQLDEGWMDDDRNDFLDDLHMDMLE EQHHQAMQFTASVLQQKKHDEDGGTTDTAT ILSNQHEKDSGVGRTDESTRNDESSEQENNG DDATASSNPLAGQRKLTCSQDTLGSGDLPFS NESFISADCTDADYLGIPVDECERFRELLELK CQVKSATPYGLYYPSGPLDAGKSDPESVDKE LELLNEELRSIELECLSIVRAHKMQQLKEQYR ESWMLHNSGFRNYNTSIDVRRHELSDITELPE KSDKDSSSAYNTGESCRSTPLTLEISPDNSLRR

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide scq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  AAEGISCPSSEGAVGTTEAYGPASKNLLSITE DPEVGTPTYSPSLKELDPNQPLESKERRASDG SRSPTPSQKLGSAYLPSYHHSPYKHAHIPAHA QHYQSYMQLIQQKSAVEYAQSQMSLVSMCK DLSSPTPSEPRMEWKVKIRSDGTRYITKRPVR DRLLRERALKIREERSGMTTDDDAVSEMKM GRYWSKEERKQHLVKAKEQRRRREFMMQSR LDCLKEQQAADDRKEMNILELSHKKMMKKR NKKIPDNWMTIQELLTHGTKSPDGTRVYNSF LSVTTV
725	2075	A	5707	3	1770	OISTEVSEAPVANDKPKTLVVKVQKKAADLP DRDTWKGRFDFLMSCVGYAIGLGNVWRFPY LCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLG QYTSIGGLGVWKLAPMFKGVGLAAAVLSFW LNIYYIVIISWAIYYLYNSFTTTLPWKQCDNP WNTDRCFSNYSMVNTTNMTSAVVEFWERN MHQMTDGLDKPGQIRWPLAITLAIAWILVYF CIWKGVGWTGKVVYFSATYPYIMLIILFFRGV TLPGAKEGILFYITPNFRKLSDSEVWLDAATQ IFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVC CINSCTSMFAGFVIFSIVGFMAHVTKRSIADV AASGPGLAFLAYPEAVTQLPISPLWAILFFSM LLMLGIDSQFCTVEGFITALVDEYPRLLRNRR ELFIAAVCIISYLIGLSNITQGGIYVFKLFDYYS ASGMSLLFLVFFECVSISWFYGVNRFYDNIQE MVGSRPCIWWKLCWSFFTPIIVAGVIFFSAVQ MTPLTMGNYVFPKWGQGVGWLMALSSMVL IPGYMAYMFLTLKGSLKQRIQVMVQPSEDIV
726	2076	A	5711	156	423	RPENGPEQPQAGSSTSKEAYI PRRDPGRTPELRGSAPRKTGANMPVRRGHVA PQNTFLGTIIRKFEGQNKKFIIANARVQNCAII
727	2077	A	5716	3	274	YCNDGFCEMTGFSRPDVMQKPCTCD HASEYFFKLCSFQVFLSFPLATIVIDVGLVVIP LVKSPNVHYVYVLLLVLSGLLFYIPLIHFKIRL AWFEKMTCYLQLLFNICLPDVSEE
728	2078	A	5737	1899	649	IQASRASPYPRVKVDFALSCHEDLLAPISEPIE WKYHSPEEEISLGPACWLWDFLRRSQQAGFL LPLSGGVDSAATACLIYSMCCQVCEAVRSGN EEVLADVRTIVNQISYTPQDPRDLCGRILTTC YMASKNSSQETCTRARELAQQIGSHHISLNID PAVKAVMGIFSLVTGKSPLFAAHGGSSRENL ALQNVQARIRMVLAYLFAQLSLWSRGVHGG LLVLGSANVDESLLGYLTKYDCSSADINPIGG ISKTDLRAFVQFCIQRFQLPALQSILLAPATAE LEPLADGQVSQTDEEDMGMTYAELSVYGKL RKVAKMGPYSMFCKLLGMWRHICTPRQVAD KVKRFFSKYSMNRHKMTTLTPAYHAENYSPE DNRFDLRPFLYNTSWPWQFRCIENQVLQLER AEPQSLDGVD
729	2079	A	5741	1	5976	PGCAARLSRARAPGPGAAGAGRKRLADPGPP PASRRLRAPGSRPRLAPCTRRAAQPAHARMA PRAAGGAPLSARAAAASPPFFQTPPRCPVPLL LLLLLGAARAGALEIQRRFPSPTPTNNFALDG AAGTVYLAAVNRLYQLSGANLSLEAEAAVG PVPDSPLCHAPQLPQASCEHPRRLTDNYNKIL QLDPGQGLVVVCGSIYQGFCQLRRRGNISAV AVRFPPAAPPAEPVTVFPSMLNVAANHPNAS TVGLVLPPAAGAGGSRLLVGATYTGYGSSFF PRNRSLEDHRFENTPEIAIRSLDTRGDLAKLFT

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I—Isoleucine, K=Lysine, L-Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion FDLNPSDDNILKIKQGAKEQHKLGFVSAFLHP SDPPPGAQSYAYLALNSEARAGDKESQARSL LARICLPHGAGGDAKKLTESYIQL.GLQCAGG AGRGDLYSRLVSVFPARERLFAVFERPQGSPA ARAAPAALCAFRFADVRAAIRAARTACFVEP APDVVAVLDSVVQGTGPACERKLNIQLQPEQ LDCGAAHLQHPLSILQPLKATPVFRAPGLTSV AVASVNNYTAVFLGTVNGRLLKINLNESMQ VVSRRVVTVAYGEPVHHVMQFDPADSGYLY LMTSHQMARVKVAACNVHSTCGDCVGAAD AYCGWCALETRCTLQQDCTNSSQQHFWTSA SEGPSRCPAMTVLPSEIDVRQEYPGMILQISGS LPSLSGMEMACDYGNNIRTVARVPGPAFGHQ IAYCNLLPRDQFPPFPPNQDHVTVEMSVRVN GRNIVKANFTTYDCSRTAQVYPHTACTSCLSA QWPCFWCSQQHSCVSNQSRCEASPNPTSPQD CPRTLLSPLAPVPTGGSQNILVPLANTAFFQG AALECSFGLEEIFEA VWVNESVYRCDQVVLH TTRKSQVFPLSLQLKGRPARFLDSPEPMTVM VYNCAMGSPDCSQCLGREDLGHLCMWSDGC RLRGPLQPMAGTCPAPEIRAIEPLSGPLDGGT LLTIRGRNLGRRLSDVAHGWIGGVACEPLP DRYTVSEEIVCVTGPAPGPLSGVVTVNASKE GKSRDRFSYVLPLVHSLEPTMGPKAGGTRITI HGNDLHVGSELQVLVNDTDPCTELMRTDTS ACTMPEGALPAPVPVCVRFERRGCVHGNLTF WYMQNPVITAISPRRSPVSGGRTITVAGERFH MVQNVSMAVHHIGREPTLCKVLNSTLITCPSP GALSNASAPVDFFINGRAYADEVAVAEELLD PEEAQRGSRFRLDYLPNPQFSTAKREKWIKH HPGEPLTLVHVSTKGAGKEQDSLGLQSHEY RVKIGQVSCDIQIVSDRIHCSVNESLGAAVGQ LPITIQVGNFNQTIATLQLGGSETAIIVSIVICSV LLLSVVALFVFCTKSRRAERYWQKTLLQME EMESQIREEIRKGFAELQTDMTDLTKELNRSQ GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT LNSQGSSQAQETHPLLGGWKESLCAAVGQ LPTIQVGNFNQTIATLQLGGSETAIIVSIVICSV LLLSVVALFVFCTKSRRAERYWQKTLLQME EMESQIREEIRKGFAELQTDMTDLTKELNRSQ GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT LNSQGSSQAQETHPLLGEWKIPESCRPNMEE GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD RCSLASLLTIALHGKLEYYTSIMKELLVDLID ASAAKNPKLMTRRTESVVEKMLTNWMSICM YSCLRETVGEPFFLLLCAIKQQINKGSIDAITG KARYTLNEEWLLRENIEAKPRNLNVSFQGCG MDSLSVRAMDTDTLTQVKEKILEAFCKNVPY SQWPRAEDVDLEWFASSTQSYILRDLDDTSV VEDGRKKLNTLAHYKIPEGASLAMSLIDKKD NTLGRVKDLDTEKYPHLVLIPTDELAEPKKSH RQSHRKKNLPPEYFRIVQRYYKOIQDMTPLS
					,	PDTLHIWKTNSLPLRFWVNILKNPQFVFDIDK TDHIDACLSVIAQAFIDACSISDLQLGKDSPTN KLLYAKEIPEYRKIVQRYYKQIQDMTPLSEQE MNAHLAEESRKYQNEFNTNVAMAEIYKYAK RYRPQIMAALEANPTARRTQLQHKFEQVVAL MEDNIYECYSEA
730	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ VANGKGNQRNMGSPQPSLLAFERNLELQIMG LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT LKD
731	2081	A	5747	1	382	FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC FRVDEVNWTTWNTNVGIINEDPGNCEGVKRT

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	[	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq+		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
{			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
j		ļ.		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	!			peptide		/=possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
ł	i					LSFSLRSSRVSGRHWKNFALVPLLREASARD
l	į	ļ	ļ	ŀ		RQSAQPEEVYLRQFSGSLKPEDAEVFKSPAAS
	2000	<u> </u>		100		GEK
732	2082	A	5753	198	3	AQAESSTVASPEATAGPLCTRIPNVPPPTPIRP
722	2002	<u> </u>	FOF A	<u> </u>	2000	PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
733	2083	A	5754	2	2223	AAGPPGLEÄEGRAPESAGPGPGGDAAETPGL
1				ŀ	1	PPAHSGTLMMAFRDVTVQIANQNISVSSSTAL
			]	ļ		SVANCLGAQTVQAPAEPAAGKAEQGETSGR
i	ļ			}		EAPEAPAVGREDASAEDSCAEAGASGAADG
ſ		]	1	ĺ	[	ATAPKTEEEEEEEETAEVGRGAEAEAGDLEQ
	ļ	Į.				LNRTSTSTKSAKSGSEASASASKDALQAMILS
	}	].			i	LPRYHCENPASCKSPTLSTDTLRKRLYRIGLN
	ŀ		1	i		LFNINPDKGIQFLISRGFIPDTPIGVAHFLLQRK
ł		ŀ	ŀ	ì	1	GLSRQMIGEFLGNSKKQFNRDVLDCVVDEM
				<u>.</u>		DFSSMELDEALRKFQAHIRVQGEAQKVERLIE
	ŀ			i		AFSQRYCMCNPEVVQQFHNPDTIFILAFAIILL
	i					NTDMYSPNIKPDRKMMLEDFIRNLRGVDDG
ļ	l			l	]	ADIPRELVVGIYERIQQKELKSNEDHVTYVTK
	[	1			i	VEKSIVGMKTVLSVPHRRLVCCSRLFEVTDV
						NKLQKQAAHQREVFLFNDLLVILKLCPKKKS
						SSTYTFCKSVGLLGMQFQLFENEYYSHGITLV TPLSGSEKKOVLHFCALGSDEMOKFVEDLKE
				ĺ		SIAEVTELEOIRIEWELEKQQGTKTLSFKPCGA
ľ	ĺ	i		Ī	ĺ	QGDPQSKQGSPTAKREAALRERPAESTVEVSI
					]	HNRLQTSQHNSGLGAERGAPVPPPDLQPSPPR
!			ŀ			QQTPPLPPPPPTPPGTLVQCQQIVKVIVLDKPC
l						LARMEPLLSQALSCYTSSSSDSCGSTPLGGPG
}			ŀ		}	SPVKVTHQPPLPPPPPPYNHPHQFCPPGSLLH
						GHRYSSGSRSLV
734	2084	Α -	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGTP
7.54	2004	^	3786	6	302	IDDVMRVLDIDEFPQSGNYETIGGFMMFMLR
i				J		KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLVT
		1				RIDSKATALSPKLPDAKDKEESVA
735	2085	A	5827	1	1257	MVFSAVLTAFHTGTSNTTFVVYENTYMNITL
, 33	2005	1	3027	·	1237	PPPFQHPDLSPLLRYSFETMAPTGLSSLTVNST
		l				AVPTTPAAFKSLNLPLQITLSAIMIFILFVSFLG
		ľ	i			NLVVCLMVYQKAAMRSAINILLASLAFADM
						LLAVLNMPFALVTILTTRWIFGKFFCRVSAMF
		1			1	FWLFVIEGVAILLIISIDRFLIIVQRQDKLNPYR
		1		i	}	AKVLIAVSWATSFCVAFPLAVGNPDLQIPSRA
			1			PQCVFGYTTNPGYQAYVILISLISFFIPFLVILY
						SFMGILNTLRHNALRIHSYPEGICLSQASKLGL
		İ				MGLQRPFQMSIDMGFKTRAFTTILILFAVFIVC
		1	:	Ì		WAPFTTYSLVATFSKHFYYQHNFFEISTWLL
		ļ	]		]	WLCYLKSALNPLIYYWRIKKFHDACLDMMP
						KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTVV
736	2086	A	5870	3	268	FTRSDELARHYRTHTGEKRFSCPLCPKOFSRS
				-		DHLTKHARRHPTYHPDMIEYRGRRRTPRIDPP
			[			LTSEVESSASGSGPGPAPSFTTCL
737	2087	A	5871	2	521	LTWPOLFLETLPELLHMSRPAEDGPSPGALVR
,	2001	1		-		RSSSLGYISKAEEYFLLKSRSDLMFEKOSERH
						GLARRLTTARRPPASSEQAQQELFNELKPAV
			1			DGANFIVNHMRDQNNYNEEKDSWNRVART
				i		VDRLCLFVVTPVMVVGTAWIFLQGVYNQPPP
			[			QPFPGDPYSYNVQDKRFI
738	2088	Α	5881	1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDCG
,50	2000	^	7001	•	1100	LLDSSKLCDYENRFNTSKGGELPDRPAGVGV
						YSAMWQLALTLILKIVITIFTFGMKIPSGLFIPS
			1		<u> </u>	MAVGAIAGRILGVGMEQLAYYHQEWTVFNS
		L			L	THE COMMISSION OF THE PART THE PART THE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	•	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ŀ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ŀ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1			ļ	peptide	_	/=possible nucleotide deletion, \=possible
ł	•	}	i	sequence	{	nucleotide insertion
			<b>-</b>	<del>                                     </del>		WCSQGADCITPGLYAMVGAAACLGGVTRMT
				:	İ	VSLVVIMFELTGGLEYIVPLMAAAMTSKWVA
1						DALGREGIYDAHIRLNGYPFLEAKEEFAHKTL
		l l				AMDVMKPRRNDPLLTVLTQDSMTVEDVETII
		1			1	SETTYSGFPVVVSRESQRLVGFVLRRDLIISIE
						NARKKQDGVVSTSIIYFTEHSPPLPPYTPPILK
1		1		1		LRNILDLSPFTVTDLTPMEIVVDIFRKLGLRQC
			ŀ		,	LVTHNGRLLGIITKKDVLKHIAQMANQDPDSI
						LFN
739	2089	Α	5892	2	916	TLQLAASVPFFAISLISWWLPESARWLIINGKP
		1				DOALQELRKVARINGHKEAKNLTIEVLMSSV
				1		KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV
				1		VNFSLLISYYGLVFDLQSLGRDIFLLQALFGA
				1		VDFLGRATTALLLSFLGRRTIQAGSQAMAGL
			{	i	{	AILANMLVPQDLQTLRVVFAVLGKGCFGISL
				1		TCLTIYKAELFPTPVRMTADGILHTVGRLGA
						MMGPLILMSRQALPLLPPLLYGVISIASSLVVL
	ŀ					FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE
		1				AFTVESTSLLEIVALHGAL
740	2090	A	5900	2	426	RPIKTLGIGFHFSVDGVHFLTQREVQNLWKE
		l	}			NLIILDTAKKHGYEVVDTFTITMGRYKEFLQG
			1			KCGCHFHEVVKSKLSKEYNFIKMKRSRNHIM
		1	ł	l		GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV
ļ				}		CSEILLSRMCANKRTM
741	2091	Α	5910	3	412	RMPESTLLIICENGYILEAPLPTIKQEEDDHDV
- 1						VSYEIKDMCIKCFHFSSVKSKILRLIEIEKRER
						QRELKEKIREERRNKLAAEMGEDGEKEFQEE
		ľ	ľ		İ	EEEKEEEEEEEPLPEIFIPSTPSPILCGFYSEPG
					l	KFWV
742	2092	Α	5936	1	482	MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV
		ļ	ł	1		TQMGNDKSIKCEQNLGHDTMYWYKQDSKK
		1				FLKIMFSYNNKELIINETVPNRFSPKSPDKAHL
		1	ļ	1	•	NLHINSLELGDSAVYFCASSQDTALQSHCIPV
-					j	HKPPGSARKLQGSVCTCTQGSSLHSLMASDG
						VPVC
743	2093	A	5938	1	1566	MNSFFGTPAASWCLLESDVSSAPDKEAGRER
		1	1	1		RALSVQQRGGPAWSGSLEWSRQSAGDRRRL
		1	1	1		GLSRQTAKSSWSRSRDRTCCCRRAWWILVPA
		l l	ł	1	Į	ADRARRERFIMNEKWDTNSSENWHPIWNVN
				1		DTKHHLYSDINITYVNYYLHQPQVAAIFIISYF
			1			LIFFLCMMGNTVVCFIVMRNKHMHTVTNLFI
		j	]	1		LNLAISDLLVGIFCMPITLLDNIIAGWPFGNTM
		1				CKISGLVQGISVAASVFTLVAIAVDRFQCVVY
		1		ļ		PFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLH
				1		VQEEKYYRVRLNSQNKTSPVYWCREDWPNQ
			1	[	1	EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLF
		J		1		RAAVPHTGRKNQEQWHVV\$RKKQKIIKMLLI
		l				VALLFILSWLPLWTLMMLSDYADLSPNELQII
		1				NIYTYPFAHWLAFGNSSVNPITYGFFNENFRRG
		t				FQEAFQLQLCQKRAKPMEAYALKAKSHVLIN
		ĺ	1	ĺ		TSNQLVQESTFQNPHGETLLYRKSAEKPQQE
	200:	<del> </del>	6066	<del> </del>	707	LVMEELKETTNSSEI
744	2094	A	5966	149	327	SHVCVSHYAGSSGCPAGAGAGAVALGISAVA
		ı	1	L	L	LYDYQGGRLGVARGAWYMEAPDIRQGDM
745						
. , ,	2095	A	5970	413	856	GAPHTDWAWAPTPMSGLGSGRGRQGTLASS
	2095	A	5970	413	856	PLSLPLLLAGVTGILATELFDQMARPAACMV
	2095	A	5970	413	856	PLSLPLLLAGVTGILATELFDQMARPAACMV CGALMWIMLILVGLGFPFIMEALSHFLYVPFL
	2095	A	5970	413	856	PLSLPLLLAGVTGILATELFDQMARPAACMV

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	scq-	1	USSN	location	corresponding	I-Isoleucine, K-Lysine, L-Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino acid residue	M-Methionine, N=Asparagine, P=Proline, O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
}		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		İ		peptide	sequence	/=possible nucleotide deletion, \=possible
ļ ļ				Sequence	}	nucleotide insertion
746	2096	A	5971	3	1343	AQTARRIIGLELDTEGHRLFVAFSGCIVYLPLS
/40	2000	11	33.1	١	'343	RCARHGACQRSCLASQDPYCGWHSSRGCVDI
1		ŀ	ļ			RGSGGTDVDQAGNQESMEHGDCQDGATGSQ
1 (			Ì	ŀ		SGPGDSAYGVRRDLPPASASRSVPIPLLLASV
l			ŀ			AAAFALGASVSGLLVSCACRRAHRRRGKDIE
·					ţ	TPGLPRPLSLRSLARLHGGGPEPPPPSKDGDA
ĺ		i	į		İ	VQTPQLYTTFLPPPEGVPPPELACLPTPESTPE
				1	ł	LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR
				İ		GGHAAGGPAPRVLVRPPPPGCPGQAVEVTTL
				ĺ		EELLRYLHGPQPPRKGAEPPAPLTSRALPPEP
l		]		J	}	APALLGGPSPRPHECASPLRLDVPPEGRCASA
i l					1	PARPALSAPAPRLGVGGGRRLPFSGHRAPPAL
		1	1	1		LTRVPSGGPSRYSGGPGKHLLYLGRPEGYRG
		Ì	Ì	ŀ		RALKRVDVEKPQLSLKPPLVGPSSRQAVPNG
L		Ĺ	<u> </u>	<u> </u>		GRFNF
747	2097	A	5998	2	754	DHASLPCSWNHRFDVETRHVFIGDHSGQVTI
					}	LKLEQENCTLVTTFRGHTGGVTALCWDPVQ
1		{	1			RVLFSGSSDHSVIMWDIGGRKGTAIELQGHN
1		1	]			DRVQALSYAQHTRQLISCGGDGGIVVWNMD
				}	ĺ	VERQETPEWLDSDSCQKCDQPFFWNFKQMW
				Ì		DSKKIGLRQHHCRKCGKAVCGKCSSKRSSIPL MGFEFEVRVCDSCHEAITDEERAPTATFHDSK
, [			l		]	HNIVHVHFDATRGWLLTSGTDKVIKLWDMT
1 !		[	1			PVVS
748	2098	A	6001	2	747	AMVFGGVVPYVPQYRDIRRTQNADGFSTYV
/40	2000	^	0001	-	'~'	CLVLLVANILRILFWFGRRFESPLLWOSAIMIL
1 1						TMLLMLKLCTEVRVANELNARRRSFTAADS
1 1			1	i	ļ	KDEEVKVAPRRSFLDFDPHHFWQWSSFSDYV
						QCVLAFTGVAGYITYLSIDSALFVETLGFLAV
1						LTEAMLGVPQLYRNHRHQSTEGMSIKMVLM
					ļ	WTSGDAFKTAYFLLKGAPLQFSVCGLLQVLV
		İ		1		DLAILGQAYAFARHPQKPAPHAVHPTGTKAL
749	2099	Α	6002	2	447	GRPDRSELVRMHILEETFAEPSLQATQMKLK
						RARLADDLNEKIAQRPGPMELVEKNILPVDSS
l i			Ì			VKEAIIGVGKEDYPHTQGDFSFDED\$SDALSP
1 1		1		ĺ		DQPASQESQGSAASPSEPKVSESPSPVTTNTP
1.50	0100	1				AQFASVSPTVPEFLKTPPTAD
750	2100	Α	6004	2	427	LLTQAMLVLPHRPQWFTPGPRLQAQGPCQEG
1 1		ļ		1		WRWELRLRNYVPEDEDLNKRRVPQAKPDAV
[		]				QEKVKEQLEAAKPEPVIEEVDLAKLAPRKPD
		1				WDLKRDVAKKLEKLLKRTQRAIAELIRERLK   GQEDSLDSAVDAATEHKTC
751	2101	_	6007	33	1280	TDQAKVDNQPEKLVRSAEDVSTVPTQPDNPF
'31	2101	A	0007	33	1200	SHPDKLKRMSKSVPAFLQDESDDRETDTASE
		1		1		SSYQLSRHKKSPSSLTNLSSSSGMTSLSSVSGS
j 1						VMSVYSGDFGNLEVKGNIQFAIEYVESLKEL
						HVFVAQCKDLAAADVKKQRSDPYVKAYLLP
1 1		ł	1			DKGKMGKKKTLVVKKTLNPVYNEILRYKIEK
1		ĺ		ĺ		QILKTQKLNLSIWHRDTFKRNSFLGEVELDLE
1 1						TWDWDNKQNKQLRWYPLKRKTAPVALEAE
1 1		1	1			NRGEMKLALQYVPEPVPGKKLPTTGEVHIWV
		1		1		KECLDLPLLRGSHLNSFVKCTILPDTSRKSRQ
		1				KTRAVGKTTNPIFNHTMVYDGFRPEDLMEAC
				l		VELTVWDHYKLTNQFLGGLRIGFGTGK\$YGT
, I		l		1		EVDWMDSTSEEVALWEKMVNSPNTWIEATL
<u> </u>						PLRMLLIAKISK
752	2102	Α	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL
				i '		SQVGGLGRFQMLHLVFILPSLMLLIPHILLENF
		ı	1	t .		AAAIPGHRCWVHMLDNNTGSGNETGILSEDA

			1.555	-		4 11
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ł	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	į.		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	i		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide		/=possible nucleotide deletion, \=possible
		l	L	sequence		nucleotide insertion
		]	[ · ·	-		LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG
		ŀ	<b>}</b>			TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKW
		l	1	į		DLVCDYQSLKSVVQFLLLTGMLVGGIIGGIIV
			1			SDRFGRRFILRWGLLQLAITDTCAAFAPTFPV
		1		1		YCVLRFLAGFSSMIIISNNSLPITEWIRPNSKAL
	1	1		1		VVILSSGALNIGQIILGGLAYVFRDWQTLHVV
	1			!		ASVPFFVFFLLSRWLVESARWLIITNKLDEGL
			1			KALRKVARTNGIKNAEETLNIEVVRSTMQEE
			1	ļ	1	LDAAQTKTTVWDLFRNPSMRKRICILVFLRK
		ļ		į.		KNLKEKA
753	2103	Α	6043	1	1470	DSFESILRLIFEIHHSGEKGDIVVFLACEQDIEK
		1				VCETVYQGSNLNPDLGELVVVPLYPKEKCSL
		}	1	1		FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN
						SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ
		1		i	i	SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP
						LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF
	1		ļ.			MNRPAPESLMQALEDLDYLAALDNDGNLSE
l	1	1		1	1	FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA
		1			1	AMVTAPNCFSHVPHGAEEAALTCWKTFLHPE
			ł			GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRD
						YFLNCSALRMADVIRAELLEIIKRIELPYAEPA
	<b> </b>		į.			FGSKENTLNIKKALLSGYFMQIARDVDGSGN
	}					YLMLTHKQVAQLHPLSGYSITKKMPEWVLF
	ł			1	1	HKFSISENNYIRITSEISPELFMQLVPQYYFSNL
		1				PPSESKDILQQVVDHLSPVSTMNKEQQMCET
ĺ	1	1	1	ı	1	CPETEQRCTLQ
754	2104	A	6055	2	394	YYALHHWPFPDLLCOTTGAIFQMNMYGSCIF
754	2104	11	0055	1		LMLINVDRYAAIVHPLRLRHLRRPRVARLLC
	1	1				LGVWALILVFAVPAARVHRPSRCRYRDLEVR
		1	1			LCFESFSDELWKGRLLPLVLLAEALGFLLPLA
			İ			AVVYSS
755	2105	A	6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE
133	2103	J ''	0037	-	1 1/2	RNARSVKITKRPTKLLIAPESAAPEEALGPAEE
						PEPGRARRSDTHTFNRLFRRDEEGRRPLTVVL
	1					QGPAGIGKTMAAKKILYDWAAGKLYQGQVD
	1	1	1			FAFFMPCGELLERPGTRSLADLILDQCPDRGA
	1				}	PVPQMLAQPQRLLFILDGADELPALGGPEAAP
		1			1	CTDPFEAASGARVLGGLLSKALLPTALLLVTT
	1	1			1	RAAAPGRLQGRLCSPQCAEVRGFSDKDKKK
		1	1			YFYKFFRDERRAERAYRFVKENETLFALCFV
	1	1	1	1	(	PFVCWIVCTVLRQQLELGRDLSRTSKTTTSVY
		1				LLFITSVLSSAPVADGPRLQGDLRNLCRLARE
	1	1			1	GVLGRRAQFAEKELEQLELRGSKVQTLFLSK
		]				KELPGVLETEVTYQFIDQSFQEFLAALSYLLE
		1			i	DGGVPRTAAGGVGTLLRGDAQPHSHLVLTT
		1				RFLFGLLSAERMRDIERHFGCMVSERVKOEA
	1	1	1	!	1	LRWVOGOGOGCPGVAPEVTEGAKGLEDTEE
			1		1	
		1			1	PEEEEGEEPNYPLELLYCLYETQEDAFVRQA LCRFPELALORVRFCRMDVAVLSYCVRCCPA
		1			1	1 = -
	1	1				GQALRLISCRLVAAQEKKKKSLGKRLQASLG
	ļ	<del> </del>		L		GG
756	2106	Α	6060	12	436	SGRPTRPAKPTGQGMGRFMLTLVCQGSIMMS
		1				ARDLIMNNLTELQPGLFHHLRFLEELRLSGNH
	1	1			[	LSHIPGQAFSGLYSLKILMLHNNQLGGIPAQA
		1.			[	LWELPSLQSLRLDANLISLVPERSFEGLSSLRH
		Ι,	1		1	LWLDDNALTEIPS
757	2107	Α	6063	54	419	ITPLGLGAADMCAFPWLLLLLLQEGSQRRL
757	2107	A	6063	54	419	ITPLGLGAADMCAFPWLLLLLLLQEGSQRRL WRWCGSEEVVAVLQESISLPLEIPPDEEVENII WSSHKSLATVVPGKEGHPATIMVTNPHYQG

						·
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ĺ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ĺ		İ	peptide		/-possible nucleotide deletion, \-possible nucleotide insertion
		<u> </u>	<u> </u>	sequence		QILTMLLRSLQQPSASWPRDCSSSCSW
758	2100	A	6066	125	438	IGISCPATIFVPMFSHSLIGIGEEYQLPYYNMV
130	2108	A	0000	123	438	PSDPSYEDMREVVCVKRLRPIVSNRWNSDEC
	l		l	l	i	LRAVLKLMSECWAHNPASRLTALRIKKTLAK
						MVESQDVKI
759	2109	A	6072	3	650	PGRRFRPAALEERAMEKLREKVPFONRGKGT
139	2109	A	00/2	3	1 630	LSSIIPNNSDTRKATETTSLSSKPEYVNPDFRW
	ł		ļ			SKDPSSKSGNLLETSEVGWTSNPEELDPIRLA
			ŀ			LLGKSGLSCQVGSATSHPVSCQEPIDEDQRISP
	!				ļ	KDKSTAGREFSGQVSHQTTSENQCTPIPSSTV
	i					HSSVADMQNMPAAVHALLTQPSLSAAPFAQ
			1		l	RYLGTLPSTGSTTLPQCHAGNATVW
760	2110	A	6077	3	730	PLRLTLMEEVLLLGLKDREGYTSFWNDCISSG
/00	2110	^	00//	, ,	'30	LRGCMLIELPLRGRLQLEACGMRRKSLLTRK
			]	1		VICKSDAPTGDVLLDEALKHVKETOPPETVO
		1	l		}	NWIELLSGETWNPLKLHYQLRNVRERLAKNL
						VEKGVLTTEKQNFLLFDMTTHPLTNNNIKQR
				ļ		LIKKVOEAVLDKWVNDPHRMDRRLLALIYL
				Ì		AHASDVLENAFAPLLDEQYDLATKRVRQLLD
			]	į.		LDPEVECLKANTNEVLWAVVAAFTK
761	2111	A	6078	833	390	IVSFHLSGFKKFVRPFSFLSVHGLOVDEYHSV
701	2111	_^	1 00/8	655	370	HQKLSADMADHSNLIRSLLVGAEDARLMRD
					<u> </u>	MKTMKSRYMELYDLNRDLLNGYKIRWNNH
			1			TELLGNLKAVNQAIQRAGRLRVGKPKNQVIT
!						ACRDAIRSNNINTLFKIMRVGTASS
762	2112	A	6079	2	2686	KKAITCGEKEKQDLIKSLAMLKDGFRTDRGS
702	}	^	0075	1 -	2000	HSDLWSSSSSLESSSFPLPKQYLDVSSQTDISG
	İ			ł.		SFGINSNNQI.AEKVRLRLRYEEAKRRIANLKI
	ļ			i		QLAKLDSEAWPGVLDSERDRLILINEKEELLK
	l	1	1	l		EMRFISPRKWTQGEVEQLEMARKRLEKDLQ
	l		[	]		AARDTQSKALTERLKLNSKRNQLVRELEEAT
į	i	1	ĺ	ĺ		RQVATLHSQLKSLSSSMQSLSSGSSPGSLTSSR
j	İ				İ	GSLVASSLDSSTSASFTDLYYDPFEQLDSELQ
İ	1					SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ
	İ	l	Į.			KAEGGGRLQALRSLSGTPKSMTSLSPRSSLSS
						PSPPCSPLMADPLLAGDAFLNSLEFEDPELSA
					ľ	TLCELSLGNSAQERYRLEEPGTEGKQLGQAV
		1		1		NTAQGCGLKVACVSAAVSDESVAGDSGVYE
	1	i		1		ASVQRLGASEAAAFDSDESEAVGATRIQIALK
				[		YDEKNKQFAILIIQLSNLSALLQQQDQKVNIR
	!	į.		l '		VAVLPCSESTTCLFRTRPLDASDTLVFNEVFW
				ļ		VSMSYPALHQKTLRVDVCTTDRSHLEECLGG
	1	ł		}	į	AQISLAEVCRSGERSTRWYNLLSYKYLKKQS
		1				RELKPVGVMAPASGPASTDAVSALLEQTAVE
		l				LEKRQEGRSSTQTLEDSWRYEETSENEAVAE
						EEEEEVEEEEGEEDVFTEKASPDMDGYPALK
		1				VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF
	1	ì		}		LRGSTIIRSKTFSPGPQSQYVCRLNRSDSDSST
		1				LSKKPPFVRNSLERRSVRMKRPSPPPQPSSVK
		1		1		SLRSERLIRTSLDLELDLQATRTWHSQLTQEIS
		ļ			, ,	VLKELKEQLEQAKSHGEKELPQWLREDERFR
					]	LLLRMLEKRMDRAEHMGELQTDKMMRAAA
	l	1				KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR
				1	I	MNIPALSADDV
		ļ				
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE
763	2113	A	6082	3	1558	
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE VLENLTQGKMCLVPGKTRKLLFKFVAKTED

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SEQ ID Not of peptide solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide sequence solide s							
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Pesidue of pepide   sequence   y=Tyrosine, X=Uaknown, **Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possible nucleotide insertion   v=Siop codon, /*possib	uence	i	ł	914	ng to first	acid residue	
			i	<b>{</b>	amino acid	of peptide	
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VIVQ\$HEKTQIRDVKLTAGLKPGQDANLTQ\$   THVTLAGTELCESEYPALLTDIVGDLHPGQ   LEKMLYVRCGTVGSRNFLYVYSYLINTTUE     ERKVCKHDEPTVTETVPFPDAVKEVSTKF   EHLERVTADIPFLIMTDLLSASPWALTUTSS]     ERKPTVTDQLESQVDNVLGTGESASECF   CLQCPSLGNIEGGVATCHYIISWKRTSAMEN     EHLERVTADIPFLIMTDLLSASPWALTUTSS]   LEAPSMITTUDQLESQVDNVLGTGESASECF   CLQCPSLGNIEGGVATCHYIISWKRTSAMEN     EHLERVTADIPFLIMTDLLSASPWALTUTSS]   LEQRIKILBGTGEGMLYNFYPUMAGYQQLPS   LANKLILRPINTLDVQDVEISVEPSDAMFSGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE     ELFVEYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLLVQDVEISVEPSDAMFSGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVGE     LEVKYHLQNKTDLVQDVEISVEPSDAMFSGE   LEVKYHLQNKTDLVGE     LEVKYHLQNKTDLVGE   LEVKYHLQNKTDLVGE   LEVKYHLQNKTDLVGE     ERKHYMYSOEIDLEADTVATLVATLVA   LEVKYHLQNG   LEVKYHLQNKTDLVGE     ERKHYMYSOEIDLEADTVATLVA   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQNG   LEVKYHLQN		1		1	1		1 '
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine.
nucl-	peptide		in	nucleotide location	location	
cotide	scq-	Į.	USSN 09/496		to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	914	correspondi ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	j		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ĭ	1	1	peptide	sequence	/=possible nucleotide deletion, \=possible
	Į.	1		sequence		nucleotide insertion
	<del></del>		<del> </del>	sequence		RIILFGRELQALSEQLGREYGKNLAHTEMLOD
						AFSLLAYSDPWSCPVGQQLDPIQREPVCAAL
		1				NSAILESONLPKOPPLMLALGOASECLRLMA
		1				RAGLGSCSFARVDDYLH
770	2120	A	6125	. 2	570	YFGLNLHVOHLGNNVFLLOTLFGAVILLANC
,,0	2120	1 ^	012	_	1 370	VAPWALKYMNRRASQMLLMFLLAICLLAIIF
		1				VPOEMOMLREVLATLGLGASALANTLAFAH
	i	l l	Ì			GNEVIPTIIRARAMGINATFANIAGALAPLMM
1						ILSVYSPPLPWIIYGVFPFISGFAFLLLPETRNK
	i	1	í			PLFDTIQDEKNERKDPREPKQEDPRVEVTQF
771	2121	A	6126	909	353	RSFVLDTASAICNYNAHYKNHPKYWCRGYF
,,,,	2121	1 ^	0120	100	1 333	RDYCNIIAFSPNSTNHVALRDTGNQLIVTMSC
l			J			LTKEDTGWYWCGIQRDFARDDMDFTELIVT
			1			DDKGTLANDFWSGKDLSGNKTRSCKAPKVV
		ł	Į			RKADRSRTSILIICILITGLGIISVISHLTKRRRS
ľ	ı	ľ	{			QRNRRVGNTLKPFSRVLTPKEMAPTEQM
772	2122	A	6148	7	810	FVLGILALSHTISPFMNKFFPASFPNRQYQLLF
' ' -		1	01.0	<b>'</b>	•••	TOGSGENKEEIINYEFDTKDLVCLGLSSIVGV
ŀ					j	WYLLRKHWIANNLFGLAFSLNGVELLHLNN
ļ			1			VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS
ľ			l			FEAPIKLVFPODLLEKGLEANNFAMLGLGDV
			l			VIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF
l	į	ł	[			GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLV
	i	1				ALAKGEVTEMFSYEESNPKDPAAVTESKEGT
		i	1			EASASKGLEKKEK
773	2123	A	6161	3	1088	COPMLYTRKNHPKLLLRRTESVAEKMLTNW
ľ		ľ	ĺ			FTFLLYKFLKESAGEPLFMLYCAIKHQMEKG
l		ļ				PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV
i		1				NPENENAPEVPVKGLDCDTGTQAKEKLLDA
		i	<u> </u>			AYKGVPYSQRPKAADMDLEWRQGRMARIIL
			1			QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV
			1			ALVPKQTSAYNISNSSTFTKSLSRYESMLRTA
ŀ		ĺ				SSPDSLRSRTPMITPDLESGTKLWHLVKNHDH
ļ	ļ	İ	ì			LDQREGDRGSKMVSEIYLTRLLATKGTLQKF
	1	1				VDDLFETIFSTAHRGSALPLAIKYMFDFLDEQ
i			1			ADKHQIHDADVRHTWKSNCLPLRFWVNVIK
	<u> </u>		<u> </u>			NPQFVFDIHKNSITDACLSVV
774	2124	A	6163	860	125	KTAVKKRNLNPVFNETLRYSVPQAELQGRVL
		1				SLSVWHRESLGRNIFLGEVEVPLDTWDWGSE
	1	İ				PTWLPLQPRVPPSPDDLPSRGLLALSLKYVPA
	}	1	1		,	GSEGAGLPPSGELHFWVKEARDLLPLRAGSL
	]	1	1			DTYVQCFVLPDDSRASRQRTRVVRRSLSPVF
						NHTMVYDGFGPADLRQACAELSLWDHGALA
	1					NRQLGGTRLSLGTGSSYGLQVPWMDSTPEEK
225	7105	1.	710.		202	QLWQALLEQPCEWVDGLLPLRTNLAPRT
775	2125	A	6191	2	392	ARGIGSLGRDHSGSGGGTGMAGAWVRKAAD
	1					YVRSKDFRDYLMSTHFWGPVANWGLPIAAIT
	1	1				DMK/KSPEIISRRMTFAL*CYSLTFVRFAHYVQ
	[	[				\PWNWLMLGCHTAVDFDQLISSMPCISHGMT     ASASAL
226	2126	-	6217	,	ยาว่า	
776	2126	A	6217	1	827	FRGYWGVREAFTDASWSGGLGPGKPGMKIT
	]	Į	]			ROKHAKKHLGFFRNNFGVREPYQILLDGTFC
	}					QAALRGRIQLREQLPRYLMGETQLCTTRCVL
	1	ļ				KELETLGKDLYGAKLIAQKCQVRNCPHFKNA
		1	'			VSGSECLLSMVEEGNPHHYFVATQDQNLSVK
1	1	J				VKKKPGVPLMFIIQNTMVLDKPSPKTIAFVKA
	1	}				VESG\RLSQCMRKKVSNISKRNRV**KTLNRG RRKKRKKISGPNPLSCLKKKKKAPDTQSSASE
	!	1				KKRKRKRISGPNPLSCLKKKKAPDTQSSASE KKRKRKRIRNRSNPKVLSEKQNAEGE
L	L	J	1	<u>. – – –</u>		AMAMAMINING TAY LOCALINAEUE

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SEQ ID	SEQ ID	Met hod	SEQ ID NO:	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of peptide	поп	in NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	Luciica		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Herree	Í	i	1 /11	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	***,	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
777	2127	A	6236	1038	1402	YYQISSLPSIVGNGIFLWLLICIFLAKQGGSRL*
	1	į	1		}	FOPFGRPRGGGHLRSGVLGQPGQHGETP/SFF
	1	}				YNSKISPALWGPPVIPSALGGEAGKSL*PRRQ
	Ì	1	1			RFQRGGIAPLPSRVRGRAKLFLKKK
778	2128	Α	6237	422	913	ASFFHHHRGAFLLLLAIPGS*GQDQSLIHWSN
	ł	ł	1	1		AVSNAD\LLDLK\N*LDH\LEEKMPL\EVKVVP
					Ì	PQVL\SEPN*RSGGCFSAPSFEVPPWTGEVKP/
	1					SPQRDGGALG\QGPLGIPSDSILALLKKQT*RA
	1					LLNWPLGSLRRSSCFGGQDGQDLKPRSGLGC
				1		NSFRYRR
779	2129	A	6249	420	36	ARAPSPSFSVRDVELSDPARERGEMPVAVGP
				[		YGQSQPSCFDRVKMGFVMGCAVGMAAGAL
			1	1		FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM
	i					MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH
		L		L	L	QSQPMY
780	2130	Α	6263	415	1380	RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG
				ļ		TDYWLYSRGVCRTKSTSDNETSRKNEEVMT
	<b>!</b>					HSGLWRTCCLEGAFRGVCKKIDHFPEDADYE
						QDTAEYLLRAVRASSVFPILSVTLLFFGGLCV
	1		í	1	ĺ	AASEFHRSRHNVILSAGIFFVSAGLSNIIGIIVYI
	1					S\ANAGRTPGQR\DSKKSYSYGWSF/YFSGAFS
			1			FIIGR/IIC*GVGLPWHIYIEKHQQLRAKSHSEF
						LKKSTFARLPPYRYRFRRRSSSRSTEPRSRDLS
		1		1		PISKGFHTIPSTDISMFTLSRDPSKITMGTLLNS
	ļ	ĺ		Į		DRDHAFLQFHNSTPKEFKESLHNNPANRRTT
701	2121		(274	922	210	PV PURVED FOR AREA VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VEROUS VERO
781	2131	A	6274	832	318	RIIKVKDLKQTLAIKTAŸPRCKCLVEMDQIFH
		1	1			LQVKQKQLACLCTWQARDPDCPPSTKVVL/L
		}	}	j		VGPGMGCMVALFQDSIAWSNKSMPSSLSAIS QSPCQVQAPEGPSSFHLPTLSFTTCLSWQGGD
				]	1	LEFLGDLKGCSELKNFQELITQSALVHPKADV
		ĺ		1		WWYCGRPLLGTLPSN
782	2132	A	6281	1324	393	WISLPSSLLCRKNGSSAEDDRR\GEPSAEEAEG
702	2132	^	0231	1324	323	EREDWGIGSA*SVGAVSKVPSARF*RTYPS\E
			]			DEEEVTHOKSSSSDSNSEEHRKKKTSRSRNK
						KKRKNKSSKRKHRKYSDSDSNSESDTNSDSD
		1		1		DDKKRVKAKKKKKKKKKKKKKKKKKKKKK
		,		ŀ		ESSDSSCKDSEEDLSEATWMEQPNVADTMDL
	J	i	}	1	1	IGPEAPIIHTSQDEKPLKYGHALLPGEGAAMA
		1				EYVKAGKRIPRRGEIGLTSEEIGSFECSGYVM
		1				SGSRHRRMEAVRLRKENQIYSADEKRALASF
	1	1				NQEERRKRESKILASFREMVHKKTKGKDDK
783	2133	A	6305	201	1032	WDDYPQGALRREAAEGLHFLGPPGRVRGQ
						LRGITGPAWYCHSPSHSLLSAFCHLPTPSRCP
		[	1	1		AMARPPVPGSVVVPNWHES/RRGQGVPGLHS
		i				AQEPPAGVWAA*AASAAAA\LSIDTASYKIFV
	I	1	1	ŀ		SGKSGVGKTALVAKLAGLEVPVVHHETTGIQ
	ţ	1		i		TTVVFWPAKLQASSRVVMFRFEFWDCGESA
	l					
		}				LKKFDHMLLACMENTDAFLFLPSFTDRASFE
		<u> </u>			ļ	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT
						DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP GQPEAGPEGAQERPSQAAPAVEAEGPGSSQA
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP GQPEAGPEGAQERPSQAAPAVEAEGPGSSQA PRKPEGAQARTAQSGALRDVSEELSRQLEDIL
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP GQPEAGPEGAQERPSQAAPAVEAEGPGSSQA PRKPEGAQARTAQSGALRDVSEELSRQLEDIL STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR QSDEVGDRDHRRPQEKKKAKGLGKEITLLM
784	2134	A	6308	86	96	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT DVPERDLTAFRQAWELPLLRVKSVPGRRLG GSSPDPASLITMKNQDKKNGAAKQSNPKSSP GQPEAGPEGAQERPSQAAPAVEAEGPGSSQA PRKPEGAQARTAQSGALRDVSEELSRQLEDIL STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR

- ABA 70	T 050 10	114.	1-050	T 50 - 17	[15 27 . 1 1 1	74 41 0 0 0 0
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide		USSN	location	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496		corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence	1	914	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	i	314	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		!	residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1		sequence	/-possible nucleotide deletion, \-possible
	J	1	1	peptide		nucleotide insertion
	<del> </del> -	<b>├</b>	<del></del>	sequence	<del></del>	RSKLESLCRELQRHNRSLKEEGVQRAREEEE
	1		1	1		KRKEVTSHFQVTLNDIQLQMEQHNERNSKLR
			-	1		OENMELAERLKKLIEOYELREEHIDKVFKHK
	1	1	ł	ļ		
	1		1	1		DLQQQLVDAKLQQAQEMLKEAEERHQREKD
	1		ì			FLLKEAVESQRMCELMKQQETHLKQQLALY TEKFEEFONTLSKSSEVFTTFKOEMEKMTKKI
	}	J	į.	ļ		
	1	ļ	1			KKLEKETTMYRSRWESSNKALLEMAEEKTV
	1	1	1	l		RDKELEGLQVKIQRLEKLCRALQT/GAQ*PVR
	L	<del> </del>	<del> </del>		L	GQRWGSHRTSAVRIFS
785	2135	A	6319	1493	889	SPQGPLLRSVSPVSAGASSVTPGGAQPGVTTT
	}	Į.	}	}		PPSLVAVAPAPGSAAGPAAGWQ*HAGCR/WT
	1	ŀ	1			KLPWSWGMRPMKIFFSEEYRSISTRISHDAL*
	1	1		1		EKCTQPAKPLSMIR\TGSSVSPG/PLVKWNWT
	i	l				RREFRNSGTRVVSSCCGMSCMYSFLGHCSV/S
	1	1		i	ĺ	QDLPLVHVDVGWQPPLGPTVGLRPGLLPLHD
		1				TTPCQKLVVDDLDWA
786	2136	A	6320	551	135	RWLPVAECDSSCVGCTGEGPGNCKECISGYA
	İ			1		REHGQCADVDECSLAEKTCVRKNENCYNTP
	1					GSYVCVCPDGFEET/RRCLCAAGRG*SHRRRK
	i		1			PDTAALPRRPVMCRTYPLNYSEGCPVENVAL
		<u> </u>		<u> </u>	<u> </u>	RMPSPAVDSGGERLPAL
787	2137	A	6330	1693	227	DYVLTAELHRQRSPGVSFGLSVFNLMNAIMG
l	1.	i	į.	1	1	SGILGLAYVMANTGVFGFSFLLLTVALLASYS
	1		İ	1		VHLLLSMCIQTAYLGP*TNYFMVLPAH*LTCL
	1		1	İ		PLIEFLQSL*NSL\*AVTSYEDLGLFAFGLPGKL
	i	1	i			VVAGTIIIQNIGAMSSYLLIIKTELPAAIAEFLT
	1		1		1	GDYSRYWYLDGQTLLIIICVGIVFPLALLPKIG
	ſ	ĺ	ĺ .	1		FLGYTSSLSFFFMMFFALVVIIKKWSIPCPI.TI.
	1	1	1	•		NYVEKGFQISNVTDDCKPKLFHFSKESAYALP
	l		Ì			TMAFSFLCHTSILPIYCELQSPSKKRMQNVTN
	1	l	ļ		ļ	TAIALSFLIYFISALFGYLTFYD/GTTKAQRGE
	!	ļ				VTCHRIKDKVESELLKG***IP*SHDVVVMT\V
	1	ļ				KLCILFAVLL\TVPLIHFPARKAVTMMFFSNFP
	1	1			ļ	FSWIRHFLITLALNIIIVLLAIYVPDIRNVFGVV
				1		GASTSTCLIFIFPGLFYLKLSREDFLSWKKLGV
						GCFC/LLSFKTSILRNSLSVYIILPASRKSIYFKI
788	2138	A	6351	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTM
	[	1		t		SASFVPNGASLEDCHCNLFCLADLTGIKWKK
	ļ	1	ļ	}		YVWQGPTSAPILFPVTEEDPILSSFSRCLKADV
		}				LG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLF
		ł	l .		•	TMTYQKKKMECGRMDFPMNAVLCFSKAVH
		1	1			NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN
	i		1	ĺ		KSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
						LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQ
	i				'	AFKMSDSATKKLIGEWKQFYPISCCLKEMSE
				ŀ		EKQEDMDWEDDSLAAVEVLVAGVRMIYPAC
						FVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPAS
	1	1	1	1		TRDPAMSSVTLTPPTSPEEVQTVDPQSVQKW
						VKFSSVSDGFNSDSTSHHGGKIPRKLANHVV
		1	l			DRVWQECNMNRAQNKRKYSASSGGLCEEAT
	1	l	1	Į		AAKVASWDFVEATQRTNCSCLRHKNLKSRN
			1	l		AGQQGQAPSLGQQQQILPKHKTNEKQEKSEK
						PQKRPLTPFHHRVSVSDDVGMD\ADS\ASQRL
					1	V\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTE
						MANSPQPPPLSP\HPCDVVDEGVTKTPSTPQS
		l	1		}	QHFYQMPTPDPLVPSKPMEDRIDSLSQSFPPQ
		[	1			YQEAVEPTVYVGTAVNLEEDEANIAWKYYK
			1		}	FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESV
					]	TSVTELMVQCKKPLKVSDELVQQYQIKNQCL
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LPVGPLLRALATCHALSRLQDTPVGDPMDLK MVESTGWVLEEEPAADSAFGTQVLAVMRPP LWEPQLQAMŒEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHPPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL		1	1	1	[		MNML
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MVESTGWVLEEPAADSAFGTQVLAVMRPP LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL		1		1	1 <sup>-</sup>	1	
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SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL	l	1	1	i	l	]	
QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL	ł			i	ĺ	l .	VPTDFAQMLQSYTAAGYRVVALASKPLPSVP
QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL		1	1	1	1	!	SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP
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LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL		1		1	1	1	
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KAADVGISLSQAEASVVSPFTSSMASIECVPM	1	1	1	1	l -	I	EOKTELVCELOKLOYCVGMCGDGANDCGAL
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Ì				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y-Tyrosine, X-Unknown, *-Stop codon,
ł		1		peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	]					VIREGROSLDTSFSVFKYMALYSLTQFISVLIL
						YTINTNLGDLQFLAIDLVITITVAVLMSRTGP
1				İ		ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
Ì			1	į		VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
	1	ļ	1			ENTVVFSLSSFQYLILAAAVSKGAPFR\RPLTN
			1	ĺ		NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
				:	ļ	NITDTGFKLLLVGLVTLNFVGGLHAGERARP
1			1	t .		VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
ļ	ļ.				İ	PPLPAGPLR
790	2140	A	6380	76	1059	SSAGSARKLQVMALAARLWRLLPFRRGAAP
			1			GSRLPAGTSGSRGHCGPCRFRGFEVMGNPGT
			İ			FKRGLLLSALSYLGFETYQVISQAAVVHATA
	İ	1	1	!		KVEEILEQADYLYESGETEKLYQLLTQYKESE
		1				DAELLWRLARASRDVAQLSRTSEEEKKLLVY
t		ļ		i		EALEYAKRA/L/EKNESSFASHKWYAICLSDV
		1				GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
		1				IHLMGIWCYTFAEMPWYQRRIA*NACLQLPP
	1					*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
ł			İ			KTYLKLHNKKLAAFWLMKAKDYPAHTEED
		}	1			KQIQTEAAQLLTSFSEKN
791	2141	A	6434	3	1460	IALLIVDGLAWDDOGGLALLHISPSKLIL*QDS
1 '71	2141	<u> </u>	0434	•	1400	SGMS/YVMVRCTITRAFFKSLLCHICQYSIGPQ
	1		i			*VT\CPGQDACKE*KSTAN*GG*RE**PQVLFF
1					<b>;</b>	AFLSNPAVKFGRMSKKQRDSLYAEVQKHQQ
1	l					RLQEQRQQSGEAEALARVYSSSISNGLSNLN
ł					i	NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
1		1	-			DOSGLDMT\GIKQIKQEPIYDLTSVPNLFTY\SS
			1			FNNGQLAPGITMTEIDRIAQNIIKSHLETCQY
1			1			TMEELHQLAWQTHTYEEIKAYQSKSREALW
		1				QQCAIQITHAIQYVVEFAKRITGFMELCQNDQ
	1		i			ILLLKSGCLEVVLVRMCRAFNPLNNTVLFEG
	1		ł		1	KYGGMQMFKALGSDDLVNEAFDFAKNLCSL
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		1				QLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ   EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
1		}	1	ļ		VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
			1			NPDCATACK
702	21.42	<b>+</b>	- ZA40	92	791	SRGTFRCFCRDFFPCFSNMRLFLWNAVLTLFV
792	2142	A	6440	92	781	
1	1	1				TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
1	1	1				MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
1		1		1		LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
}		1	1	1		LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
1			1			ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
			1			GAVVNESHHDALVEDIFDKEDEDKDGFISAR
		<u> </u>	ļ. <u>.</u>	L		EFTYKHDEL
793	2143	A	6446	3201	152	PRLKRLVVTEEDGGARPEALGKIAPRTPAELG
		1			!	ARADQELVTALMCDLRRPAAGGMMDLAYV
	1	1	1	1	1	CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
1				1		DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
]	1	ļ	}	l		EAITC\LEWDQSGFPGFLFSRWPTGQIK\CWS
1	1		1	!	1	MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
1			1	1		WLH\NGVKLALHVEKSGASSFGEKFSR\VKFS
	1			(		P\SLTLF\GGNAMEGWIAVTVSGLVTVSLLQ\P
			1	<b>)</b>		SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
	1			1		VVATADGSSA\SPVQFYKVCVSVVSEKCRIDT
		1		1		DILPSLFMRCTTDLNRKDKFPAITHLKFLARD
1	1	}				MSEQVLLCASSQTSSIVECWSLRKEGLPVNNI
	1		1		9	FQQISPVVGDKQPTILKWRILSATNDLDRVSA
	i		1	·		VALPKLPISLTNTDLKVASDTOFYPGLGLAL
1			1	1		AFHDGSVHIVHRLSLQTMAVFYSSAAPRPVD
[			[			EPAMKRPRTAGPAVHLKAMOLSWTSLALVG
L	1	1	L	l	l	PI INITIA KI GOLWALIPVINIÁPO M I OPWTAO

WO 01/57188

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  IDSHGKLSVLRLSPSMGHPLEVGLALRHLLFL LEYCMVTGYDWWDILLHVQPSMVQSLVEKL
						HEEYTRQTAALQQVLSTRILAMKASLCKLSP CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF VLDMNTLQALQQLLQWVGDFVLYLLASLPN QPCPTSEPCPTSEPSPTSEPSPTSEPSSP*SLC\G SLLRPGHSFLRDGTSLGMLRELMVVIRIWGLL KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC RDEGPASEPDEALVDECCLLPSQLLIPSLDWL PASDGLVSRLQPKQPLRLQFGRAPTLPGSAAT LQLDGLARAPGQPKIDHLRRLHLGACPTEEC KACTRCGCVTMLKSPNRTTAVKQWEQRWIK NC/LVRWALVAGAPQLPLSPAAPQLLLSYPSA APEPGCCKSHRSPWTLLGAVNLSPPCRAVEG RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT PRSLDHLHPEDRP
794	2144	Α	6490	418	585	NGDKADLENESCRAQVLMPVVPALWEAEGG GSIEPRDLRLQ*AVITPL\TPAWVTQ
795	2145	A	6499	395	1027	KLLWLPPHSEQKRSPLYHPQGPSGTTPSAPAFS SHSPPPSLLQAPSIAAFLRTHGHISASGPLRMP FPH/H*NAFLLVFPGQRSQLTS/PSHYLCREVFP DHHHHLCRLSLESSPLFHHRVLFCVPKQNVN STRAQIFCLFVHIVGCRCINTFPLHLFRLHLWL HFLQIPLCKKNKSVKLGKTVVGRGCQSAAGS DTRVRAAVGAPGLPVEPLV
796	2146	A	6503	68	936	IISALLTHSSFCVFTLCQDFFTYSSMSEEVTYA DLQFQNSSEMEKIPEIGKFGEKAPPAPSHVWR PAALFLTLLCLLLLIGLGVLASMFHVTLKIEM KKMNKLQNISEELQRNISLQLMSNMNISNKIR NLSTTLQTIATKLCRELYSKEQEHKCKPCPRR WIWHKDSCYFLSDDVQTWQESKMACAAQN ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE DS/YSWYESG*YNQPSAWVIRNAPDLNNMY CGYINRLYVQYYHCTYKQRMICEKMANPVQ LGSTYFREA
797	2147	A	6507	1	881	PGSTHASARSQVPRSAGEAAPHSRRPPGLLPH APRAASAQLEERMRDPHPGMTLQEGDCRGS QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ ESALAKLLLTCCSALRPRATQARGSSRLLVAS WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA AIWTGAVAVLAGAAAFIYEKRGGTYWALLR TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTPLWLYC WRMFPTKGVSP
798	2148	A	6528	912	2287	VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAP RFLVAFAYWNHYLSCTSPCSCYRPLCRLNFG LNVVENLALLVLTYVSSSEDF/TWVPG*GRSG

NO: of nucle peptide cotide sequence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence uence	ne.	Amino acid sequence (A=Alanine C=Cysteine	Prodicted end	Predicted	SEQ	Met	SEO ID	eco ID
nucle entide seq.	1105							SEQ ID
cotide sequence  USSN 09/496 914 914 914 914 914 914 914 914 914 914		•				1100	1 -	
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amino acid residue of peptide sequence   T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, **Stop codon, /*possible mucleotide dietion, \range possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possible mucleotide insertion   Possi		Q=Glutamine, R=Arginine, S=Serine,	acid residue		914			•
peptide sequence //possible nucleotide deletion, \=possible nucleotide insertion  EVPFEGTGLPLPHSDLPTSWCGHSLQCG  FPPAIHENAFIVFIASLGHMLLTCIL.WRI HTVSQEVDGLSLAGAPRQPRKSRTSVLE MVRWELSSNGNPGRGVLGLGLGLGNKL GQNLGL*HCVWVWETGE*KRWRLQM GVASRQ*VRNSVRGLVCHNSSAPPMY! SPTVFGGGVGG*LHVTFILHPPEVEAAG! GPSLPQRQGREHIVVILAAPACAPPHDR* REIRPSP*ELGLRGEPTLSYPASCRVIRQP RKSYSWKQRLFIINTISFFSALAVYFRHN EAGYVTIFALEYTVVLTNMAFHMTAW* GNKELLITSQPEEKRF  799 2149 A 6529 1 874 FFFFQRINFIEHSGSVSLLALACDLGWCE CCLVQGGGDLVDVQTNHGEDEAGGD* DEARCKESQQEAQENLREDLCLESFAKI QIEGSFREETTRKQAALDGFPLGGG VHLHPSKEQQGQEGGGRQRGARTHHWE* EKGRRVRLRPPSGKLRADQPVRKLGGFP GLPGDTPTGYTHHAPPVSPTGASGQERG GAVSYAHASATK  800 2150 A 6544 2 662 SAQRWAVGRWGCRLLALLLLVPGFC EITFSLPDNAKQCFYEDIAQGTKCTLEFG GHYDVDCRLEDPDGKVLYKEMKQYD* TASKNGTYKFCFSNEVESTFTHKTVYFDF ETHLCFLVR/DRVSALTQMESACVSIHE, VIDYQTHFRLREAQGRSRAEDLNTRVAN GEALILL VVSIGQVFLLKSFSDKRTTTTI  801 2151 A 6556 1 1319 TPCMECIKGEGLREPQNLSGSQREPQTEG DGWRRMPRWGLLLLLWSCTFGLPTDV KRIFLKRMPSIRESLKERGVDMARLGPE* MKRLTLGNTTSSVULTNYMDTQYYGEIG PQTFKVVVDTGSSNVWYPSKCSRLYTA HKLFDASDSSSVKHNGTELTLRYSTGTV SQDITVGGITVTQMFGEVTEMPALPFMI DGVVCMGFIEQAIGRVTPIFDNIISQGVLI		T=Threonine, V=Valine, W=Tryptophan,	of peptide	amino acid		J	J	
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CTSDPQGNGVWSSPAPRCGILGHCQAPD				i				
FAKLKTQTNASDFPIGTSLKYECRPEYYO		CTSDPOGNGVWSSPAPRCGILGHCOAPDI						

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion  SITCLDNLVWSSPKDVCKRKSCKTPPDPVNG MVHVITDIQVGSRINYSCTTGHRLIGHSSAECI LSGNAAHWSTKPPICQRIPCGLPPTIANGDFIS TNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHA ERTQRDKDNFSPGQEVFYSCEPGYDLRGAAS MRCTPQGDWSPAAPTCEVKSCDDFMGQLLN GRVLFPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG RHTGKPLEVFFFGKAVNYTCDPHPDRGTSFD LIGESTIRCTSDPQGNGVWSSPAPRCGILGHC QAPDHFLFAKLKTQTNASDFPIGTSLKYECRP EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP PDPVNGMVHVITDIQVGSRINYSCTTGHRLIG HSSAECILSGNTAHWSTKPPICQRIPCGLPPTI ANGDFISTNRENFHYGSVVTYRCNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVEFRCQP GFVMKGPRRVKCQALNKWEPELPSCSRVCQ PPPEILHGEHTPSHQDNFSPGQEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALLNGRHTGFTSGDIPYGKEISYTCDPHDRR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEGFPFASPTIPINDFEFPVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFNGMVHINTDTQFGSTVNYSC NEGFRLIGSSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGGQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLIPHLLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRTTSEPHGNVWS SPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAACPHPPRKIONGHYIGGHVSI VSPAPRCEI PVGAA
						EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT
803	2153	Α	6574	2	3233	HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGQDVSARQAFQAAKIITYKDPDNPEYL EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide scq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  DGLLLYIQAVTETLAHGGTVTDGENITQRMW NRSFQGVTGYLKIDSSGDRETDPSLWDMDPE NGAFRVVLNYNGTSQELVAVSGRKLNWPLG YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV GSLSLLGILIVSFFIYRKMQLEKELASELWRVR WEDVEPSSLERHLRSAGSRLTLSGRGSNYGSL LTTEGQFQVFAKTAYYKGNLVAVKRVNRKR IELTRKVLFELKHMRDVQNEHLTRFVGACTD PPNICILTEYCPRGSLQDILENESITLDWMFRY SLTNDIVKGMLFLHNGAICSHGNLKSSNCVV DGRFVLKITDYGLESFRDLDPEQGHTVYAKK
804	2154	A	6585	2	3837	LWTAPELLRMASPPVRGSQAGDVYSFGIILQE IALRSGVFHVEGLDLSPKEIIERVTRGEQPPFR PSLALQSHLEELGLLMQRCWAEDPQERPPFQ QIRLTLRKFNRENSSNILDNLLSRMEQYANNL EELVEERTQAYLEEKRKAEALLYQILPHSVAE QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE STPMQVVTLLNDLYTCFDAVIDNFDVYKVET IGDAYMVVSGLPVRNGRLHACEVARMALAL LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGV VGLKMPRYCLFGDTVNTASRMESNGEALKI HLSSETKAVLYEEFGGFELELRGDVEMKGKG KVRTYWLLGERGSSTRG
804	2154	A	6383		383/	DAPGRPPVRLPTMELEDGVVYQEEPGGSGAV MSERVSGLAGSIYREFERLIVRYDEEVVKELIP LVVAVLENLDSVFAQDQEHQVELELLRDDNE QLITQYEREKALRKHAEEKFIEFEDSQEQEKK DLQTRVESLESQTRQLELKAKNYADQISILEE REAELKKEYNALHQRHTEMIHNYMEHLERT KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP AGDGLLTPDAQKGGETPGSEQWKFQELSQPR SHTSLKDELSDVSQGGSKATTPASTANSDVA TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV QVAQETRNVSTGSAENEEKSEVQAIIESTPEL DMDKDLSGYKGSSTPTKGIENKAFDRNTESL FEELSSAGSGLIGDVDEGADLLGMGREVENLI LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE MARVLMERNQYKERLMELQEAVRWTEMIR ASRENPAMQEKKRSSIWGFFSRLFSSSSNTTK KPEPPVNILKYNAPTSHVTPSVKKRSSTLSQLP GDKSKAFDFLSEETEASLASRREQKREQYRQ VKAHVQKEDGRVQAFGWSLPQKYKQVTNG QGENKMKNLPVPVYLRPLDEKDTSMKLWCA VGVNLSGGKTRDGGSVVGASVFYKDVAGLD TEGSKQRSASQSSLDKLDQELKEQQKFLKNQ EELSSLVWICTSTHSATKVLIIDAVQPGNILDS FTVCNSHVLCIASVPGARETDYPAGEDLSESG QVDKASLCGSMTSNSSAETDSLLGGITVVGC SAEGVTGAATSPSTNGASPVMDKPPEMEAEN SEVDENVPTAEEVATEATEGNAGSAEDTVDIS QTGYYTEHVFTDPLGVQPEDLSPVYQSSND SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYILLDLGRPIIISIRCMTVVHDKVWCG YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ LAWVGDGVWVSIRLDSTLRLYHAHTYQHLQ DVDIEPYVSKMLGTGKLGFSFVRITALMVSC

446.75	7 6 5 7 5 T 5	1 34.4	1 050	I bester i	Thurston - 3 3	Amino gold gapyan as (A - Alanina C-Curtain
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide		in	nucleotide	3	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1		sequence	/-possible nucleotide deletion, \=possible
		1	1	peptide	ĺ	
	Ļ		<b>_</b>	sequence		nucleotide insertion
			ļ			NRLWVGTGNGVIISIPLTETVILHQGRLLGLR
			1	1	ł	ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
		Ì	i			FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
		<u> </u>	1	<b>↓</b>		ISPQSSSSGTDLTGDKGRGHLHRSLVVRRP
805	2155	A	6605	469	2602	FGRLLWGTAFKSWKMKAPIPHLILLYATFTQ
	İ	1	1			SLKVVTKRGSADGCTDWSIDIKKYQVLVGEP
						VRIKCALFYGYIRTNYSLAQSAGLSLMWYKS
						SGPGDFEEPIAFDGSRMSKEEDSIWFRPTLLQ
	-	ĺ	ľ			DSGLYACVIRNSTYCMKVSISLTVGENDTGL
						CYNSKMKYFEKAELSKSKEISCRDIEDFLLPT
	ļ			1		REPEILWYKECRTKTWRPSIVFKRDTLLIREV
					1	REDDIGNYTCELKYGGFVVRRTTELTVTAPL
	ļ	ļ				TDKPPKLLYPMESKLTIQETQLGDSANLTCRA
		ľ				FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE
	}	1				SDI\KILKEHLGEQEVSISLIVDSVEEGDLGNYS
	1		1		1	CYVENGNGRRHASVLLHKRELMYTVELAGG
					1	LGAILLLLVCLVTIYKCYKIEIMLFYRNHFGA
		1	ļ			EELDGDNKDYDAYLSYTKVDPDQWNQETGE
	1	i				EERFALEILPDMLEKHYGYKLFIPDRDLIPTGT
	İ		J	}	]	YIEDVARCVDQSKRLIIVMTPNYVVRRGWSIF
			1		ł	ELETRLRNMLVTGEIKVILIECSELRGIMNYQE
						VEALKHTIKLLTVIKWHGPKCNKLNSKFWKR
	ļ		1			LQYEMPFKRIEPITHEQALDVSEQGPFGELQT
	1			İ		VSAISMAAATSTALATAHPDLRSTFHNTYHS
	j	1	l l			QMRQKHYYRSYEYDVPPTGTLPLTSIGNQHT
				1		YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA
	<u> </u>					ILPLLPRETSISSVIW
806	2156	Α	6614	3	1584	NSARGGVGVRGARAMATVQEKAAALNLSAL
	Ì	1	1	j		HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT
		}		]	ļ	QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
			l	ĺ		IQNKYFGDVDIPRAKVVRVCQALMDYKVFE
	1	1	ì			AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD
	ļ		1			SQLGKENKLYSPARYADALFKSSDIRSASLED
	1	t	1		1	LWENLSLKPANSPHVNISTTLSPQVINEVWQE
	1	1	}	ļ		ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK
		1			ĺ	RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA
	]	1			1	AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE
	1	1			1	LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV
					1	NGKTEIALEATQLLLKLLDFQNREEFRRLLYF
					1	MAVAANPSEFKLQKESDNRMVVKRIFSKATV
		İ			1	DNKNLSKGKTDLLVLFL\MDHQKDVFKIPGT
	1	1	1	1	ĺ	L\HKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI
	-				1	DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA
		1	L	<u> </u>	<u> </u>	KEKKK\LLGQFYKCHPDIFIEHFGD
807	2157	A	6615	4198	2094	FGIVGTFALETDELDSDRDPAIFSLCDFGAMR
						PQILLLALLTLGLAAQHQDKVPCKM/VKML
	ł	1			1	CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD
	-				1	LSGNQLRSILASPLGFYTALRHLDLSTNEISFL
		1			]	QPGAFQALTHLEHLSLAHNRLAMATALSAG
					}	GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS
				ļ	Ī	LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS
	ļ	1	1	1	Ì	NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD
		1			1	FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT
		1				WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR
					1	LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS
			1		1	GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL
		1		1	}	NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE
	1	1			i	TLELGARALG\SLRTLLLQGNALRDLPPYTFA
		i			1	NLASLQRLNLQGNRVSPCGGPDEPGP\SGCV\
	Ī				1	AFSGITSLRSLSLVDNEIELLRAGAFLHTPLTE

SFQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M-Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LDLSSNPGLEVATGALGGLEASLEVLALQGN GLMVLQVDLPCFICLKRLNLAENRLSHLPAW
		}				TQAVSLEVLDLRNNSFSLLPGSAMGGLETSLR RLYLQGNPLSCCGNGWLAAQLHQGRVDVDA TQDLICRFSSQEEVSLSHVRPEDCEKGGLKNI NLIILTFILVSAILLTTLAACCCVRRQKFNQQ YKA
808	2158	A	6619	153	1852	FKALSQYIYTNTHLEREAAFEVAILLRRMEEG ARHRNNTEKKHPGGGESDASPEAGSGGGGV ALKEIGLVSACGIIVGNIIGSGIFVSPKGVLEN AGSVGLALIVWIVTGFITVVGALCYAELGVNI PKSGGDYFYVKDIFGGLAGFLRLWIAVLVIYP TNQAVIALTFSNYVLQPLFPTCFPPESGLRLLA AICLLLTWVNCSSVRWATRVQDIFTAGKLL ALALIIIMGIVQICKGEYFWLEPKNAFENFQEP DIGLVALAFLQGSFAYGGWNFLNYVTEELV DPYKNL\PRAIFISIP\LVTFVYVFANV/ALYVT AMSPQEL\LAS\NAVAVTFGEKLLGVMAWIM PISVALSTFGGVNGSLFTSSRLFFAGAREGHLP SVLAMIHVKRCTPIPALLFTCISTLLMLVTSD MYTLINYVGFINYLFYGVTVAGQIVLRWKKP DIPRPIKINLLFPIIYLLFWAFLLVFSLWSEPVV CGIGLAIMLTGVPVYFLGVYWQHKPKCFSDFI ELLTLVSQKMCVVVYPEVERGSGTFFANED MEEQQQPMYQPTPTKDKDVAGQPQP
809	2159	A	6621	1041	223	QDSRKMLPSTSVNSLVQGNGVLNSRDAARH TAGAKRYKYLRRLFRFRQMDFEFAAWQMLY LFTSPQRVYRNFHYRKQTKDQWARDDPAFL VLLSIWLCVSTIGFGFVLDMGFFETIKLLLWV VLIDCVGVGLLIATLMWFISNKYLVKRQSRD YDVEWGYAFDVHLNAFYPLLVILHFIQLFFIN HVILTDTFIGYLVGNTLWLVAVGYYIYVTFL GYSVGLLFFSALPFLKNTVILLYPFAPLILLYG LSLALGWNFTHTLCSFYKYRVK
810	2160	A	6623	160	822	SPASGHCRLNGAAVAMFGCLVAGRLVQTAA QQVAEDKFVFDLPDYESINHVVVFMLGTIPFP EGMGGSVYFSYPDSNGMPVWQLLGFVTNGK PSAIFKISGLKSGEGSQHPFGAMNIVRTPSVAQ IGISVELLDSMAQQTPVGNAAVSSVDSFTQFT QKMLDNFYNFASSFAVSQVPDDTQ/RPSEMF IPANVVLKWYENFQRRTSTEPSLLENIIWIKIN F
811	2161	A	6627	18	3367	LEGSLNTERAKYYLTITMPHFTVTKVEDPEEG AAASISQEPSLADIKARIQDSDEPDLSQNSITG EHSQLLDDGHKKARNAYLNNSNYEEGDEYF DKNLALFEEEMDTRPKVSSLLNRMANYTNLT QGAKEHEFAENITEGKKKPTKTPQMGTFMG VYLPCLQNIFGVILFLRLTWVVGTAGVLQAF AIVLICCCCTMLTAISMSALATNGVVPAGGSY FMISRALGPEFGGAVGLCFYLGTTFAAAMYIL GAIEIFLVYIVPRAAIFHSDDALKESAAMLNN MRVYGTAFLVLMVLVVFIGVRYVNKFASLFL ACVIVSILAIYAGAIKSSFAPPHFPVCMLGNRT LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD AQKSIPIGTILAILTTSFVYLSNVVLFGACIEGV VLRDKFGDAVKGNLVVGTLSWPSPWVIVIGS FFSTCGAGLQSLTGAPRLLQAIAKDNIIPFLRV

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						FGHSKANGEPTWALLLTAAIAELGILIASLDL VAPILSMFFLMCYLFVNLACALQTLLRTPNW RPRFRYYHWALSFMGMSICLALMFISSWYYA IVAMVIAGMIYKYIEYQGAEKEWGDGIRGLS LSAARFALLRLEEGPPHTKNWRPQLLVLLKL DEDLHVKHPRLLTFASQLKAGKGLTIVGSVIV GNFLENYGEALAAEQTIKHLMEAEKVKGFCQ LVVAAKLREGISHLIQSCGLGGMKHNTVVM GWPNGWRQSEDARAWKTFIGTVRVTTAAHL ALLVAKNISFFPSNVEQFSEGNIDVWWIVHDG GMLMLLPFLLK\QHKVWRKCSIRFF\TVAQLE DNSIQMKKDLATFLYHLRIEAEVEVVEMHDS DISAYTYERTLMMEQRSQMLRHMRLSKTER DREAQLVKDRNSMLRLTSIGSDEDEETETYQ EKVHMTWTKDKYMASRGQKAKSMEGFQDL LNMRPDQSNVRRMHTAVKLNEVIVNKSHEA KLVLLNMPGPPRNPEGDENYMEFLEVLTEGL ERVLLVRGGGSEVITIYS
812	2162	Α	6628	66	640	AVCTMSEMAELSELYEESSDLQMDVMPGEG DLPQMEVGSGSRELSLRPSRSGAQQLEEEGP MEEEEAQPMAAPEGKRSLANGPNAGEQPGQ VAGADFESEDEGEEFDDWEDDYDYPEEEQLS GAGYRVSAALEEADKMFLRTREPALDGGFQ MHYEKTPFDQLAFIEELF\SLMVVNRLTEELG CDEIIDRE
813	2163	A	6630	708	1355	AKMGÄYKYIQELWRKKQSDVMRFLLRVRC WQYRQLSALHRAPRPTRPDKARRLGYKAKQ GY/VYIYIGFVFAVIYRIRVRRGGRKRPVPKG ATYGKPVHHGVNQLKFARSLQSVAEERAGR HCGALRVLNSYWVGEDSTYKFFEVILIDPFHK AIRRNPDTQWITKPVHKHREMRGLTSAGRKS RGLGKGHKFHHTIGGSRRAAWRRNTLQLH RYR
814	2164	A	6635	201	1705	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLR DSEDRSDSRAAQPAHDSGHGDDESPSTSSGT AGTSSVPELPGFYFDPEKKRYFRLLPGHNNCN PLTKESIRQKEMESKRLRLLQEEDRRKKIARM GFNASSMLRKSQLGFLNVTNYCHLAHELRLS CMERKKVQIRSMDPSALASDRFNLILADTNS DRLFTVNDVTVGGSKYGIINLQSLKTPTLKVF MHENLYFTNRKV\NSVCWASLNHLDSHILLC LMGLAETPGCATLLPASLFVNSHPAGIDRPG\ MLCSFRIPGAWSCAWSLNIQANNCFSTGLSR RVLLTNVVTGHRQSFGTNSDVLAQQFALMA PLLFNGCRSGEIFAIDLRCGNQGKGWKATRLF HDSAVTSVRILQDEQYLMASDMAGKIKLWD LRTTKCVRQYEGHVNEYAYLPLHVHEEEGII. VAVGQDCYTRIWSLHDARLLRTIPSPYPASKA DIPSVAFSSRLGGSRGAPGLLMAVGQDLYCY SYS
815	2165	A	6643	659	3282	NKNILEVPSARTTRIMGDHLDLLLGVVLMAG PVFGIPSCSFDGRIAFYRFCNLTQVPQVLNTTE RLLLSFNYIRTVTASSFPFLEQLQLLELGSQYT PLTIDKEAFRNLPNLRILDLGSSKIYFLHPDAF QGLFHLFELRLYFCGLSDAVLKDGYFRNLKA LTRLDLSKNQIRSLYLHPSFGKLNSLKSIDFSS NQIFLVCEHELEPLQGKTLSFFSLAANSLYSR VSVDWGKCMNPFRNMVLEILDVSGNGWTV DITGNFSNAISKSQAFSLILAHHIMGAGFGFHN IKDPDQNTFAGLARSSVRHLDLSHGFVFSLNS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion  RVFETLKDLKVLNLAYNKINKIADEAFYGLD
						NLQVLNLSYNLLGELYSSNFYGLPKVAYIDL QKNHIAIIQDQTFKFLEKLQTLDLRDNALTTIH FIPSIPDIFLSGNKLVTLPKINLTANLIHLSENR LENLDILYFLLRVPHLQILII.NQNRFSSCSGDQ TPSENPSLEQLFLGENMLQLAWETELCWDVF EGLSHLQVLYLNHNYLNSLPPGVFSHLTALR GLSLNSNRLTVLSHNDLPANLEILDISRNQLL APNPDVFVSLSVLDITHNKFICECELSTFINWL NHTNVTIAGPPADIYCVYPDSLSGVSLFSLSTE GCDEEEVLKSLKFSLFIVCTVTLTI.FLMTILTV TKFRGFCFICYKTAQRLVFKDHPQGTEPDMY KYDAYLCFSSKDFTWVQNALLKHLDTQYSD QNRFNLCFEERDFVPGENRPANIQDAIWNSR KIVCLVSRHFLRDGWCLEAFSYAQGRCLSDL NSALIMVVVGSLSQYQLMKHQSIRGFVQKQQ YLRWPEDLQDVGWFLHKLSQQILKKEKEKK KDNNIPLQTVATIS
816	2166	A	6649	63	3811	RDRAGVRPAGKQHAAAAFYDVGGDRPWDS GNTQLPPRNPVKANAMFGAGDEDDTDFLSPS GARLASLFGLDQAAAGHGNEFFQYTAPKQP KKGQGTAATGNQATPKTAPATMSTPTILVAT AVHAYRYTNGQYVKQGKFGAAVLGNHTTR EYRILLYISQQQPVTVARIHVNFELMVRPNNY STFYDDQRQNWSIMFESEKAAVEFNKQVCIA KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE VAYTGWLFQNHVLGQVFDSTANKDKLLIKL LGSGKVIKGWEDGMLGMKKGGKRLLIVPPA CAVGSEGVIGWTQATDSILVFEVEVRRVKIA KDSGSDGHSVSSRDSAAPSPIPGADNLSADPV VSPPTSIPFKSGEPALRIKSNSLSEQLAINTSPD AVKAKLISRMAKMGQPMLPILPPQLDSNDSEI EDVNTLQGGGQPVVTPSVQPSLQPAHPALPQ MTSQAPQPSVTGLQAPSAALMQVSSLDSHSA VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ PVRPLYPAPLSQPPHFQGSGDMASFLMTEAR QHNTEIRMAVSKVADKMDHLMTKVEELQKH SAGNSMLIPSMSVTMETSMIMSNIQRIIQENER LKQEILEKSNRIEEQNDKISELIERNQRYVEQS NLMMEKRNNSLQTATENTQARVLHAEQEKA KVTEELAAATAQVSHLQLKMTAHQKKETEL QMQLTESLKETDLLRGQLTKVQAKLSELQET SEQAQSKFKSEKQNRKQLELKVTSLEEELTDL RVEKESLEKNLSERKKKSAQERSQAEEEIDEI RKSYQEELDKLRQLLKKTRVSTDQAAAEQLS LVQAELQTQWEAKCEHLLASAKDEHLQQYQ FVCAQRDAYQQKLVQLQEKSVCFA\CLALQA QITALTKQNEQHIKELEKNKSQMSGVEAAAS DPSEKVKKIMNQVFQSLRREFELEESYNGRTI LGTIMNTIKMVTLQLLNQQEQEKEESSSEEEE EKAEERPRRPSQEQSASASSGQPQAPLNRERP ESPMVPSEQVVEEAVPLPPQALTTSQDGHRR KGDSEAEALSEIKDGSLPPELSCIPSHRVLGPP TSIPPEPLGPVSMDSECEESLAASPMAAKYPDN PSGK\VCVREVAPDGPLQESSTRLSLTS\DPEE GDPLALGPESPGEPQPPQLKKDDVTSSTGPHK ELSSTEAGSTVAGAALRPSHHSQRSSLSGDEE DELFKGATLKALRPKAQPEEDEDEVSMKGR PPPTPLFGDDDDDDDDWLG FFRSSSDNGSPIRQYE/HSTPAHQGPVMGLEG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  KS/ARNSQLRIVLVGKTGAGKSATGNSILGRK VFHSGIAAKSITKKCEKRSSSWKETELVVVD
						TPGIFDTEVPNAETSKEIIRCILLTSPGPHALLL VVPLGRYTEEEHKATEKILKMFGERARSFMIL IFTRKDDLGDTNLHDYLREAPEDIQDLMDIFG DRYCALNNKATGAEQEAQRAQLLGLIQRVV RENKEGCYTNRMYQRAEEEIQKQTQAMQEL HRVELEREKARIREEYEEKIRKLEDKVEQEKR KKQMEKKLAEQEAHYAVRQQRARTEVESKD GILELIMTALQIASFILLRLFAED
818	2168	A	6660	357	1890	APSGSWTRVVLTLDPCSLRSRSPRSLLDPGMP GISARGLSHEGRKQLAVNLTRVLALYRSILDA YIIEFFITDNLWDTLPCSWQEALDGLKPPQLA TMLLGMPGEGEVVRYRSVWPLTLLALKSTA CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR KHVRPKKQHEIRRLGELVKKLSDFT/GLHPGC RRGLRPGHILSRFMALGLGLMVKSIEGDQRL VERAQRLDQELLQALEKEEKRNPQVVQTSPR HSPHHVVRWVDPTALCEELLLPLENPCQGRA RLLLTGLHACGIDLSVALLRHFSCCPEVVALA SVGCCYMKLSDPGGYPLSQWVAGLPGYELP YRLREGACHALEEYAERLQKAGPGLRTHCY RAALETVIRRARPELRRPGVQGIPRVHELKIEE YVQRGLQRVGLDPQLPLNLAALQAHLAQEN RVVAFFSLALLLAPLVETILILDRLLYLQEQA LSP\GFHAELLPIFSPELSPRNLVLVATKMPLG QALSVLETEDS
819	2169	A	6661	65	2686	SGSGHCLAEAASMGPWGWKLRWTVALLLA AAGTAVGDRCERNEFQCQDGKCISYKWVCD GSAECQDGSDESQETCLSVTCKSGDFSCGGR VNRCIPQFWRCDGQVDCDNGSDEQGCPPKTC SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE ASCPVLTCGPASFQCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECIHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRDWSDEPIKECGTNECLDNNGGCS IIVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARVDMRSCLTEGVEAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNP VYQKTTEDEVHICHNQDGYSYPSRQMVSLED DVA
820	2170	A	6666	17	4146	ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI EGYLHILLISKAEDYRSYRFPKLTVITEYLLLF RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ł	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	!	USSN	location	corresponding	I-Isoleucine, K-Lysine, L-Leucine,
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uence		Į.	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciico		*	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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i		ļ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/-possible nucleotide deletion, \-possible
	ŀ			sequence		nucleotide insertion
	<del>                                     </del>	·	<del> </del>			EMTNLKDIGLYNLRNITRG\AIRIEKNADLCYL
Į.					<u> </u>	STVDWSLILDAVSNNYIVGNKPPKECGDLCP
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1			ļ	1		GTMEEKPMCEKTTINNEYNYRCWTTNRCQK
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í	i	Ì		<b>j</b>	ļ.	RCVDRDFCANILSAESSDSEGFVIHDGECMQE
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l	1	!		1	1	NKDVEPGILLHGLKPWTQYAVYVKAVTLTM
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l	ł	i	1	1	<b>}</b>	NSSSQLIVKWNPPSLPNGNLSYYIVRWQRQP
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i	ļ	1		ł	ł	ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE
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l	1	ł	1	<b>{</b>	ł	NTTMSSRSRNTTAADTYNITDPEELETEYPFF
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	1	į .				DORECVSROEYRKYGGAKLNRLNPGNYTARI
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l	İ	1	1	ĺ		ALPVAVLLIVGGLVIMLYVFHRKRNNSRLGN
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821	2171	Α	6691	106	825	GRVLFRGCGVGHKGQVLMGTFILAQDWLSE
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	L				10.50	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
823	2173	Α	6727	3	4063	PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG
			j.		1	NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
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						SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS VGGQNPSTGGISADRTQGNIGCGGDTDPGQS

SEQ ID NO: of nucl- ectide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
824	2174	A	6732	2440	365	SSQPSQDGQESNVPSVGSLADPDYLNTPQMN: TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL SDSVMNIFKDRNFDSCCICACNMNIKGADVG LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSGL FLEDELDIFGKNSDIGQAAERRLMMCQSTFL PQVEGTKKPQEPPISLLLLLQNQHTQPFASLN FLDYISSNNRQTLPCVSWSYDRVQADNNDY WTECFNALEQGRQYVDNPTGGKVDEALVRS ATVHSWPHSNVLDISMLSSQDVVRMLLSLQP FLQDAIQKKRTGRTWENIQHVQGPLTWQQFH KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT ISPFSLPFWERLLLDPYGGHRDVAYIVVCPEN EALLEGAKTFFRDLSAVYEMCRLGQHKPICK VLRDGIMRVGKTVAQKLTDELVSEWFNQPW SGEENDNHSRLKLYAQVCRHHLAPYLATLQL DSSLLIPPKYQTPPAAAQGQATPGNAGPLAPN GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV PPVSSSASAPGISQISTTSSSGFSGSVGGQNPST GGISADRTQGNIGCGGDTDPGQSSSQPSQDG QESVTERERIGIPTEPDSADSHAHPPAVVYM VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD NLPEHMRNSFILQIVPCQYMLQTMKDEQVFY IQYLKSMAFSVYCQCRPLPTQIHIKSLTGFGP AASIEMTLKNPERPSPIQLYSPPFILAPIKDKQT ELGETFGEASQKYNVLFVGYCLSHDQRWLL ASCTDLHGELLETCVVNIALPNRSRRSKVSAR KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR LGHGELKDWSILLGECSLQTISKKLKDVCRM CGISAADSPSILSACLVAMEPQGSFVVMPDAV TMGSVFGRSTALNMQSSQLNTPQDASCTHIL VFPTSSTIQVAPANYPNEDGFSPNNDDMFVDL PFPDDDMDNDIGILMTGNLHSSPNSSPVPSPGSP SGIGVGSHFQHSRSQGERLLSREAPEELKQQP LALGYFVSTAKAENLPQWFWSSCPQAQNQC PLFLKASLHHHISVAQTDELLPARNSQRVPHP LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVIIFVVLTQLYNAIMNIL VEEGLGRRTPPGGRRGPVTPARPGPDSVRR
824	21/4	A	6/32	2440	365	RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGGGGGGGTKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQNELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA KYKEWLPHLLVAGFDPLILLCNSWIDSVSIDT LIFTLEFTNWKTLAPAVERMLSARASNAWIL QQHIATVPSLTHLCRLEIRSSLKSERLRSDSYIS

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SEQ ID	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of		hod	ID NO:	beginning	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	<b>!</b>	USSN	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496		to last amino	M=Methionine, N=Asparagine, P=Proline,
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uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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	ţ	ļ		peptide	sequence	/=possible nucleotide deletion, \=possible
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825	2175	A	6735	277	1252	RIMGLEDRGVQMLLTTVGAFAAFSLMTIAVG
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	1					ATYNSDRDNSFLQVHNCIQKENKDSLHSNTA
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826	2176	A	6744	3	5177	SDDLRTGLFQDVQDAESLKLPGVYEVLFYNE
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				1		EDPDISTADLGDVLQDPCSLEYWDELQKVFV
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				1		WANTNTVHKSVAIKLVHNLTSPKWKDGGNG
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				1		CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS
			1	1		SLPCWDLMPDISQSVLDASLLQKQIMLGFSPA
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				1		ENGFCTRAIVLTYQEHLGVTYLTLSEDPSPRV
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		l		İ		VADFFRLPYEGLTRGPGAFVSGVSRGTTSFVK
				Í		HISKGTLTSITNLATSLARNMDRLSLDEEHYN
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SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion VGKGIMGVFTKPIGGAAELVSQTGYGILHGA GLSQLPKQRHQPSD\VHADQAPNSHVKYVW KMLQSLGRPEVHMALDVVLVRGSGQEHEGC LLLTSEVLFVVSVSEDTQQQAFPVTEIDCAQD
827	2177	A	6748	2	1662	SKQNNLLTVQLKQPRVACDVEVDGVRERLSE QQYNRLVDYITKTSCHLAPSCSSMQIPCPVVA AEPPPSTVKTYHYLVDPHFAQVFLSKFTMVK NKALRKGFP FVGAPRRGNPFGSPGNPGRHQGPCHRPRGTK ASGVSPTLWRPQAAATGLEMPSSGRALLDSP LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN VGGSRFVLSQQALSCFPHTRLGKLAVVVASY RRPGALAAVPSPLELCDDANPVDNEYFFDRS
						SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI QYWGIDELSIDSCCRDRYFRRKELSETLDFKK DTEDQESQHESEQDFSQGPCPTVRQKLWNIL EKPGSSTAARIFGVISIIFVGVSIINMALMSAEL SWLDLQILEILEYVCISWFTGEFVLRFLCVRD RCRFLRKVPNIIDLLAILPFYITLLVESLSG\SQT TQEL\ENVGAHCPGCLRLLRAL\RMLKAWGR HSTGLRSLGMTITQCYEEVGLLLFLSVGISIF STVEYFAEQSIPDTTFTSVPCAWWATTSMT TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI AIINDRFSACYFTLKLKEAAVRQREALKKLTK NIATDSYISVNLRDVYARSIMEMLRLKGRER ASTRSSGGDDFWF
828	2178	A	6786	5672	1360	GTHPASSGPVPLPPAAVSAATREELGEPVPFV TASSGFQSMHSSNPKVRSSPSGNTQSSPKSKQ EVMVRPPTVMSPSGNPQLDSKFSNQGKQGGS ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK NGAGNGAKGKGKERSISADSFDQRDPGTPN DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS TEMANKAAEAVLKGQVETIVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLPQQPPAPANQ DQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEFTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMWHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKIPDGRNFPPQGIFSGPGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRFFLPMSQGPGSNSOLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNFTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNIKAPLTMASPAMLGNVESG GPPPTASQPASVNIPGSLPSSTPYTMPPEPTL SQNPLSIMMSR\MSKFAMPS\SNPGYNHDAI

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829	2179	A	6797	433	3	ASFFNFSICICKIILEVGPPVGHPAHDDVGGRH GPGGR/GSRSPRSLQCAPGGGRRSGCPAGSSP ASTCPPSPGGSGADRFGPSPPPPSREAAPTAG AAASSTSSGASCPPVPASSRWGVRSRTRSGSG GEREPRDRPSERPRLV
830	2180	A	6800	3	1911	LPERAFGPRTPRAPRRRRRILLSPPPRPPPLDREPRAPGPWLCPSRAGTAQDPARIRERRGRVAGGAAGPAMELRARGWWLLCAAAALVACARGDPASKSRSCGEVRQIYGAKGFSS\DVPQAEISGEHLRICPQGYTCCTSEMEENLANRSHAELETALRDSSRVLQAMLATQLRSFDDHFQHILNDSERTLQATFPGAFGELYTQNARAFRDLYSELRLYYRGANLHLEETLAEFWARLERLFKQLHPQLLLPDDYLDCLGKQAEALRPF\GEAP\RELRLATTRA\FVAAR\SFVQGLGVAS\DVVRKVAQVPLG\PEC\SRAVIEAGSYC\ALHCVGVPGARPCPDYCRNVLKGCLANQADLDAEWRNLLDSMVLITDKFWGTSGVESVIGSVHTWLAEAINALQDNRDTLTAKVIQGCGNPKVNPQGPGPEKRRRGKLAPREPPSGTLEKLVSEAKAQLRDVQDFWISLPGTLCSEKMALSTASDDRCWNGMARGRYLPEVMGDGLANQINNPEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRGANGNVFEVEVDITKPDMTIRQIMQLKIMTNRLRSAYNGNDVDFQDASDDGSGSGSGGGCLDDLCGRKVSRKSSSSTIPLTHALPGLSEQEGQKTSAASCPQPPTFLLPLLLFLALTVARPRWR
831	2181	A	6808	2	1522	ASRHGMTPGALLMLLGALGPPLAPGVRGSEA EGRLREKLFSGYDSSVRPAREVGDRVRVSVG LILAQLISLNEKDEEMSTKVYLDLEWTDYRLS WDPAEHDGIDSLRITAESVWLPDVVLLNNND GNFDVALDISVVVSSDGSVRWQPPGIYRSSCS IQVTYFPFDWQNCTMVFSSYSYDSSEVSLQT GLGPDGQGHQEIHIHEGTFIENGQWENIHKPS RLIQPPGDPRGGREGQRQEVIFYLIRIKPLFY LVNVIAPCILITLLAIFVFYLPPDAGEKMGLSIF ALLTLTVFLLLLADKVPETSLSVPIIKYLMFT MVLVTFSVILSVVVLNLHHRSPHTHQMPLWV RQIFIHKLPLYLRLKRPKPERDLMPEPPHCSSP GSGWGRGTDEYFIKKPPSDFLFFKPNRFQPEL SAPDLRRFIDGPNRAVALLPELREVVSSISYIA RQLQEQEDHDALKEDWQFVAMVVDRLFLW TFIIFTSVGTL\VIFLDATYHLPPPDPFP
832	2182	A	6824	71	1079	ETMAKNPPENCEDCHILNAEAFKSKKICKSLK ICGLVFGILALTLIVLFWGSKHFWPEVPKKAY DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGN GTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI KVIPEFSEPEEEIDENEEITITFFEQSVIWVPAE KPIENRDFLKNSKILEICDNVTMYWINPILAIS

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833	2183	A	6846	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGP GVMESKEERALNNLIVENVNQENDEKDEKE QVANKGEPLALPLNVSEYCVPRGNRRFRVR QPILQYRWDIMHRLGEPQARMREENMERIGE EVRQLMEKLREKQLSHSLRAVSTDPPHHDHH DEFC\LMP
834	2184	A	6851	3	2024	PNGVALLHI.PGAAVIPNTNYMFQDALGGRSR GSREESPAPSRAPASASLWRRLVVVEAKMAA HAAAAQAAAQAAHAEAADSWYLALLGF AEHFRTSSPPKIRLCVHCLQAVFPFKPPQRIEA RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS QQIPQFEDVKFEAASLLSELYCQENSVDAAKP LLRKAIQISQQTPYWHCRLLFQLAQLHTLEKD LVSACDLLGVGAEYARVVGSEYTRALFLLSK GMLLMERKLQEVHPLLTLCGQIVENWQGN PIQKESLRVFFLVLQVTHYLDAGQVKSVKPC LKQLQQCIQTISTLHDDEILPSNPADLFHWLP KEHMCVLYYLVTVMHSMQAGYLEKAQKYT DKALMQLEKLKMLDCSPILSSFQVILLEHIIM CRLVTGHKATALQEISQVCQLCQQSPRLFSN HAAQLHTLLGLYCVSVNCMDNAEAQFTTAL RLTNHQELWAFIVTNLASVYIREGNRHQEVVL LYSLLERINPDHSFPVSSHCLRAAAFYVRGLF SFFQGRYNEAKRFLRETLKMSNAEDLNRLTA CSLVLLGHIFYVLGNHRESNNMVVPAMQLAS KIPDMSVQLWSSALLRDLNKACGNAMDAHE AAQMHQNFSQQLLQDHIEACSLPEHNLITWT DGPPPVQFQAQNGPNTSLASLL
835	2185	A	6855	334	1268	PTRRPILPLTSPKAISVPSPLÖGKQHTLVKSCL SVSGIGGFLVSLSSRMKLQTLAVSVTALKFWS AYVPCQTQDRDALRLTLEQIDLIRRMCASYSE LELVTSAKALNDTQKLACLIGVEGGHSLDNS LSILRTFYMLGVRYLTLTHTCNTPWAESSAK GVHSFYNNISGLTDFGEKVVAEMNRLGMMV DLSHVSDAVARRALEVSQAPVIFSHSAARGV CNSARNVPDDILQLLEEERWAFVMVSLFHGE LIQWQPIRPMCSTVADHFDHIKAVIGSKFIGI GGDYDGAGKYRKKTTCKAPWRTSSRMSS
830	2180		0802	313	11	PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNPAGHLGLGSSFGT GPGSGRPPP
837	2187	A	6863	2	1615	VLRGQRGPAGGLAEERRRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI LWQRSA\AEDQRTSTYNGDIRETRIDQENKD

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838	2188	A	6865	6291	739	AGPLEPRVQGAMALQLWALTLLGLLGAGAS LRPRKLDFFRSEKELNHLAVDEASGVYYLGA VNALYQLDAKLQLEQQVATGPVLDNKKCTP PIEASQCHEAEMTDNVNQLLLVDPPRKRLVE CGQLLKGI\CALRALSNISLRLFYEDGSGEKSF VASNDEGVATVGLVSSTGPGGDRVLFVGKG NGPHDNGIIVSTRLLDRTDSREAFEAYTDHAT YKAGYLSTNTQQFVAAFEDGPYVFFVFNQQD KHPARNRTLLARMCREDPNYYSYLEMDLQC RDPDIHAAAFGTCLAASVAAPGSGRVLYAVF SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN ACYTGTREARDIFYKPFHGDIQCGGHAPGSSK SFPCGSEHLPYPLGSRDGLRGTAVLQRGGLN LTAVTVAAENNHTVAFLGTSDGRILKVYLTP DGTSSEYDSILVEINKRVKRDLVLSGDLGSLY AMTQDKVFRLPVQECLSYPTCTQCRDSQDPY CGWCVVEGRCTRKAECPRAEEASHWLWSRS KSCVAVTSAQPQNMSRRAQGEVQLTVSPLPA LSEEDELLCLFGESPPHPARVEGEAVICNSPSS IPVTPPGQDHVAVTIQLLRRGNIFLTSYQYPF YDCRQAMSLEENLPCISCVSNRWTCQWDLR YHECREASPNPEDGIVRAHMEDSCPQFLGPSP LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD LLKFMEPVTMQESGTFAFRTPKLSHDANETL PLHLYVKSYGKNIDSKLHVTLYDCSFGRSDC SLCRAANPDYRCAWCGGQSRCVYEALCNTT SECPPPVTIRIQPETGPLGGGIRITILGSNLGVQ AGDIQRISVAGRNCSFQPERYSVSTRIVCVIEA AFTPFTGGVEVDVFGKLGRSPPNVQFTFQQP KPLSVEPQQGPQAGGTTLTHGTHLDTGSQED VRVTLNGVPCKVTKFGAQLQCVTGPQATRG QMLLEVSYGGSPVPNPGIFFTYRENPVLRAFE PLRSFASGGRSINVTGQFSLIQRFAMVVIAEP LQSWQPPREAESLQPMTVVGTDYVFHNDTK VVFLSPAVPEEPEAYNLTVLIEMDGHRALLRT EAGAFEYVPDFTFENFTGGVKKQVNKLIRAR GTNLNKAMTLQEAEAFVGAERCTMKTLTET DLYCEPPEVQPPPKRRQKRDTTHNLPEFIVKF GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM VVVIAVSVYCYWRKSQQAEREYEKIKSQLEG LEESVRDCKKEFTDLMIEMEDQTINDVHEAG GIPVLDYKTYTDRVFFLPSKDGDKDVMITGKL DIPEPRRPVVEQALYQFSNLLNSKSFLINFHT L\ENQPEFSARAKVYFASLLTVALHGKLEYYT DIMHTLFLELLEQYVVAKNPKLMLRRSETVV ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI KHQVEKGPVDAVQKKAKYTLNDTGLLGDD VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ VKEKIIDQVYRGPPCSCWPRPDSVVLEWPG STAQILSDLDLTSQREGRWKRVITLMHYNVR DGATLILSKVGVSQQPEDSQQDLPGERHALL EEENRVWHLVRPTDEVDEGKSKRGSVKEKE RTKAITEIYLTRLLSVKGTLQQFVDNFFQSVL APGHAVPPAVKYFFDFLDEQAEKHNIQDEDTI

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839	2189	A	6872		1485	RARRLALQCHVCVCALTPGEQSGRRLPGQT WLMFSCFCFSLQDNSFSSTTVTECDEDPVSLH EDQTDCSSLRDENNKENYPDAGALVEEHAPP SWEPQQQNVEATVLVDSVLRPSMGNFKSRKP KSIFKAESGRSHGESQETEHVVSSQSECQVRA GTPAHESPQNNAFKCQET\VRL\QPRIDQRTAT SPKDAFETR\QDLNEEEAAQVHGVKDPAPAS TQSVLA\DGTDSADPSPVHKDGQNEADSAPE DLHSVGTSRLLLYHITDGDNPTAVRHGCSL/F SGQSQRFNLDPESAPSPPSTQQFMMPRSSSRC SCGDGKEPQTITQLTKHIQSLKRKIRKFEEKFE QEKKYRPSHGDKTSNPEVLKWMNDLAKGRK QLKELKLKLSEEQGSAPKGPPRNLLCEQPTVP RENGKPEAAGPEPSSSGEETPDAALTCLKERR EQLPPQEDSKVTKQDKNLIKPLYDRYRIIKQIL STPSLIPTIVSQDTCMLLLCTDV
840	2190	A	6873	2	2054	FFRFYFSFIRLFAMSLADLTKTNIDEHFFGVAL ENNRRSAACKRSPGTGDFSRNSNASNKSVDY SRSQCSCGSLSSQYDYSEDFLCDCSEKAINRN YLKQPVVKEKEKKKYNVSKISQSKGQKEISV EKKHTWNASLFNSQIHMIAQRRDAMAHRILS ARLHKIKGLKNELADMHHKLEAILTENQFLK QLQLRHLKAIGKYENSQNNLPQIMAKHQNEV KNLRQLLRKSQEKERTLSRKLRETDSQLLKT KDILQALQKLSEDKNLAEREELTHKLSIITTK MDANDKKIQSLEKQLRLNCRAFSRQLAIETR KTLAAQTATKTLQVEVKHLQQKLKEKDREL EIKNIYSHRILKNLHDTEDYPKVSSTKSVQAD RKILPFTSMRHQGTQKSDVPPL/TTKGKKATG NIDHKEKSTENHEIPHCVNKLPKQEDSKRKY EDLSGEEKHLEVQII.LENTGRQKDKKEDQEK KNIFVKEEQELPPKIIEVIHPERESNQEDVLVR EKFKRSMQRNGVDDTLGKGTAPYTKGPLRQ RRHYSFTEATENLHHGLPASGGPANAGNMR YSHSTGKHLSNREEMELEHS\DSGYEPSFGKS SRIKVKDTTFRDKKSSLMEELPGSGYVLKTD QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII
841	2191	A	6874	3	2867	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG NAPAPGTPAASGWQPPTYHSGRAFSARYPRP SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA DHAVRPLHGARGGQPPVPQQHVLERQVQLS QGQNVVIKVKPPSKSGSASASGAQRGSLEEFE DTPWSDQRPREGEGEPPRGQLQPSRPTRARG TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP REPRRTVSESVIAVKASFPSSALPPRTGVALG RKLGSHSVASCAPQLLGDRRVDAGHTDQPVP SGSVGGPARPASGPRQAREASLVVTCRTNKF RKNNYKWVAASSKSPRVARRALSPRVAAEN VCKASAGMANKVEKPQLIADPEPKPRKPATS SKPGSAPSKYKWKASSPSASSSSFRWQSEAG SKDHASQLSPVLSRSPSGD\RPALAHSGLKPLS GETPLSAYKVKTRTKIIRRRGSTSLPGDKKSG TSPAATAKSHLSLRRRQALRGKSSPVLKKTPN

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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nucl-	peptide	ŀ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methiorline, N=Asparagine, P=Proline,
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ļ	J		l .	ļ.		QIWRLITNFLFFGPVGFNFLFNMIFLYRYCRM
	ì	!	1		•	LEEGSFRGRTADFVFMFLFGGFLMTLFGLFVS
	1	1	1		ŀ	L/VFLGPGLYNN/GSSMCGAE\EPLCPHELLRP
			1			SQLPGPLSALGAHGIFLVVGELNHCGPFGYCS
1				1		WTHIFFLGRCISQSTWWNKNSENTIYFESYF
844	2194	A	6928	902	366	HRLCMPIQGACGERME/FSLLLPGLECNGVIL
"	1	١.,				AHCNLRLPGSSNSPASASQVAGITGVCHHAR
J	]	1	J	I	]	
			1	1	l	LIFVFSVETGFLHAGQAGLELLTSGDPPASAS
	1	1	1	1	1	QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
		L	L	L		LM
845	2195	Α	6939	1660	317	LYPENLGESLFPILLLPPPWPDGGRPCCVEMS
1		1				TRAKKLRRIWRILEEKESVAGAVQTLLLRSQE
ł	l	1	1	1	{	GGV\TSAAASTLSEPPRRTQESRTRTRALGLPT
			1	I	1	LPMEKLAASTEPQGPRPVLGRESVQVPDDQD
	1		1	[	Į.	FRSFRSECEAEVGWNLTYSRAGVSVWVQAV
		1	1	I	Ì	1
			1	[		EMDRTLHKIKCRMECCDVPAETLYDVLHDIE
}	}	1		1		YRKKWDSNVIETFDIARLTVNADVGYYSWR
	ſ		[	[	ſ	CPKPLKNRDVITLRSWLPMGADYIIMNYSVK
	1			1	1	HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT
	1		1	I		YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK
	1		1		1	MYKACLKYPEWKQKHL\PHFKPWL\HPEQSP
		ļ	1	1		LPSLALS\ELSVOHADS\LENIDESAV\AESREE
	l	ł	1	1	l	R\MGGAGGEG\SDDDTSLYAEAPHRFRETETG
	1			1		1
			1	l		PGAGRALGAAAAPALSPLHPPGTWWHRARP
i	i	1	1	!	l	RRVLQPGWTEPQ

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D-Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
846	2196	A	6944	42	2672	RRKMAGCRGSLCCCRWCCCCGERETRTPE ELTILGETQEEEDEILPRKDYESLDYDRCINDP YLEVLETMDNKKGRRYEAVKWMVVFAIGV CTGLVGLFVDFFVRLFTQLKFGVVQTSVEECS QKGCLALSLLELLGFNLTFVFLESLLGLIEFVE AGSGITEGKCYLYARQVPGLVRLPTLLWKAL GVLLTVAAMLLINGLGSPMIHSGSVVGAGLPQ FQSISLRKIQFNFPYFRSDRYGKNKRDFVSAG AAAGVAAAFGAPIGGTLFSLEEGSSFWNQGL TWKVLFCSMSATFTLNFFRSGIQFGSWGSFQL PGLLNFGEFKCSDSDKKCHLWTAMDLGFFV VMGVIGGLLGATFNCLNKRLAKYRMRNVHP KPKLVRVLESLLVSLVTTVVVFVASMVLGEC RQMSSSSGIGNDSFQLQVTEDVNSSIKTFFCP NDTYNDMATLFFNPQESAILQLFHQDGTFSPV TLALFFVLYFLLACWTYGISVPSGLFVPSLLC GAAFGRLVANVLKSYIGLGHIYSGTFALIGAA AFLGGVVRMTISLTVILIESTNEITYGLPIMVT LMVGKWTGDFFNKGNYDIHVGLRGVPLLEW ETEVEMDKLRASDIMEPNLTVVPPHTRIQSLV SILRTTVHHAFPVVTENRGNEKEFMKGNQLIS NNIKFKKSSILTRAGEQRKRSQSMKSYPSSEL RNMCDEHIASEEPAEKEDLLQQMLERRYTPY PNLYPDQSPSEDWTMEERFRPLTFHGLILRSQ LVTLLVRGVCYSESQSSASQPRLSYAEMAED YPRYPDIHDLDLTLLNPRMIVDVTPYMNPSPF TVSPNTHVSQVFNLFRTMGLRHLPVVNAVGE IVGIITRHNLTYEFLQARLRQHYQTI
847	2197	A	6951	3	1994	NTNSSSVTNSAAGVEDLNIVQVTVPDNEKER LSSIEKIKQLREQVNDLFSRKFGEAIGVDFPVK VPYRKITFNPGCVVIDGMPPGVVFKAPGYLEI SSMRRILEAAEFIKFTVIRPLPGLELSNGEYST VGKRKIDQEGRVFQEKWERAYFFVEVQNIST CLICKRSMSVSKEYNLRRHYQTNHSKHYDQY MERMRDEKLHELKKGLRKYLLGLSDTECPE QKQVFANPSPTQKSPVQPVEDLAGNLWEKLR EKIRSFVAYSIAIDEITDINNTTQLAIFIRGVDE NFDVSEELLDTVPMTGTKSGNEIFSRVEKSLK NFCINWSKLVSVASTGTPPMVDANNGLVTKL KSRVATFCKGAELKSICCIIHPESLCAQKLKM DHVMDVVVKSVNWICSRGLNHSEFTTLLYEL DSQYGSLLYYTEIKWLSRGLVLKRFFESLEFI DSFMSSRGKPLPQLSSIDWIRDLAFLVDMTM HLNALNISLQGHSQIVTQMYDLIRAFLAKLCL WETHLTRNNLAHFPTLKLVSRNESDGLNYIP KIAELKTEFQKRLSDFKLYESELTLFSSPFSTKI DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ LFSIMKLSKTKYCSQLKDSQWDSVLHIAT
848	2198	A	6985	3	289	SVQYLPGRPTRTHASTDAPLMLKPTPLPSKTK ASAPVQCLLLMAATFSPQGLAKPHSGTIPITVC CFNAINTKIPIQRLESYTRITNIQCPKEAVM
849	2199	A	6999	963	5	LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP MYFFLSHL\AVVDIAYACNTVPRMLVNLLHP AKPISFAGRMMQTFLFSTFAVTECLLLVVMS YDLYV\AICHPLRYLAIMTWRVCITLAVTSWT TGVLLSLIHLVLLLPLPFCRPQKIYHFFCEILA VLKLACADTHINENMVLAGAISGLVGPLSTIV VSYMCILCAILQIQSREVQRKAFCTCFSHLCVI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ŀ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	ļ	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
40		1	***	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	l	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \-possible
Ì			Į.	sequence	ŀ	nucleotide insertion
<del> </del>	<del></del>		<del> </del>	Soquence	<del> </del>	GLFYGTAIIMYVGPRYGNPKEQKKYLLLFHS
1	}					LFNPMLNPLICSLRNSEVKNTLKRVLGVERAL
850	2200	Λ	7001	1	1011	MGNDSVSYEYGDYSDLSDRPVDCLDGACLAI
850	2200	1 1	7001	*	1011	DPLRVAPLPLYAAIFLVGVPGNAMVAWVAG
1						KVARRRYGATWLLHLAVADLLCCLSLPILAV
					İ	PIARGGHWPYGAVGCRALPSIILLTMYASVLL
			ļ			LAALSADLCFLALGPAW\CLRFS/GACGVQVA
			Ì			CGAAWTLALLLTVPSAIYRRLHQEHFPARLQ
ľ	i		ľ			CVVDYGGSSSTENAVTAIRFLFGFLGPLVAVA
Ì						SCHSALLCWAARRCRPLGTAIVVGFFVCWAP
	1		ļ			YHLLGLVLTVAAPNSALLARALRAEPLIVGL
						ALAHSCLNPMLFLYFGRAQLRRSLPAACHW
1	J		J			ALRESOGODESVDSKKSTSHDLVSEMEV
851	2201	A	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASI
931	2201	A	7011	1	2310	SRGVLVCDECCSVHRSLGRHISIVKHLRHSA
1	1		Į.		[	WPPTLLQMVHTLASNGANSIWEHSLLDPAQV
Ĭ	1	1				QSGPALKQTPKDKV\HPIKSEFIRAKYQMLAF
	1	ļ				VHKLPCRDDDGVTAKDLSKQLHSSVRTGNLE
		ļ				TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG OTLOAELLVVYGADPGSPDVNGRTPIDYARO
1	ļ.		j			
1	Į.					AGHHELAERLVECQYELTDRLAFYLCGRKPD
1						HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
		ĺ				SNRLFEELAMDVYDEVDRRENDAVWI.ATQN
1						HSTLVTERSAVPFLPVNPEYSATRNQGRQKL
1	1	İ		1	1	ARFNAREFATLIIDILSEAKRRQQGKSLSSPTD
			+			NLELSLRSQSDLDDQHDYDSVASDEDTDQEP
	ļ					LRSTGATRSNRARSMDSSDLSDGAVTLQEYL
	1					ELKKALATSEAKVQQLMKVNSSLSDELRRLQ
}	i					REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
ĺ	{		Į.			TPMAPGGSTHRRDRQAFSMYEPGSALKPFGG
						PPGDELTTRLQPFHSTELEDDAIYSVHVPAGL
-						YRIRKGVSASAVPFTPSSPLLSCSQEGSRHTSK
l		ľ	ľ		ĺ	LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
		l				LGKEEDFHPELESLDGDLDPGLPSTEDVILKT     EQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
		1			}	VTEMASLFPKRPALEPVRSSLRLLNASAYRLQ
		ŀ	,			SECRKTVPPEPGAPVDFQLLTQQVIQCAYDIA
	1	J	1			KAAKQLVTITTREKKQ
8.52	2202	A	7016	484	1777	RISKIOVYYSTGYSSRKMNPTLGLAIFLAVLL
1 002	2202	l ^	1010	704	1///	TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
	1	1	]			KELARONMOLGFKLLKKLAFYNPGRNIFLSP
						LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
1	1	i	1		i	EKDLHEGFHYIIHELTQKTQDLKLSIGNTLFID
		1	1		}	QRLQPQRKFLEDAKNFYSAETILTNFQNLEM
1	1	l				AOKOINDFI/ESKTHGKINNLIENIDPGTVMLL
1	1	!				ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
						VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
		l	]			NITAIFILPDEGKLKHLEKGLOVDTFSRWKTL
	1	l				LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
						KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
l	l		1			
		1				DERGTEGAAGTGAQTLPMETPLVVKIDKPYL LLIYSEKIPSVLFLGKIVNPIGK
947	2202	<u> </u>	7017	1	2702	
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
Į		j	j			ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
	]					ANVSKKVSWSGRDRDDEEAAPLLRRTARPG
						GGTPLLNGAGPGAARQSPRSALFRVGHMSSV
		1				ELDDELLEP\DMDPPHPFPKEIPHNEKLLSLKY
	<b> </b>	1				ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
1	1	1				WVICALIGILTGLVACFIDIVVENLAGLKYRVI KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV
L	<u> </u>	L	<u> </u>			MUSIL FRIDKT I ENGGLST SLLLWATENAAT V

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first arnino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N-Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LVGSVIVAFIEPVAAGSGIPQIKCFLNGVKIPH
						VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE KRDFVSAGAAAGVSAAFGAPVGGVLFSLEEG ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG NMWDLSSPGLINFGRFDSEKMAYTIHEIPVFI AMGVVGGVLGAVFNALNYWLTMFRIRYIHR PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL QGGSMSYPLQLFCADGEYNSMAAAFFNTPEK SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG AAIWADPGKYALMGAAAQLGGIVRMTLSLT VIMMEATSNVTYGFPIMLVLMTAKIVGDVFIE GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV MSTPVTCLRRREKVGVIVDVLSDTASNHNGF PVVEHADDTQPARLQGLILRSQLIVLLKHKVF VERSNLGLVQRRLRLKDFRDAYPFFPIQSIH VSQDERECTMDLSEFMNPSPYTVPQEASLPR VFKLFRALGLRHLVVVDNRNQVVGLVTRKD LARYRLGKRGLEELSLAQTGPKAQATAEGRV AGAAQQPCQLRAVTLEDLGLLLAGGLASPEP LSLEELSERYESSHPTSTASVPEQDTAKHWNQ LEQWVVELQAEVACLREHKQRCERATRSLL RELLQVRARVQLQGSELRQLQQEARPAAQAP EKEAPEFSGLQNQMQALDKRLVEVREALTRL RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVITDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL
855	2205	A	7058	3	1441	QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL EDGNFLKLANNGTVLRASHGTKMMTPEVLA EAYGKKEWKHFLSDTGMACRSGKYYFYDN

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide feletion, \=possible nucleotide KDIVAAIQHNYKMSAFKENCGIYFPEIKRDPG RYLHSRPESVKKWLRQLKNAGKILLLITSSHS DYCRLLCA\YILGNDFTDLFDIVITNALKPGFP SHLPSQRPFRTLENDEEQEALPSLDKPGWYSQ GNAVHLYELLKKMTGKPEPKVVYFGDSMHS DIFPARHYSNWETVLILEELRGDEGTRSQRPE ESEPLEKKGKYEGPKAKPLNTSSKKWGSFFI DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI EAIAELPLDYKFTRFSSSNSKTAGYYPNPPLV LSSDETLISK
856	2206	A	7082	396	1635	SSPSVFEFEHAVQPVFTMEFLKTCVLRRNACT AVCFWRSKVVQKPSVRRISTTSPRSTVMPAW VIDKYGKNEVLRFTQNMMMPIIHYPNEVIVK VHAASVNPIDVNMRSGYGATALNMKRDPLH VKIKGEEFPLTLGRDVSGVVMECGLDVKYFK PGDEVWAAVPPWKQGTLSEFVVVSGNEVSH KPKSLTHTQAASLPYVALTAWSAINKVGGLN DKNCTGKRVLILGASGGVGTFAIQVMKAWD AHVTAVCSQDASELVRKLGADDVIDYKSGSV EEQLKSLKPFDFILDNVGGSTETWAPDFLKK WSGATYVTLVTPFLLNMDRLGIADGMLQTG VTVGSKALKHFWKGVHYRWAFFMASGPCL DDIAELVDAGKIRPVIEQTFPFSKVPEAFLKV ERGHARGKTVINVV
857	2207	A	7088	320	2417	LRRRKMTPQSLLQTTLFLLSLLFLVQGAHGR GHREDFRFCSQRNQTHRSSLHYKPTPDLRISIE NSEEALTVHAPFPAAHPASRSFPDPRGI.YHFC LYWNRHAGRLHLLYGKRDFLLSDKASSLLCF QHQEESLAQGPPLLATSVTSWWSPQNISLPSA ASFTFSFHSPPHTGAHNASVDMCELKRDLQL LSQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMGSFEEDRINATVWKLQPTAGLQ DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE KVLGIVVQNTKVANLTEPVVLTFQHQLQPKN VTLQCVFWVEDPTLSSPGHWSSAGCETVRRE TQTSCFCNHLTYFAVLMVSSVEVDAVHKHY LSLLSYVGCVVSALACLVTIAAYLCSRVPLPC RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPV ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG YNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAVHRTPEGVIYPS MCWIRDSLVSYITNLGLFSLVFLFNMAMLAT MVVQILRLRPHTQKWSHVLTLLCLSLVLGULP WALIFFSFASGTFQLVVLYLFSIITSFQGFLIFI WYWSMRLQARGGPSPLKSNSDSARLPISSGS TSSSRI
858	2208	A	7091	185	415	DAGAVKSSDTNIWFRGMCDDKKGHRCPS*G QPQHFHVAFHTEAEGAMFYFRLHVIHRVMQS QQQLFPSTLFSWLLE
859	2209	A	7136	3	302	FFFWRÖSLALLPRLECSGATGAHCNLHFPGSS DCPTSAS*IAGITGACYHAWLLFVFLAETGFH HVGQGGLELLTSSDPSGSASQSAGITGVSHCT WPI
860	2210	A	7156	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAV PAPKVPIKMQVKHWPSEQDPEKAWGARVVE PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGR GPILPGTKAWMETEDTLGRVLSPEPDHDSLY

SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M-Methionine, N-Asparagine, P-Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
Ì	ļ	1	1	peptide		/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
1		1				HPPPEEDQGEERPRLWVMPNHQVLLGPEEDQ
}				}		DHIYHPQ*GSRGHHCPRPVPRPRLLGLGPSLP CPS
861	2211	A	7161	1220	1003	NYVCTIAF*EKKMGF*LSLSCLVLLFVLFLDCI
1 801	2211	1 ^	/101	1220	1005	LTTTTRIMFHCTYLFASVCLSLLNTLLSPNCL
}		ļ			j	KSAMILO
862	2212	Α	7211	665	847	LKYYHITMGIYKTGKKVIL*KSSMSNRFSVIF
						YKNIQKLSFSNYVYHQNYVFSSDWSYDF
863	2213	A	7212	924	1273	HGSSCALGDLAPG*LPSGPVLSSPAVRL*RKP
ł	Į.	1			1	LVWDSPSCLPATGPT*GLVLVLGGPDCT*WA
	Ì	ĺ		!	ĺ	RGQHEHKRMRAP*SCRVTVNLAKKKKKTDQ
			L	<u> </u>		CIKPNYQSPPKECDYNILANSVA
864	2214	Α	7214	845	1619	SDKGGKKADRKNHLRHAFPLLPHRVRERLH
1				j		DPKVPVDADHVQGQDPGRAAHDIHGEDVTE
ĺ						KVSKDPLAPDEVGDTDEGHDRHGHREVGQR HGHDQEEVAYEERACEGGKFATVEVTDKPV
1		l	į	ł	{	DEALREAMPKVAKYAGGTNDKGIGMGMTV
		1		!		PISFAVFPNEDGSLQKKLKVWFRIPNQFQSDP
}		ł			}	PAPSDKSVKIEEREGITVYSMQFGGYAKEAD
		ļ	1			YVAQATRLRAALEGTATYRGDIYFCTGYDPP
		l		1	}	MKPYGRRNEIWLLKT
865	2215	Α	7246	559	682	RRLGAVAHAYTSSTLGGRGGWIT*GQELQTS
		<u> </u>		<u> </u>		LANMAKPRLY
866	2216	Λ	7257	641	1310	TCTYKYLMGWIRGRRSRHSWEMSEFHNYNL
i		ł		İ	{	DLKKSDFSTRWQKQRCPVVKSKCRENASPFF FCCFIAVAMGIRFIIMVAIWSAVFLNSLFNQEV
1	ļ	l		1	j	QIPLTESYCGPCPKNWICYKNNCYQFFDESKN
1		f		ĺ	ĺ	WYESQASCMSQNASLLKVYSKEDQDLLKLV
		Ì	-			KSYHWMGLVHIPTNGSWQWEDGSILSPNLLT
İ	! ! .	l		1	ĺ	IIEMQKGDCALYASSFKGYIENCSTPNTYICM
		l				QRTV
867	2217	Α	7288	151	396	SIKIIEAFGSNGPDFWFFRYWSP*LFRQQVVFI
ļ		J	)		ŀ	MPFFQTLWLMNANRFCSIFTTTNVANNCWW
060	2210	<del>   </del>	7200		272	TPYHCWLSVVVCRCESHGI PDTVIGGRGSGGKEFGRWVLW*VFE*RLGTP
868	2218	Α	7298	3	2/2	KGSCPAGGSRMVSESD*EGRGC*ASYPCAC*
					!	AGS*WR*GSRPAGRGTPPRSLSHARPP
869	2219	A -	7332	1223	332	PRRDAEDRDESCLNPAFPIGLLHPNSVNSMAR
]		] •		l		FLTLCTWLLLLGPGLLATVRAECSQDCATCS
	]	1		l		YRLVRPADINFLACVMECEGKLPSLKIWETC
}	1	)	}	i		KELLQLSKPELPQDGTSTLRENSKPEESHLLA
						KRYGGFMKRYGGFMKKMDELYPMEPEEEA
}	}	]		j		NGSEILAKRYGGFMKKDAEEDDSLANSSDLL
1	1			]		KELLETGDNRERSHHQDGSDNEEEVSKRYGG
[		}	Į	l	ŀ	FMRGLKRSPQLKEKAKELQKRYGGFMRRVG POKW*MTSPONRYGGFLKRFAEALPSDEEGE
İ						SYSKEVPEMEKRYGGFMRF
870	2220	A	7382	216	1018	EIHORLTERTOFLDESRKNPNS*QANLLRGGG
ا ۵٫۰	2220	^	7502		1010	AGOGRGREGAESGGSRGEGPGSDGRLPATGD
]	}	1	1	l	}	FWSPRSQRRGCCGRRAPRPEAMENGAVYSPT
]	1			Į		TEEDPGPARGPRSGLAAYFFMGRLPLLRRVL
ł	1		1	}	}	KGLQLLLSLLAFICEEVVSQCTLCGGLYFFEF
				ļ		VSCSAFLLSLLILIVYCTPFYERVDTTKVKSSD
Į	}	1	}	Ì	}	FYITLGTGCVFLLASIIFVSTHDRTSAEIAAIVF
						GFIASFMFLLDFITMLYEKRQESQLRKPENTT
	1 200:	<del> </del>	12403	ļ	102	RAEALTEPLNA
871	2221	A	7403	3	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVN DPGNMSFVKETVDKLLTGFRCFREREAAPRR
1				}		ALRGAALPGESEAGDPESLRSSVNADWIQYS
				<del></del>	<u> </u>	1

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	}	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M-Methionine, N-Asparagine, P-Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ĺ	I	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ł	l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ		I	peptide	•	/possible nucleotide deletion, \possible
	L	<u> </u>		sequence		nucleotide insertion
			1			DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
		L	<u> </u>		L	PFIC
872	2222	Α	7413	1061	359	FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
				ļ		PGGS*PQATLHLDRMRVSASPTKEIQVKKYK
	i	]	1			CGLIKPCPANYFAFKICSGAANVVGPTMCFED
	1	{		[	1	RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
						KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
	1	1		1	(	YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
)		}	1	j	i	SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
						GWPELLEMEGCMPPKPF
873	2223	Α	7429	2242	2394	ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
				<u> </u>	L	DHPGQHCETPSLLKIERKLF
874	2224	Α	7468	146	894	PCTSCVLWATLHLPASTRKAPQAECGMISITE
		ŀ	•			WQKIGVGITGFGIFFILFGTLLYFDSVLLAFGN
1	Į.				!	LLFLTGLSLIIGLRKTFWFFFQRHKLKGTSFLL
				1	1	GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
ſ	ĺ	1			i	AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE
	ł	1	Ì			MSSLNLDHWLKGAKREEWEPPPQSPALTHSP
j	Į.	l	-	Ì	ł	TYPGPPQVQKERNGAEQLTSNPQVDSRGCQE
					}	AEMQTPRRLGWGWYHTLTLYLWEEK
875	2225	Α	7498	91	251	GEKPVPTWLQDEAGQWLLGFVAQPWGWPG
		1	1	1	0	SERHEP*HGGVLFRLGPSAPPGKL
876	2226	A	7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN
					ļ	ILGGQGGWIA*GQEFKTSLGNTVRPCLYK
877	2227	Α	7566	2	940	GCAPDTRFFVPEPGGRGAAPWVALVARGGC
			ł	ļ		TFKDKVLVAARRNASAVVLYNEERYGNITLP
[	1					MSHAGTGNIVVIMISYPKGREILELVQKGIPV
		1				TMTIGVGTRHVQEFISGQSVVFVAIAFITMMII
İ		]	1			SLAWLIFYYIQRFLYTGSQIGSQSHRKETKKVI
l	1	1	}	1	ļ	GQLLLHTVKHGEKGIDVDAENCAVCIENFKV
ľ						KDIIRILPCKHIFHRICIDPWLLDHRTCPMCKL
ŀ						DVIKALGYWGEPGDVQEMPAPESPPGRDPAA
-	1	1				NLSLALPDDDGSDESSPPSASPAESEPQCDPSF
	1	1	}	1	1	KGDAGENTALLEAGRSDSRHGGPIS
878	2228	Α	7586	315	1232	ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLR
Į.		1	1		}	RGRMQAACWYVLFLLQPTVYLVTCANLTNG
	Į.		İ		1	GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS
Į.	İ	1	i	1		QTFRGKENDTDLDLRYDTPEPYSEQDLWDW
1		}				LRNSTDLQEPRPRAKRRPIVKTGKFKKMFGW
Į.		1			1	GDFHSNIKTVKLNLLITGKIVDHGNGTFSVYF
İ	1	1		1	1	RHNSTGQGNVSVSLVPPTKIVEFDLAQQTVID
!				1		AKDSKSFNCRIEYEKVDKATKNTLCNYDPSK
-		1				TCYQEQTQSHVSWLCSKPFKVICIYISFYSTD
		1		1		YKLVQKVCPDYNYHSDTPYFPSG
879	2229	A	7605	479	391	TESWKLKWWSPTCLDQLNGSAPGNVFIHG
880	2230	A	7612	93	659	DAAVAMTAQGGLVANRGRRFKWAIELSGPG
'		Ţ -				GGSRGRSDRGSGQGDSLYPVGYLDKQVPDTS
	,					VOETDRILVEKRCWDIALGPLKQIPMNLFIMY
ł		1		1	l	MAGNTISIFPTMMVCMMAWRPIQALMAISAT
l		1		1	1	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK
					l	COSMGLLPTHASDWLAFIEPPERMEFSGGGL
ļ						LL
881	2231	A	7615	291	1452	SPOKTMRSHTITMTTTSVSSWPYSSHRMRFIT
١ ٠٠٠		1.	1 /013		1	NHSDOPPONFSATPNVTTCPMDEKLLSTVLTT
		1		1		SYSVIFIVGLYGNIIALYVFLGIHRKRNSIOIYL
		1		1		LNVAIADLLLIFCLPFRIMYHINQNKWTLGVIL
	1		1	1		CKVVGTLFYMNMYISILLGFISLDRYIKINRSI
l					ļ	QQRKAITTKQSIYVCCIVWMLALGGFLTMIIL
		1	1		1	TLKKGGHNSTMCFHYRDKHNAKGEAIFNFIL
	<del></del>	1		1	<u> </u>	THE TOTAL OF THE PARTY OF THE P

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  VVMFWLIFLLILSYIKIGKNLLRISKRRSKFPN SGKYATTARNSFIVLIFTICFVPYHAFRFIYISS QLNVSSCYWKEIVHKTNEIMLVLSSFNSCLDP VMYFLMSSNIRKIMCQLLFRRFQGEPSRSEST
882	2232	A	7617	67	379	SEFKPGYSLHDTSVAVKIQSSSKST RQMALLKANKDLISAGLKEFSVLLNQQVFND PLVSEEDMVTVVEDWMNFYINYYRQQVTGE PQERDKALQELRQELNTLANPFLAKYRDFLK SHELPSHPPPSS
883	2233	A	7622	400	215	KVKTCRYNPKYSAANDTGFVDIPSREKDLAK AVATVGPISVAVGASHVFFQFYKKGKHLSS
884	2234	A	7638	2640	2861	APVLILQMVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLRKVSECRQMGPGALEQFP GLSCHTSHSG
885	2235	A	7642	201	455	PSRGKMELEAMSRYTSPVNPAVFPHLTVVLL AIGMFFTAWFFVYEVTSTKYTRDIYKELLISL VASLFMGFGVLFLLLWVGIYV
886	2236	A	7692	61	569	APENPFSRQHFNSETKVKLSLKTGTWLGNHA HLGEHFSTHHELGLSGKVVGFLVKNILEVIRN GGMETRHPGKVSSWFHRWDSRAEQHNHAE HHEDVPQGDEDSKVSEAQQEFPDVVTCAGLP GLLPKALRVLLFQLKVQHRPGIHQQRPEQQD VSDHRYGRSVRQNRK
887	2237	A	7693	85	315	NPGCCLPVAMRTSYLLLFTLCLLLSEMASGG NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTK IQGTCYRGKAKCCK
888	2238	A	7702	242	1298	APSHRRYLSPSRSAGQLGNMALERLCSVLK VLLITVLVVEGIAVAQKTQDGQNIGIKHIPAT QCGIWVRTSNGGHFASPNYPDSYPPNKECIYI LEAAPRQRIELTFDEHYYIEPSFECRFDHLEVR DGPFGFSPLIDRYCGVKSPPLIRSTGRFMWIKF SSDEELEGLGFRAKYSFIPDPDFTYLGGII.NPIP DCQFELSGADGIVRSSQVEQEEKTKPGQAVD CIWTIKATPKAKIYLRFLDYQMEHSNECKRNF VAVYDGSSSIENLKAKFCSTVANDVMLKTGI GVIRMWADEGSRLNRFRMLFTSFGGASPAQA ALSFCHSNMCINNSLVCNGVQNCAYPWDEN HC
889	2239	A	7707	185	2911	CHYIMNPSTHHPASAGGSILGLFDFFGLGLGE MTMDALLARLKLLNPDDLREEIVKAGLKCGP ITSTTRFIFEKKLAQALLEQGRLSSFYHHEA GVTALSQDPQRILKPAEGNPTDQAGFSEDRDF GYSVGLNPPEEEAVTSKTCSVPPSDTDTYRAG ATASKEPPLYYGVCPVYEDVPARNERIYVYE NKKEALQAVKMIKGSRFKAFSTREDAEKFAR GICDYFPSPSKTSLPLSPVKTAPLFSNDRLKDG LCLSESETVNKERANSYKNPRTQDLTAKLRK AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ EGCRYNVMHVAAKENQASICQLTLDVLENP DFMRLMYPDDDEAMLQKRIRYVVDLYLNTP DKMGYDTPLHFACKFGNADVVNVLSSHHLI VKNSRNKYDKTPEDVICERSKNKSVELKERIR EYLKGHYYVPLLRAEETSSPVIGELWSPDQTA EASHVSRYGGSPRDPVLTLRAFAGPLSPAKAE DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGRELAHELGYPWVEYWEFLGCFVDLSSQE GLQRLEEYLTQQEIGKKAQQETGEREASCRD KATTSGSNSISVRAFLDEDDMSLEEIKNRQNA ARNNSPPTVGAFGHTRCSAFPLEQEADLIEAA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	t	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ŀ	ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
İ		İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
}		1		peptide	}	/-possible nucleotide deletion, \-possible
	<del> </del> -	<del> </del>	<del> </del>	sequence	ļ	nucleotide insertion
1		į	1		ĺ	EPGGPHSSRNGLCHPLNHSRTLAGKRPKAPR
	ļ	}	J .	ļ	]	GEEAHLPPVSDLTVEFDKLNLQNIGRSVSKTP DESTKTKDQILTSRINAVERDLLEPSPADQLG
	į	1			ļ	NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV
						TREPARRLFLFGEEPSKLDQDVLAALECADV
}	ļ	J	]	]	]	DPHQFPAVHRWKSAVLCYSPSDRQSWPSPAV
	1	1				KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP
L		l				GLGSPGRYSPVHGSQLRRMARLAELAAL
890	2240	Α	7711	360	269	RHMPVIPALWEAEVGGLLEPRSSRSAWATE
891	2241	A	7721	61	1175	KLPWEPSFLIKMQIIRHSEQTLKTALISKNPVL
ļ	]					VSQYEKLDAGEQRLMNEAFQPASDLFGPITL
ł		[	i i			HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN
1	i I	ĺ	í í		•	KRSIYIQSIGSLGNTRIISEEYIKWLTGYCKAYF
}	j .					YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
			i i			AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
1	1	1	i			WNFVFGQASLTDGVGIFSFARYGSDFYSMHY
	j .	}	ļ			KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLR
						SCKTLTHEIGHIFGLRHCQWLACLMQGSNHL
1	}	1				EEADRRPLNLCPICLHKLQCAVGFSIVERYKA
1				1		LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
892	2242	Α	7723	2	1650	EAFKEWKEWIIKCLAVLQK SAPTAPARPCRAERGSGGGMLALLAASVALA
} "		1.	ا لعاد	-	1000	VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL
1						PAMPMQGAQSPEEELRAAVLQLRETVVQQ
						KETLASARAIRELTGKLARCEGLAGGKARGA
1				ļ		GATGKDTMGDLPRDPGHVVEQLSRSLQTLK
1 1			1			DRLESLEPLPAMPMQGGAQSPEEELRAAVLO
1				i		LRETVVQQKETLASARAIRELTGKLARCEGL
1 1	l j		)	ļ		AGGKARGAGATGKDTMGDLPRDPGHVVEQ
[	!	į	1	1	ĺ	LSRSLQTLKDRLESLEHQLRANVSNAGLPGD
		1	ĺ	j		FREVLQQRLGELERQLLRKGAELEDEKSLLH
)				1		NETSAHRQKTESTLNALLQRVTELERGNSAF
	[	!		[	ĺ	KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
		i				ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE
]	]	1		j		WGNNPIELLINDKVAQLPLFVSDGKWHHICV
<b>l</b> [	ĺ	[		[		TWTTRDGMWEAFQDGKKLGTGENLAPWHPI   KPGGVLILGQEQDTVGGRFDATQAFVGELSQ
i i	I	i		ľ		FNIWDRVLRAQEIVNIANCSTNMPGNIIPWVD
L				1		NNVDVFGGASKWPVETCEERLLDL
893	2243	A	7729	3554	2419	LTAGTAMNYPLTLEMDLENLEDLFWELDRL
	İ		1	ĺ	1	DNYNDTSLVENHLCPATEGPLMASFKAVFVP
			I			VAYSLIFLLGVIGNVLVLVILERHRQTRSSTET
	{		1	Ī	- 1	FLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
	ſ	1		ſ	•	LCKTVIALHKVNFYCSSLLLACIAVDRYLAIV
		ļ	1		Į	HAVHAYRHRRLLSIHITCGTIWLVGFLLALPEI
1 1	1	1	1	1	ļ	LFAKVSQGHHNNSLPRCTFSQENQAETHAWF
	}	1		l	l	TSRFLYHVAGFLLPMLVMGWCYVGVVHRLR
	j			l	!	QAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV
}	1	- 1	}	Ì	}	IFLOTLARLKAVDNTCKLNGSLPVAITMCEFL
				į		GLAHCCLNPMLYTFAGVKFRSDLSRLLTKLG
894	2244	A	7738	670	287	CTGPASLCQLFPSWRRSSLSESENATSLTTF
		.	, , , , ,	0/0	20/	FVTRAGRWGAGARVRGGAGGMASGAARWL
		- 1				VLAPVRSGALRSGPSLRKDGDVSAAWSGSGR SLVPSRSVIVTRSGAILPKPVKMSFGLLRVFSI
						VIPFLYVGTLISKNFAALLEEHDIFVPEDDDDD
	1		- 1	}		D D
895	2245	A	7753	119		APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR
		}				LWLSLFLHAGKEAPHCPRTRPL
896	2246	A	7754	1		SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIM
			<del></del> -			THE TAXABLE PARTIES AND A PART

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  QVSTAALAVLLCTMALCNQVLSAPLAADTPT ACCFSYTSRQIPQNFIADYFETSSQCSKPSVIFL TKRGRQVCADPSEEWVQKYVSDLELSA
897	2247	A	7761	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPL RPLSRHPLSSGSPETSAAAIMLLTVRHGTVRY RSSALLARTKNNIQRYFGTNSVICSKKDKQSV RTEETSKETSESQDSEKENTKKDLLGIIKGMK VELSTVNVRTTKPPKRRPLKSLEATLGRLRRA TEYAPKKRIEPLSPELVAAASAVADSLPFDKQ TTKSELLSQLQOHEEESRAQRDAKRPKISFSNI ISDMKVARSATARVRSRPELRIQFDEGYDNYP GQEKTDDLKKRKNIFTGKRLNIFDMMAVTKE APETDTSPSLWDVEFAKQLATVNEQPLQNGF EELIQWTKEGKLWEFPINNEAGFDDDGSEFH EHIFLEKHLESFPKQGPIRHFMELVTCGLSKNP YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF KLRPWKFLFRNN
898	2248	Α	7775	85	496	SCOTTOPPAOSCSTGTMRIMLLFTAILAFSLA QSFGAVCKEPQEEVVPGGGRSKRDPDLYQLL QRLFKSHSSLEGLLKALSQASTDPKESTSPEK RDMHDFFVGLMGKRSVQPDSPTDVNQENVP SFGILKYPPRAE
899	2249	Α	7785	179	703	PFHLGASSNTFRLQVQTQESKAQKEVKMGFI FSKSMNESMKNQKEFMLMNARLQLERQLIM QSEMRERQMAMQIAWSREFLKYFGTFFGLA AISLTAGAIKKKKPAFLVPIVPLSFILTYQYDL GYGTLLERMKGEAEDILETEKSKLQLPRGMIT FESIEKARKEQSRFFIDK
900	2250	A	7789	1465	300	VWLPLKSYKIRSPSLHCQCEIFREEFLFSSLQE GRDKDTFSKMAMVSEFLKQAWFIENEEQEY VQTVKSSKGGPGSAVSPYPTFNPSSDVAALH KAIMVKGVDEATIIDILTKRNNAQRQQIKAAY LQETGKPLDETLKKALTGHLEEVVLALLKTP AQFDADELRAAMKGLGTDEDTLIEILASRTN KEIRDINRVYREELKRDLAKDITSDTSGDFRN ALLSLAKGDRSEDFGVNEDLADSDARALYEA GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNKVLDLELKGDIEKCLTAIVKCA TSKPAFFAEKLHQAMKGVGTRHKALIRIMVS RSEIDMNDIKAFYQKMYGISLCQAILDETKGD YEKILVALCGGN
901	2251	A	7796		807	VEFHPQRARAGARAPSMGVLLTQRTLLSLVL ALLFPSMASMAAIGSCSKEYRVLLGQLQKQT DLMQDTSRLLDPYIRIQGLDVPKLREHCRERP GAFPSEETLRGLGRRCFLQTLNATLGCVLHRL ADLEQRLPKAQDLERSGLNIEDLEKLQMARP NILGLRNNIYCMAQLLDNSDTAEPTKAGRGA SQPPTPTPASDAFQRKLEGCRFLHGYHRFMH SVGRVFSKWGESPNRSRRHSPHQALRKGVRR TRPSRKGKRLMTRGQLPR
902	2252	Α	7802	2	721	TAARRRQKGTAARRLQKGTAARRRQKGTAA RRRQKGTAARRPQKGTAARRRQKGTAARRR QKGTAARRRQKGTAARRPQKGTAARRRQKG TAARRRQKGTAARRRQKGLAIASRGCPCASR AGGVRGAGSRLRAMAPKVFRQYWDIPDGTD CHRKAYSTTSIASVAGLTAAAYRVTLNPPGTF LEGVAKVGQYTFTAAAVGAVFGLTTCISAHV REKPDDPLNYFLGGCAGGLTLGARTHNYGIG AAACVYFGIAASLVKMGRLEGWEVFAKPKV

SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	, nou	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
1 .	dence	i	914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	ľ	1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
1		1	1	residue of	sequence	
			1	peptide		/=possible nucleotide deletion, \=possible
L				sequence		nucleotide insertion
903	2253	A	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA
	İ		1		1	VSTVFSTSSLMLALSRHSLLSPLLSVTSFRRFY
J	ŀ		1	ļ	1	RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
	1		1			ARLLYESRKRGMLENCILLSLFAKEHLQHMT
			1	1		EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
1	1					EIFENEVMALLRDFAKNKNKEQRLRAPDLEY
		1	i	i	Í	LFEKPR
904	2254	A	7813	40	821	GAGRALGHLETGAGDVAAALPARKFPRSLLG
1 704	2254	1	7013	1 70	021	AGARLTGWTMNVFRILGDLSHLLAMILLLGK
1			ļ			IWRSKCCKGISGKSQILFALVFTTRYLDLFTNF
		1			1	
ł	ł	l	ł	}	1	ISIYNTVMKVVFLLCAYVTVYMIYGKFRKTF
1 .	ì	İ	1	1		DSENDTFRLEFLLVPVIGLSFI ENYSFTLLEIL
		[	1			WTFSIYLESVAILPQLFMISKTGEAETITTHYL
ŀ		1	i			FFLGLYRALYLANWIRRYQTENFYDQLAVVS
		1	1		ſ	GVVQTIFYCDFFYLYVTKGRSWDDSNADTGL
						RSYSSI
905	2255	Α	7817	1399	881	LSNKDVLSPQLKDENSKLRRKLNEVQSFSEA
	ļ.	1	1		i	QTEMVRTLERKLEAKMIKEESDYHDLESVVQ
i		1	1			QVEQNLELMTKRAVKAENHVVKLKQEISLL
l .	ł	ł	i	<u> </u>	t	QAQVSNFQRENEALRCGQGASLTVVKQNAD
l .		ł				VALQNLRVVMNSAQASIEQLVSGAETLNLVA
Ì		}			ľ	EILKSIDRISEVKDEEEDS
906	2256	A	7822	3	1462	DSPRNRFEILGRPTRTPTRPGPRPAMEDLDAL.
900	2236	A	/022	•	1402	
1	1		1	1	ļ	LSDLETTTSHMPRSGAPKERPAEPLTPPPSYG
l			1			HQPQTGSGESSGASGDKDHLYSTVCKPRSPK
1	1	j	i	ļ		PAAPAAPPFSSSSGVLGTGLCELDRLLQELNA
		1				TQFNITDEIMSQFPSSKVASGEQKEDQSEDKK
		[	1		ſ	RPSLPSSPSPGLPKASATSATLELDRLMASLSD
		1	Ì			FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG
ļ		1	1	ĺ		KGSLDTMLGLLQSDLSRRGVPTQAKGLCGSC
		ł	1			NKPIAGQVVTALGRAWHPEHFVCGGCSTAL
			1	ļ		GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI
		1	1	1		RHKMVTALGTHWHPEHFCCVSCGEPFGDEG
		1		1		FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN
ĺ	1	1	1	1	1	YISALSALWHPDCFVCRECFAPFSGGSFFEHE
	1	1	1	}	1	GRPLCENHFHARRGSLCATCGLPVTGRCVSA
I	1	1	1	ļ	1	LGRRFHPDHFTCTFCLRPLTKGSFQERAGKPY
j	I		]	1	1	COPCFLKLFG
907	2257	A	7828	1792	1671	FIYVNOSFAPSPDOEVGTLYECFGSDGKLVLH
1 ~~.	'	' *	1,020	1	1	YCKSQAWG
908	2258	A	7842	110	1172	KLSCPCSHGTRVTAVRGPRLKAGVOWHDLG
200	2238	^	/84Z	110	1172	,
	1	1	J	1	J	SLOPPPSGLKQSSHLSLSSSWDFRHAPTHPET
1				1		YTCPKMIEMEQAEAQLAELDLLASMFPGENE
			1	1		LIVNDQLAVAELKDCIEKKTMEGRSSKVYFTI
1				1		NMNLDVSDEKMAMFSLACILPFKYPAVLPEI
			1	1		TVRSVLLSRSQQTQLNTDLTAFLQKHCHGDV
l	]	J	1	1		CILNATEWVREHASGYVSRDTSSSPTTGSTVQ
		1	1	i	Ì	SVDLIFTRLWIYSHHIYNKCKRKNILEWAKEL
	}	1	1	1	1	SLSGFSMPGKPGVVCVEGPQSACEEFWARLR
ł	1		1	1		KLNWKRILIRIIREDIPFDGTNDETERQRKFSIF
Į.		l	1	l		EEKVFSVNGARGNHMDFGQLYQFLNTKGCG
1			1			DVFQMFLWV
909	2259	A	7870	3067	2923	EGICVYTFIYVHMYTRTCMHTYPYMYMNSV
303	2239	1	/8/0	300,	2763	LISSEILLIPSKYLFESK
-	22.62	<b>L.</b>	7004	212	4074	
910	2260	Α	7884	212	4874	GALTWSHPLLAVCPQGVWLGSTPSGSPALLP
		1				PSHRVNAEPGCVVTNACASGPCPPHANCRDL
			1			WQTFSCTCQPGYYGPGCVDACLLNPCQNQG
1	i		i			SCRHLPGAPHGYTCDCVGGYFGHHCEHRMD
1	1	1	l	1		QQCPRGWWGSPTCGPCNCDVHKGFDPNCNK
			•	·	•	·

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  TNGQCHCKEFHYRPRGSDSCLPCDCYPVGST SRSCAPHSGQCPCRPGALGRQCNSCDSPFAEV TASGCRVLYDACPKSLRSGVWWPQTKFGVL ATVPCPRGALGLRGAGAAVRLCDEAQGWLE PDLFNCTSPAFRELSLLLDGLELNKTALDTME AKKLAQRLREVTGHTDHYFSQDVRVTARLL AHLLAFESHQQGFGLTATQDAHFNENLLWA GSALLAPETGDLWAALGQRAPGGSPGSAGLV RHLEEYAATLARNMELTYLNPMGLVTPNIML SIDRMEHPSSPRGARRYPRYHSNLFRGQDAW DPHTHVLLPSQSPRPSPSEVLPTSSSIENSTTSS VVPPPAPPEPEPGISIIILLVYRTI.GGLLPAQFQ AERRGARLPQNPVMNSPVVSVAVFHGRNFLR GILESPISLEFRLLQTANRSKAICVQWDPPGLA EQHGVWTARDCELVHRNGSHARCRCSRTGT FGVLMDASPRERLEGDLELLAVFTHVVVAVS VAALVLTAAILLSLRSLKSNVRGIHANVAAA LGVAELFLLGIHRTHNQLVCTAVVILLHYFF LSTFAWLFVQGLHLYRMQVEPRNVDRGAMR FYHALGWGVPAVLLGLAVGLDPEGYGNDFC CWISVHEPLIWSFAGPVVLVVMNGTMFLLA ARTSCSTGQREAKKTSALTLRSSFLLLLLVSA SWLFGLLAVNHSILAFHYLHAGLCGLQGLAV LLLFCVLNADARAAWMPACLGRKAAPEEAR PAPGLGPGAYNNTALFEESGLIRTLGASTVSS VSSARSGRTQDQDSQRGRSYLRDNVLVRHGS AADHTDHSLQAHAGPTDLDVAMFHRDAGA DSDSDSDLSLEEERSLSIPSSESEDDNGRTRGRFQRPLCRAAQSERLLTHPKDVDGNDLLSYWPA LGECEAAPCALQTWGSERRLGLDTSKDAAN NNQPDPALTSGDETSLGRAQQRKGILKNRL QYPLVPQTRGAPELSWCRAATLGHRAVPAAS YGRIYAGGGTGSLSQPASRYSSREQLDLLLRR QLSRERLEEAPAPVLRPLSRPGSQECMDAAPG RLEPKDRGSTLPRQPPRDYPGAMAGRFGSR DALDLGAPREWLSTLPPSRTALGHPCDPPPLP LSPQRQLSRDPLLPSRPDSRFALGDDLLLRR PLSPRGDGCMDAAPG RLEPKDRGSTLPRQPPRDYPGAMAGRFGSR DALDLGAPREWLSTLPPSRTADLDPQPPPLP LSPQRQLSRDPLLPSRPDSNSGPSHGP
					•	NNQPDPALTSGDETSLGRAQRQRKGILKNRL QYPLVPQTRGAPELSWCRAATLGHRAVPAAS YGRIYAGGTGSLSQPASRYSSREQLDLLLRR QLSRERLEEAPAPVLRPLSRPGSQECMDAAPG RLEPKDRGSTLPRRQPPRDYPGAMAGRFGSR DALDLGAPREWLSTLPPPRRTRDLDPQPPPLP
911	2261	Α	7890	21	806	EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG SCRPKARSSSARWALTCCLVLLPFLAGLTTYL LVSQLRAQGEACVQFQALKGQEFAPSHQQV YAPLRADGDKPRAHLTVVRQTPTQHFKNQFP ALHWEHELGLAFTKNRMNYTNKFLLIPESGD YFIYSQVTFRGMTSECSEIRQAGRPNKPDSITV VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE DKTFFGAFLL
912	2262	A	7891	1263	111	ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ PVPYILKKIFQDREAAATTGVSRDLCYVKELG VRGNVLRFLPDQGFFLYPKISQASSCLQKLL YFNLSAIKEREQLTLAQLGLDLGPNSYYNLGP ELELALFLVQEPHVWGQTTPKPGKMFVLRSV

SFQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion PWPQGAVHFNILLDVAKDWNDNPRKNFGLFL EILVKEDRDSGVNFQPEDTCARLRCSLHASLL VVTLNPDQCHPSRKRRAAIPVPKLSCKNLCH RHQLFINFRDLGWHK WIIAPKGFMANYCHGE CPFSLTISLNSSNYAFMQALMHAVDPEIPQAV CIPTKLSPISMLYQDNNDNVILRHYEDMVVD ECGCG
913	2263	A	7892	15	849	ASRLPRGPGCGADMRPLLGLLLVFAGCTFAL YLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAE LRELSEVLREYRKEHQAYVFLLFCGAYLYKQ GFAIPGSSFLNVLAGALFGPWLGLLLCCVLTS VGATCCYLLSSIFGKQLVVSYFPDKVALLQR KVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPI LNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTS LDALFSWDTVFKLLAIAMVALIPGTLIKKFSQ KHLQLNETSTANHIHSRKDT
914	2264	A	7893	815	959	KSGWVWWLTPLIPALWEAQTEGSLRPEVKN RLSNITRPFFSKKKKILV
915	2265	A	7909	3	641	HASGPGGLLRRRRGSGANMPVARSWVCRKT YVTPRRPFEKSRLDQELKLIGEYGLRNKREV WRVKFTLAKIRKAARELLTLDEKDPRRLFEG NALLRRLVRIGVLDEGKMKLDYILGLKIEDFL ERRLQTQVFKLGLAKSIHHAHVLIQQCHIRVR EQVVNILFFTVRLDSQKHIDFSLCFPIGVANPS HVKRKNASKGQGGAGARDDEEEE
916	2266	A	7914	3	967	VAHTQWHTCQRLSQLTHRSILKYLLIDTHAC QVLILKHTIIASLSLPSCQECFPSSIPSASHMVS HPHPPPSPRWGQTPEGLPAASPCGPGPRSCFS SILPTGDSWGMLACLCTVLWHLPAVPALNRT GDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLN YLGPPFNEPDFNPPRLGAETLPRATVDLEVW RSLNDKLRLTQNYEAYSHLLCYLRGLNRQAA TAELRRSLAHFCTSLQGLLGSIAGVMAALGY PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL LKELQTWLWRSAKDFNRLKKKMQPPAAAVT LHLGAHGF
917	2267	A	7921	2	1166	RPRRGQGLVQEVQTENVTVAEGGVAEITCRL HQYDGSIVVIQNPARQTLFFNGTRALKDERFQ LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED THHQIATLTVLVAPENPVVEVREQAVEGGEV ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ ENGKVWSVASTVRFRVDRKDDGGIIICEAQN QALPSGHSKQTQYVLDVQYSPTARIHASQAV VREGDTLVLTCAVTGNPRPNQIRWNRGNESL PERAEAVGETLTLPGLVSADNGTYTCEASNK HGHARALYVLVVYGESRLRPTEGGGAPDP GAVVEAQTSVPYAIVGGILALLVFLIICVLVG MVWCSVRQKGSYLTHEASGLDEQGEAREAF LNGSDGHKRKEEFFI
918	2268	A	7938	3	2653	RRRLPPASPPSSSVSSSLSPSAVVMACRWSTK ESPRWRSALLLLFLAGVYGNGALAEHSENVH ISGVSTACGETPEQIRAPSGITSPGWPSEYPAK INCSWFIRANPGEITISFQDFDIQGSRRCNLD WLTIETYKNIESYRACGSTIPPPYISSQDHIWIR FHSDDNISRKGFRLAYFSGKSEEPNCACDQFR CGNGKCIPEAWKCNNMDECGDRSDEEICAKE ANPPTAAAFQPCAYNQFQCLSRFTKVYTCLP ESLKCDGNIDCLDLGDEIDCDVPTCGQWLKY FYGTFNSPNYPDFYPPGSNCTWLIDTGDHRK

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						VILRFTDFKLDGTGYGDYVKIYDGLEENPHK LLRVLTAFDSHAPLTVVSSSGQIRVHFCADKV NAARGFNATYQVDGFCLPWEIPCGGNWGCY TEQQRCDGYWHCPNGRDETNCTMCQKEEFP CSRNGVCYPRSDRCNYQNHCPNGSDEKNCFF CQPGNFHCKNNRCVFESWVCDSQDDCGDGS DEENCPVIVPTRVITAAVIGSLICGLLLVIALG CTCKLYSLRMFERRSFETQLSRVEAELLRREA PPSYGQLIAQGLIPPVEDFPVCSPNQASVLENL RLAVRSQLGFTSVRLPMAGRSSNIWNRIFNFA RSRHSGSLALVSADGDEVVPSQSTSREFERNH THRSLFSVESDDTDTENERRDMAGASGGVAA PLPQKVPPTTAVEATVGACASSSTQSTRGGH ADNGRDVTSVEPPSVSPARHQLTSALSRMTQ GLRWVRFTLGRSSSLSQNQSPLRQLDNGVSG REDDDDVEMLIPISDGSSDFDVNDCSRPLLDL ASDQGQGLRQPYNATNPGVRPSNRDGPCERC GIVHTAQIPDTCLEVTLKNETSDDEALLLC
919	2269	Α	7951	1674	1839	VVRVTCCPPARSTTERTNAYDEEDCVEMVAS
920	2270	A	7953	47	572	GGWNDVACHTTMYFMCEFDKKNM GGRASWPEQAKEPRREGHTDKQQTEDVLAA GLRCLPHLPAICARRMSPAFRAMDVEPRAKG VLLEPFVHQVGGHSCVLRFNETTLCKPLVPRE HQFYETLPAEMRKFTPQYKGKSQLLEGLPHW RGDVRDRGHGRPWQPSLEPSLPPTLCFPSLSS
921	2271	A	7957	612	812	FSSSWPSAQHLTPSVFNPW RSGRTVVTGIGYSKALQSSNRNTKSLLQNEF MMVYSFRALSFKESTWATFQHGGEATKSRSL SSTQ
922	2272	A	7967	1443	1660	ENITEK WKEIWMCRGNKKSCCWTFIKDRHLT VSCCKSKSGETLLICIFCSNLVGFFFFGIRGFSN WELVKPN
923	2273	Α	7981	1	3023	GSAPRAATAMARARPPPPPSPPPGLLPLLPLL LLPLLLLPAGCRALEETLMDTK WVTSELAWT SHPESGWEEVSGYDEAMNPIRTYQVCNVRES SQNWURTGFIWRRDVQRVYVELKFTVRDC NSIPNIPGSCKETFNLFYYEADSDVASASSPFW MENPYVKVDTIAPDESFSRLDAGRVNTKVRS FGPLSKAGFYLAFQDQGACMSLISVRAFYKK CASTTAGFALFPFTLTGAEPTSLVIAPGTCIPN AVEVSVPLKLYCNGDGEWMVPVGACTCATG HEPAAKESQCRPCPPGSYKAKQGEGPCLPCPP NSRTTSPAASICTCHNNFYRADSDSADSACTT VPSPPRGVISNVNETSLILEWSEPRDLGVRDD LLYNVICKKCHGAGGASACSRCDDNVEFVPR QLGLSEPRVHTSHLLAHTRYTFEVQAVNGVS GKSPLPPRYAAVNITTNQAAPSEVPTLRLHSS SGSSLTLSWAPPERPNGVILDYEMKYFEKSEG LASTVTSQMNSVQLDGLRPDARYVVQVRART VAGYGQYSRPAEFETTSERGSGAQQLQEQLP LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPEAI AYRKFTSASDVWSYGIVMWEVMSYGERPY

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide		in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
eotide	Seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	l .	l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	l	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ		peptide	1	/=possible nucleotide deletion, \=possible
			1	sequence	}	nucleotide insertion
				<b>.</b>		WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
		<u> </u>	ļ			LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
		1	1	i	1	SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
	ļ		j			WLDAIKMGRYKESFVSAGFASFDLVAQMTA
	i	ļ			ļ	EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
	<u> </u>		Ĺ	[		LPVQV
924	2274	A	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
						QLMRELDQRTEDKKAEIDILAAEYISTVKTLS
				ĺ		PDQRVERLQKIQNAYSKCKEYSDDKVQLAM
		1	İ	1		QTYEMVDKHIRRLDADLARFEADLKDKMEG
			ļ	1		SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
						EEDTPKKKKHKGG
925	2275	A	7994	447	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
		<u> </u>				SPIRCYCQHWPHCVHC
926	2276	A	7996	925	582	GPCKVCCITLAIMLQCHSFYRKDVQVEHPKS
			1	ł		LNPKYSQIENFLSADMALKRKCLLSISDLDFW
	1		ì	1		IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI
						RDTQPILPLGGRYYTTIRQ
927	2277	Α	7998	2	353	RIQRPLNSRSPNHSLFVKAELTAKQATMKLSV
			1	1		CLLLVTLALCCYQANAEFCPALVSELLDFFFI
			İ	ł		SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
		<b>_</b>	<u> </u>			MSLQKRSLIAEVLVKILKKCSV
928	2278	A	8004	130	588	LAPLRCQPGTRTQPRSHPAANDPSAAMSAAG
	]					ARGLRATYHRLLDKVELMLPEKLRPLYNHPA
			1			GPRTVFFWAPIMKWGLVCAGLADMARPAEK
		1	i			LSTAQSAVLMATGFIWSRYSLVIIPKNWSLFA VNFFVGAAGASQLFRIWRYNQELKAKAHK
929	2279	A	8007	2	1016	EFARRVFIAAREMSLLRSLRVFLVARTGSYP
929	22/9	^	8007	*	1018	AGSLLRQSPQPRHTFYAGPRLSASASSKELLM
		i				KLRRKTGYSFVNCKKALETCGGDLKQAEIWL
			1	l		HKEAQKEGWSKAAKLQGRKTKEGLIGLLQE
	ļ			İ		GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
			1			GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
		ļ	1	1		GPDREGSLKDQLALAIGKLGENMILKRAAWV
		1	i	1		KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
	į.				1	ALVICETSEOKTNLEDVGRRLGOHVVGMAPL
	l	1	1		{	SVGSLDDEPGGEAETKMLSQPYLLDPSITLGQ
		ł		i		YVQPQGVSVVDFVRFECGEGEEAAETE
930	2280	Α	8008	3	1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL
				1		GLVPLTDDTSHAGPPGPGRALLECDHLRSGV
			[	Į.		PGGRRRKDWSCSLLVASLAGAFGSSFLYGYN
			ļ	1		LSVVNAPTPYIKAFYNESWERRHGRPIDPDTL
	!	[		1	ŀ	TLLWSVTVSIFAIGGLVGTLIVKMIGKVLGRK
				ĺ	•	HTLLANNGFAISAALLMACSLQAGAFEMLIV
	ŀ	l		1	1	GRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
	}		1	1		QVTAIFICIGVFTGQLLGLPELLGKESTWPYLF
	ŀ			1		GVIVVPAVVQLLSLPFLPDSPRYLLLEKHNEA
	1		-	1		RAVKAFQTFLGKADVSQEVEEVLAESRVQRS
	)	}	]	J.		IRLVSVLELLRAPYVRWQVVTVIVTMACYQL
				1	1	CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTGG
	1					IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLFF
	}	1		<b>\</b>		GTLTTTLTLQDHAPWVPYLSIVGILAIIASFCSG
	1	1		1		PGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSN
		ĺ		1	1	FAVGLLFPFIQKSLDTYCFLVFATICITGAIYL
	1			[		YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
	1		<u> </u>			DSAVTDGKINGRP
					L = 410	A LO LIBRO AT INVESTIGATION OF THE LOT OF TH
931	2281	A	8009	861	300	AAĞAVVSAMPKAKGKTRRQKFGYSVNRKRL
931	2281	A	8009	861	300	NRNARRKAAPRIECSHIRHAWDHAKSVRQNL AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

NO: of NO: of hod ID NO: beginning nucleotide D=Aspartic Ac	quence (A=Alanine C=Cysteine, eid, E=Glutamic Acid, ne, G=Glycine, H=Histidine,
nucl- peptide in nucleotide location F=Phenylalanir cotide seq- USSN location corresponding I=Isoleucine, K seq- uence 09/496 correspondi to last amino M=Methionine	ne, G=Glycine, H=Histidine,
cotide seq- USSN location corresponding I=Isoleucine, K seq- uence 09/496 correspondi to last amino M=Methionine	ne, O=Grycine, ri=Histiaine,
seq- uence 09/496 correspondi to last amino M=Methionine	
uence     1914   ng to lifst   acid residue   U=Glutamine,	
	K-Arginine, S-Serine, V=Valine, W=Tryptophan,
	=Unknown, *=Stop codon,
	leotide deletion, -possible
sequence nucleotide inse	
	VLNDLEAEASLPEKKGNTLSRD
	ENHGEDYKAMARDEKNYYQD
	VYKRFYPAEWQDFLDSLQKRK
MEVE	MALINIA MANAGEMENT OF THE COLOR
797	RWRWAKSRHHCIPTVTLSKRSG
	QRQRSQRVPGKETARVLRAGK
	PWPPPPPPPPGSPGPGCRQFHQ
	ASVREMRGKVKMRRALRRAPA
STRASSRQPN	
	MAQNLKDLAGRLPAGPRGMGT
	AVAYGVRESVFTVEGGHRAIFF
	TILAEGLHFRIPWFQYPIIYDIRA
	SKDLQMVNISLRVLSRPNAQEL
	DYEERVLPSIVNEVLKSVVAKF
	AQVSLLIRRELTERAKDFSLILDD
	EYTAAVEAKQVAQQEAQRAQF
LVEKAKQEQ	RQKIVQAEGEAEAAKMLGEAL
SKNPGYIKLE	RKIRAAQNISKTIATSQNRIYLTA
	ESFTRGSDSLIKGKK
934 2284 A 8023 255 982 SQFSLSQVLV	/DSAEEGSLAAAAELAAQKREQ
RLRKFRELHI	LMRNEARKLNHQEVVEEDKRL
KLPANWEAK	KARLEWELKEEEKKKECAARG
EDYEKVKLL	EISAEDAERWERKKKRKNPDLG
FSDYAAAQL	RQYHRLTKQIKPDMETYERLRE
KHGEEFFPTS	SNSLLHGTHVPSTEEIDRMVIDLE
KQIEKRDKY	SRRRPYNDDADIDYINERNAKF
	KYTAEIKQNLERGTAV
935 2285 A 8027 59 310 LVSSTVNLLT	TEKAPWNSLAWTVTSYVFLKFL
QGGGTGSTG	MRDSALTLLGIGPSHRHSLSIRL
SQHSSPAPM	YSQTFHILVLG
936 2286 A 8032 1 639 SGRECNMAK	TYDYLFKLLLIGDSGVGKTCVL
FRFSEDAFNS	STFISTIGIDFKIRTIELDGKRIKLQ
IWDTAGQER	FRTITTAYYRGAMGIMLVYDIT
NEKSFDNIRN	NWIRNIEEHASADVEKMILGNKC
DVNDKRQVS	SKERGEKLALDYGIKFMETSAK
ANINVENAFI	FTLARDIKAKMDKKLEGNSPQG
SNQGVKITPE	OQQKRSSFFRCVLL
	ILEKYIPISANLTLTIA
	WLHVPPGLSMALSWVLTVLSLL
	ANLVPVPITNATLDRITGKWFYI
	NKSVQEIQATFFYFTPNKTEDTIF
	QCIYNTTYLNVQRENGTISRYV
	LILRDTKTYMLAFDVNDEKNW
	ETTKEQLGEFYEALDCLRIPKSD
	DKCEPLEKQHEKERKQEEGES
	OLSOPONWNFSGAGGAWSLDF
	ELARLGESIMDGKQGGMDGSKP
	LLSNPLMGDAVSDWSPMHEAA
	NLISQGWAVNIITADHVSPLHEA
	KILLKHGAQVNGVTADWHTPL
	DCVNLLLQHGASVQPESDLASP
	VECVNELLQHGASVQPESDLASP VECVNSLIAYGGNIDHKISHLGT
	QRACVKKLLESGADVNQGKGQ
	TASEELACLLMDFGADTQAKN
	VPPESPLAQLFLEREGPPSLMQL
	HIQQHHKITKLVLPEDLKQFLLH
L L CONTRACTOR OF THE CONTRACT	OT I BY A CEDE OPERATOR OF THE
	ISTARKASEPSQPSQPSQPGGHLI
ARLRTMDLH	ILFDYSEPGNFSDISWPCNSSDCI

No. of	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Included		1	1				
USSN   Sequence   19/34   19				1			
						10 11	
1914   ng to first a mino acid residue of peptide sequence			Į		1		1
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residue of peptide   sequence		Ì		1	_	of peptide	
peptide   sequence			1		residue of		
VVOTVMCPMPRKSVLLYTLSFIVIFIFVIGM   ANSVVW NVIQAKTITGVTHOLALAIADL   WVVVLTIPVWVSLVQIHAQKTITGVTHOLALAIADL   WVVVLTIPVWVSLVQIHAQKTITGVTHOLTVTHIPSS   RKEMVRRVCILVWILAFCVSLPDTYVLTVTHOMSS   RKEMVRRVCILVWILAFCVSLPDTYVLTVTHOMSS   RKEMVRRVVCILVWILAFCVSLPDTYVLTVTSSS   RKEMVRRVVCILVWILAFCVSLPDTYVLTVTHOMSS   RKINISTSVVFILARAISASSDQERIL   VISASNISTYCRSFYPEISIKEWLIGMELVSV   VLGFAVPSILAVEVILIPSHLHVI   PFICRLSHALFTALHVTOCLSILVHCCVNDVILVY   VSIRINNYRELBIKAFIRVVSAKGGITKLIDA   SRYSETEYSALEQSTK   SRKIESTSVALEQSTK   WARRIEVSALEQSTK   DMAGIMITIVSLLFLGVCAHHIPTGSVVLPS   PCCMFFVSKRIPENRVVSVQLSSRSTCLKARD   VISTIKKGQQFCGPFKQEWVQRVKKILDAKQ   KKASPRARAVAVKGPVQRYFQNOTTC   GGIGEIKQRPSCLGCLDPSILSVIMISIGLGS   VFSAVISQRSRSDILOQRGTSLTICQCVDSVVLPS   WENTON   WARRIEVSCHOOL				1	peptide	1	/-possible nucleotide deletion, \-possible
ANSYVYW NIQAKITGYUTHCYILNIALADW					sequence		nucleotide insertion
WVVLTIPVWVVSLVQINQWFMGELTCKVTH   LFSINLFGSIFILTCMSVPRVLSTYTSTPSS     RKKMVRRVCILVWLLAFCVSLPDTYYLTVTSS     RKKMVRRVVCILVWLLAFCVSLPDTYYTTSTPSS     RKKMVRRVVCILVWLLAFCVSLPDTYYTTSTPSS     RKKMVRRVVCILVWLLAFCVSLPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPDTYYTTSTPSS     RKKMVRRVVCILVWLAFCVSLIPWLAFCVSLIPTSTPSS     RKKMVRRVCIPTSTALFVSLIPTSTPSS     RKKMVRRVFTSTLAFTSTALFVSLIPTSTSTPSS     RCKMVRRVSRRPRVVSVQLSSRSTCLKADAQ     RKASPRARAVAVKGPVGRYFGNOTTC     GGGERQRPSCIGCCDPSISVMNISGLGS     RKASPRARAVAVKGPVGRYFGNOTTC     GGGERQRPSCIGCCDPSISVMNISGLGGS     RKASPRARAVAVKGPVGRYFGNOTTC     MKFVRQPGGERCAFTSTLTTGCQVDSVJTMSSVGLGS     RKASPRARAVAVKGPVGRYFGNOTTC     MKFVRQPSRDICQRGTSLTIATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTIATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTIATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQVBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBSTLTATARQSEATYESGF     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBST     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBST     VDKFPISRPNLTFSTLTVSMSFEDSNITGCQUBST     VDKFPISRPNLTFTLTSTTTSMSFEDSNITGCQUBST     VDKFPISRPNLTTSTTTSTTTSMSFEDSNITGCQUBST     VDKFPISRPNLTTSTTT			†				VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
				1			ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
RKKMMRRVCIL.WILLAFCVSLPDTYYLKT				1		1	WVVLTIPVWVVSLVQHNQWPMGELTCKVTH
VTSASNETYCRSFYPEHSIKEWLIGMELVSV						İ	LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
			ļ			1	RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
RKIIFSYVVYLVCWLPYHVAVLLDIFSILHYI		i	1	1	İ		VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
PFTCRLEHALFTALHYTQCLSL/HCCVNPVL   YSFNRNYRYELMKAFIRYSAKTGLTKLIDA    SRYSETEYSALEGSTK    PFTCRLEHALFTALHYTQCLSL/HCGVCAHHIIPTGSV/LPS    SRYSETEYSALEGSTK    PFTCRLEHALFTALHYTQCLSL/HCGVCAHHIIPTGSV/LPS    PFCCMFFYSKRIPENRVYSYQLSSRSTCLKAGV    IFTIKKGQGFCGDFXQEWVQRYMKNLDAKQ    KKASPRARAVAVKGFYQRYGNQTTC    KKASPRARAVAVKGFYQRYGNQTTC    SGIGEIKQRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGRCLDPSLSV/LMNISLGLGS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGTGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTS    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGADCGFTANGGGEK    VFSAVISGRPSCLGCGARGACCTPSTFTFINSAGERBMDVLF    VAFAVPLILGQGYEGERGLGDBYYQVYY   VTYTPSYDDFSADFTIDYSIFESEDRINKLDK    VAFAVPLILGQGYEGERGLGGDBYYQVYY   VTYTPSYDDFSADFTIDYSIFESEDRINKLDK    VAFAVPLILGQGYEGERGLGGARGADCGFTSF		ì					VI.GFAVPFSIIAVFYFLLARAISASSDQEKHSS
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SRYSETEYSALEQSTK		-			}	}	PFTCRLEHALFTALHVTQCLSLVHCCVNPVL
941   2291   A   8059   73   432   DMAGLMTIVTSLLFLGVCAHHIPTGSVVLY   PACTURE   PACTUR				İ			YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
PCCMFFVSKRIPENRVSYQLSSRSTCLKAGV   FITIKKGQQFGDBFWQRYMKIDAKQ   KKASPRARAVAVKGPVQRYPGNQTTC     942   2292   A   8067   278   1262   GGIGEIKQRFSCLGRCLDFSLSVLMNISLGLGS   VFSAVISQKPSINICQRGTSLTIQCQVDSQVT   MMFWYRQQPGQSLTLIATANQSEATTESGF   VDKFPISRPNLTFSTLTVSNMSPEDSSIYLCSA   GRQGTYEQYTGPGTRLTVTEDUKNVPPEVA   VFSAVISQKEVHISGVSTDPQPLKEQPALNDSRY   CLSSRLRVSATFWQNPRNFRCQVGYFQLSE   NDEWTQDRAKPVTQIVSAEAWGRADCGFTS   ESYQQCVLSATILYELLGKATLYAVLVSALV   LMAWVKRKDSRG   VMKVVPATRGNLPRSQLTGTHQHCQPREPRI   TASELLRRPRATARLRAHAAPPEPPLAVFAP   PSDKKELLALPVACDPVLASVMSWQAASLI   QGPGDKGDVPUEEABLAQREWQSMMQR   RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA   EVILNYGRLRSLLAQREVQHKHLKSITPPSHVVDLL   DSIEDMDLCHVVPAKKIDERACENNA   EPNKNCSKSHGGIDCSVVECCRQEHAFIGG   FKPHMDFGTISQF     944   2294   A   8073   1   797   ESARWSQLRRTLIRLSFPISCGRSHAFGGCK   MAATSGTDEPVSGELVSWAHALSLPAESYGN   DPDIEMA WAMRAMQHAVYYKLISSVDPOP   LKLTKVDQIYSEFRKNFETLRIDVLDPELK   SESAREKWRPFCLKRNGIVEDFNYGTLLRILD   CSQGYTEENTIFARIQFFAIEIARREGYNKA   VYISVQDKEGEKGVNNGGEKRADSGEEENT   KNGGEKGADSGEEKGFNNGTEKTDKGGEK   GKEADKEINKSGEKAM   VYISVQDKEGEKGVNNGGEKRADSGEEENT   KNGGEKGADSGEEKGFNRGTENKTDKGGEK   GKEADKEINKSGEKAM   GEDTLMEYLENFKKYPOTKMIFVGIKKKEER   ADLIAYLKATNE   SADRRVLG REWGRPA SERECSLCQRLRELL   NMGDVEKGKKIFIMKCSQCHTVEKGGKKIKT   GPNLIGGLFGRRTGGARGYSYTAANNKGIIW   GEDTLMEYLENFKKYPOTKMIFVGIKKKEER   ADLIAYLKKATNE   SADRRVLIGGEFEGEDETYQVVYY   YYTVFSYDDFSADFTIDYSJFESEDRI.NRLDK   DITEAIETTISLETARADHPKPYTVKPYTTEPQ   SPRSEAMPCPVLRSPIPLPPVRVPLYPRVGISC   KKVGRRILIMTLWMGVWQEEGIGR   GGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGGGSSPRELAGAAGCTTVTSQAVAARRQQFSF   SGG			<u> </u>				
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		1	ł	ł	l	ì	
1262   GGIGEIKORPSCLÜRECLIPSLSVLIMMISLGLÜS					•		
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MMFWYRQPGQSLTLIATANGGSEATYESGF	942	2292	Α	8067	278	1262	
VIDKPISRPNLTFSTLTVSNMSPEDSSIYLCSA   GRQGTYEQYPGFTRLTVTEDLKNVFPPEVA   VFEPSEAEISHTQKATLVCLATGFYPDHVELS   WWVNGKEVHSGYSTDPQLKEQPALNDSRY   CLSSRLRVSATFWQNPRNHFRCQVGFYGLSE   NDEWTQDRAKPVTQNVSAEAWGRADCGFTS   ESVQQGVLSATTFWQNPRNHFRCQVGFYGLSE   NDEWTQDRAKPVTQNVSAEAWGRADCGFTS   ESVQQGVLSATTFWQNPRNHFRCQVGFYGLSE   NDEWTQDRAKPVTQNVSAEAWGRADCGFTS   ESVQQGVLSATTFWQNPRNHFRCQVGFYGLSE   NDEWTQDRAKPVTQNVSAEAWGRADCGFTS   ESVQGQVLSATTFWQNLFRSQLGTHQHCQPREPKI   LMAMVKRKDSRG   WKKVPATRGNLFRSQLGTHQHCQPREPKI   TASERLRRRPRATARLRAHAAPPEPPLAVFAP   PSDRKELLALPVACDPVLASVMSWVQAASLI   QGPGKGDVPGEADESLLAQREWQSNMQR   RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA   EVILNYGRLRGTLSALLSWCHLHNNNSTLINK   INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL   DSIEDMDLCHVVPAEKKIDEAKDERLCENNA   EPNKCSKSHSGIDCSYVECCRTQEHAHSGK   PKPHMDFGTDSQF   PKPHMDFGTDSQF   PKPHMDFGTDSQF   PKPHMDFGTDSQF   PKPHMDFGTDSQF   PKPHMDFGTDSQF   LKLTKVDDQIVSEFRKNFETLRIDVLDPEELK   SESAKEKWRPFCLKFNGFIVEDFNYGTLLRLD   CSQGYTEENTIFAPRIQFFAEIARNREGYNKA   VYISVQDKEGEKGVNNGGEKRADSGEEENT   KNGGEKGADSGEKEEGINREDKTDKGGEK   GKEADKEINKSGEKAM   VYISVQDKEGEKAMSGEENT   KNGGEKGADSGEKEEGINREDKTDKGGEK   GKEADKEINKSGEKAM   SARTVLGLREWGRPASERECSLCQRLKREL   NMGDVEKGKKIPMKCSQCHTVEKGGKHKT   GPNLHGLFGRKTGQAPGYSTAANKNKGIIW   GEDTLMEYLLENPKKYPJGTKMIFVGIKKKEER   ADLLAYLKKATNE   GERTGKTGQAPGYSTAANKNKGIIW   SADRRVLGGREGGENFYQVVYY   YTVTPSYDDFSADFTIDSJFESEDRLNRLDK   DITEAETISLEFTARADHFRYVKPVTTEPQ   SPRSEAMPCPVLRSPIPLPVRVPLFRWGCISC   KKVGRRLLMTLWMGVVQEEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SATURDARY VGEIGR   SA			ļ	1	Į.		
GRQGTYEQYFGPGTRLTVTEDLKNYPPPEVA   VFEPSEAEISHTQKATLVCLATGFYPDHVELS   WWNGKEVHSGVSTDPQPLKEQPALNDSRY   CLSSRLRVSATFWQNRFNHFRCQVQFYGLSE   NDEWTQDRAKPVTQIVSAEA WGRADCGFTS   ESYQQGVLSATILVEILLGKATLYAVLVSALV    LMAMVKRKDSRG   STORT			1			<u> </u>	
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CLSSRLRVSATFWQNPRNHFRCQVQFYGLSE   NDEWTQDRAKPVTQIVSAEAWGRADGGFTS		i	ĺ	1	•	!	
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SYQQGVLSATILYEILLGKATLYAVLVSALV			ĺ		1	1	
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943   2293   A   8070   1   879   MVKVVPATRGNLPRSQLTGTHQHCQPREPKI TASERLRRPRATARLRAHAPPEPPLAVFAP PSDRKELALPVACOPVIASVMSWVQAASLI QGPGDKGDVFDEEADESLLAQREWQSNMQR RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA EVILNYGRLRGTLSALLSWCHLHNNNSTLINK INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL DSIEDMDLCHVVPAEKKIDEAKDERLCENNA EFNKNCSKSHSGIDCSYVECCRTQEHAHSGK PKPHMDFGTDSQF   ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK MAATSGTDEPVSGELVSVAHALSLPAESYGN DPDIEMAWAMRAMQHAEVYYKLISSVDPQF LKLTKVDDQIYSEFRKNFETLRIDVLDPEELK SESAKEW RRFFCLKFNGIVEDFNYGTLLRLD CSQGYTEENTIFAPRIQFFAIEIARNREGYNKA VYISVQDKEGEKGVNNGGEKRADSGEEENT KNGGEKGADSGEEKGFMEDKTDKGGEK GKEADKEINKSGEKAM   2   505   GAATLLRSASSAARKAAEAFQVWLHLHRYL SADRRVLGLREWGRPASERECSLCQRLKREL NMGDVEKGKKIFIMKCSQCHTVEKGGKIKT GPNLHGLFGRKTGQAPGYSYTAANKNKGIIW GEDTLMEYLENPKKYTPGTKMIFVGIKKEER ADLIAVLKKATNE   GPNLHGLFGRKTGQAPGYSYTAANKNKGIIW GEDTLMEYLENPKKYTPGTKMIFVGIKKEER ADLIAVLKKATNE   GPREPKTTIOSITESEDRLINRLDK DITEAIETTISLETARADHPKPVTVKPVTTEPQ SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCISC KWGRRLMTLMGVWQEEIGR   GGGSSPRELAGAAGLTVTSQAVAARRQQPSF		1	1				
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		<u> </u>	<u> </u>	<u> </u>	<u> </u>	L	SRARAPAHSLRAALSLASSARSWGAVSRDRG

SEQ ID NO: of nucl- eotide scq- uence	SEQ ID NO: of peptide seq- ucnce	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
948	2298	В	8093	3905	846	PCPPAIMYQSSNKC  MEPGEVKDRILENISLSVKKLQSYFAACEDEI PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG YWVLVVHFTRREAIKQIEVLQHVATNLGRSR AWLYLALNENSLESYLRLFQENLGLLHKYYV KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA PYLDLAPYMPDYYKPQYLLDFEDRLPSSVHG SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST ASDLTSSKASTRSPTQRQNPFNEEPAETVSSS DTTPVHTTSQEKEEAQALDPPDACTELEVIRV TKKKKIGKKKKSRSDEEASPLHPACSQKKCA KQGDGDSRNGSPSLGRDSPDTMLASPQEEGE GPSSTTESSERSEPGLLIPEMKDTSMERLGQPL SKVIDQLNGQLDPSTWCSRAEPPDQSFRTGSP GDAPERPPLCDFSEGLSAPMDFYRFTVESPST VTSGGGHHDPAGLGQPLHVPSSPEAAGQEEE GGGGEGQTPRPLEDTTREAQELEAQLSLVRE GPVSEPEPGTQEVLCQLKRDQPSPCLSSAEDS GVDEGQGSPSEMVHSSEFRVDNNHLLLLMIH VFRENEEQLFKMIRMSTGHMEGNLQLLYVLL TDCYVYLLRKGATEKPYLVEEAVSYNELDY VSVGLDQQTVKLVCTNRRKQFLLDTADVAL AEFFLASLKSAMIKGCREPPYPSILTDATMEK LALAKFVAQESKCEASAVTVRFYGLVHWED PTDESLGPIPCHCSPPEGTITKEGMLHYKAGT SYLGKEHWKTCFVVLSNGILYQYPDRTDVIP LLSVNMGGEQCGGCRRANTTDRPHAFQVILS DPPCLELSAESEAEMAEWMQHLCQAVSKGVI PQGVAPSPCIPCCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWVIYLSCTSELDRLLSALNSGWKTIY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC*
949	2299	A	8095	9	2374	ARRADTVLLESPSMLQGLLPVSLLLSVAVSAI KELPGVKKYEVVYPIRLHPLHKREAKEPEQQ EQFETELKYKMTINGKIAVLYLKKNKNLLAP GYTETYYNSTGKEITTSPQIMDDCYYQGHILN EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCPS TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKL SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVYFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMYKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD

SEQ ID NO: of NO: of NO: of NO: of NO: of NO: of No: of	idine, line,
nucleotide seq- sold- sold- sold- sold- sold- sold- sold- sold- seq- uence    1	oline,  can, don, ible  CLYRROPE REYLYGG PAPPTRETC PAKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
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uence    914   ng to first amino acid residue of peptide sequence   peptide residue of peptide sequence   pe	nan, don, ible LLYRROPE REYLYGG PAPPTRETC TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
amino acid residue of peptide sequence   T=Threonine, V=Valine, W=Tryptoph y=Tyrosine, X=Unknown, **=Stop con / possible nucleotide deletion, \=possible nucleotide deletion, \=possible nucleotide insertion	don, ible FLLYRROPE REYLYGG PAPPTRETC TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
residue of peptide sequence   Y=Tyrosine, X=Unknown, *=Stop color	don, ible FLLYRROPE REYLYGG PAPPTRETC TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
950 2300 A 8100 I 1251 MGLLIMILASAVI.GSFLTILAQPF PADEAARAGEGRYYIKPVPGLLI GRDEEPSGAAPEGATPTAAPETT YFLNATILFIFELENTALTRIWV EELLQTKTAGRILEGLSLRDVFL.C RLVRPVVPSATGEPDGPEGALPA EASVEYNNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVF RSQFEGRPMPQLTSIIVNQLKKIIK KIRKPFFPYQTI.QGFEEDEEHIHI GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGL.WYKILVDLPF WGLEDGGG-CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMVDLWFHRALDTDLARFF GSVPSDSSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVPSDVSSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVPSDVDSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVPSDVDSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVPSDVDSSSKGKKCRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVPSDVDSSSKGKKCRTQKEKK RRDDGLSAAARKQRDSTPRDSEIN ANEKKEEPK  952 2302 A 8112 595 291 PSVASLARRFSGRALWPPSHSVPC LIGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEIN ANEKKEEPK  953 2303 A 8118 I 669 VCGGRDPCSTPLAKPAAGGAENI LETNILKMTTPNKTPGADPKQLE GSQAVWSLSSCKPGFGVDQLRDE SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRVGNNFHNLQEIRQL HTVPLTDNHKKPTTRFMQIAVLA THMRQIKIYTPVEESSIGKFPRCTT	ELLYRROPE ELLYRROPE EREYLYGG PAPPTRETC TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS AYLFVKLS RKHTLPNY QQWALTE VHCTLELS
950 2300 A 8100 1 1251 MGLLMILASAVLGSFLTLLAQFF PADEAARAGEGRYIKPVPGLLL GRDEEPSGAAPEGGATPTAAPETT YFLNATILFLFRELRDTALTRRWV EELLQTKTAGRLLEGLSLRDVFLG RLVRPVVPSATGEPDGPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVV RSQFEGRPMPQLTSIIVNQLKKIK KIRFKPFFPYOTLQGFEEDEEHHII GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG PS51 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMOTYEMVDKHIRRLDTDLARFI ESSDYDSSSSKGKKKGRTOKEKK KNSDEEAPKTAQKKLKURTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTM PRCSQERKKK PSSDYLDSSSKGKKKRTVREKK KNSDEEAPKTAQKKLKURTSPE 1 S952 2302 A 8112 595 291 PSVASIARFFSGRALWPPSHSVPC LHGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEIN ANEKKEEPK 1 O'CAGIRDPCSTPLAKPAAGGAENI LETNILKMTTPGNORGELARQKNMKK RRDDGLSAAARKQRDSTPRDSEIN ANEKKEEPK 2 O'CAGIRDPCSTPLAKPAAGGAENI LETNILKMTTPNKTPPGADPKQLE GSQAVWSLSSCKPGFGVDQLRDG SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVKVQNNFHNLQEIRQL HVPLTDNHKKPTTFTMQIAVLAI THMRQIKIYTPVEESSIGKFPRCTI	ELYRROPE REYLYGG PAPPTRETC TKKIKVEF GETVPFIKT AACPELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
950   2300   A   8100   I   1251   MGLLMILASAVLGSFLTLLAQFF   PPADEAARAGEGFRYIKPVPGLLL   GRDEPPGGAAPEGGATPTIAAPETT   YFLNATILFLFRELRDTALTRRWV   EELLQTKTAGRLLEGLSLRDVFL   RLVVPVYPSATGEPDOPPGEALPA   EAEVEYNGGFHLAIDVDLVFGKS.   RVYGRLRLVFTRVPFTHWFFSFVV   RSQFGRMPQLTSILVNQLKKIK   KIRFKPFFPYQTLQGFEEDEHIHI   GRI,KVTLLECSRLLEGSYDREAN   SSVWEEKQRSSIKTGTISLTAVFM   AFPGLWYKLLVDLPFWGLEDGGGCPG   CPG     951   2301   A   8108   1612   839   EVALFCFEMAAGMYLEHYLDSIE   NFQLMRDLDQRTEDLKAEIDKLA   SLSSEKLALLKQIQEAYGKCKEF   AMQTYEMVDKHIRRLDTDLARFI   ESSDYDSSSKGKKKGRTQKEKK   KNSDEEAPKTAQKKLKLVRTSPE   GSVHPSDVJDMPDPNEPTYCLC   MIGCDNPDCSIEWFHFACVGLTTM   PRCSQERKKK   SVYGEKKK   RRDDGLSAAARKQRDSTPRDSEIN   ANEKKEEPK     952   2302   A   8112   595   291   PSVASI ARREFSGRALWPPSHSVPG   LHGTTLPGGNQRELARQKNMKK   RRDDGLSAAARKQRDSTPRDSEIN   ANEKKEEPK     953   2303   A   8118   I   669   VCAGIRDPCSTPLAKPAAGGAEN   LETNILKMTTPNKTPPGADPKQLE   GSQAVWSLSSCKPGFGVOQL RDG   SDGSQPHLVNIQFRRKTTVKTLCI   SYTPSKISVRVGNNFHNLQEIRQL   HYPLTDNHKKPTRTFMIQIAVLA   THMRQIKYTPVEESSIGKFPRCTT	REYLYGG PAPPTRETC TIKKIKVEF GETVPFIKTI AACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
PPADEAARAGEGFRYIKPVPGILL GRDEEPSGAAPEGGATPTAAPETT YFLNATII.FLFRELRDTALTRIWV EELLQTKTAGRLLEGLSLRDVFLC RLVRPVVPSATGEPDOPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVI RSQFEGRPMPQLTSIIVNQLKKIIK KIRFKPFFPYQTLQGFEEDEHIHI GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NSQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMVDKHIRRLDTDLARFI ESSDYDSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKL VRTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTI PRCSQERKKK  952 2302 A 8112 595 291 PSVASIARRFSGRALWPPSHSVPC LHGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEN ANEKKEEPK  953 2303 A 8118 1 669 VCAGIRDPCSTPLAKPAAGGAENI LETNILKMTTPNKTPPGADPKQLE GSQAVWSLSSCKPGFVVQURDI SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRVGNNFHNLQEIRQL HVPVLTDNIKKFTTFMQLAVLA THMRQIKIYTPVEESSIGKFPRCTT	REYLYGG PAPPTRETC TIKKIKVEF GETVPFIKTI AACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
GRDEEPSGAAPEGGATPTAAPETE YFLNATILFIFEELRDTALTRRWV EELLQTKTAGRLLEGLSLRDVFLG RLVRPVVPSATGEPDOPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS, RVVGRLRLVFTRVPFTHWFFSFVI RSQFEGRPMPQLTSIIVNQLKKIK KIRFKPFFPYQTLQGFEEDEEHIHI GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMYDKHIRRLDTDLARFI ESSDYDSSSSKGKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTM PRCSQERKKK RRDDCISAAARKQRDSTPRDSEIN ANEKKEEPK  953 2303 A 8118 1 669 VCAGIRDPCSTPLAKPAAGGAEN  954 VCAGIRDPCSTPLAKPAAGGAEN SVEEKEPK VCAGIRDPCSTPLAKPAAGGAEN VCAGIRDPCSTPLAKPAAGGAEN SVEYPSKISVRYGNNFHNLQEIRQL SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRYGNNFHNLQEIRQL HVPLTDNHKKPTTFMQLAVLA THMRQIKIYTPVEESSIGKFPRCTI	PAPPTRETC TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
YFLNATILFLFRELRDTALTRRWV EELLQTKTAGRLLEGLSLRDVFLC RLVRPVVPSATGEPDOPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVI RSQFEGRPMPQLTSIIVNQLKKIK KIRFKPFFPYQTLQGFEEDEHHIH GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMVDKHIRRLDTDLARFI ESSDYDSSSKGKKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTI PRCSQERKKK  952 2302 A 8112 595 291 PSVASLARRFSGRALWPPSHSVPC LHGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEN ANEKKEPK  953 2303 A 8118 1 669 VCAGIRDPCSTPLAKPAAGGAEN LETNILKMTTPNKTPPGADPKQLE GSQAVWSLSSCKPGFGVDQLRDI SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRVGNNFHNLQEIRQL HYPLTDNHKKPTRTFMQIAVLA THMRQIKIYTPVEESSIGKFPRCTT	TKKIKVEF GETVPFIKTI ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
EELLQTKTAGRLLEGLSLRDVFLC RLVRPVVPSATGEPDGPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVI RSQFEGRPMPQLTSIIVNQLKKIK KIRFKPFFPYQTLQGFEEDEHHIN GRIKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMVDKHIRRLDTDLARFF ESSDYDSSSSKGKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTK PRCSQERKKK  952 2302 A 8112 595 291 PSVASLARRFSGRALWPPSHSVPC LHGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEIN ANEKKEEPK  953 2303 A 8118 1 669 VCAGIRDPCSTPLAKPAAGGAENI LETNILKMTTPNKTPPGADPKQLE GSQAVWSLSSCKPGFGVDQLRDL SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRVGNNFHNLQEIRQL HYPLTDNHKKPTRTFMIQIAVLA THMRQIKIYTPVEESSIGKFPRCTI	GETVPFIKTI AACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
RLVRPVVPSATGEPDGPEGEALPA EAEVEYNGGFHLAIDVDLVFGKS. RVVGRLRLVFTRVPFTHWFFSFVI RSQFEGRPMPQLTSIIVNQLKKIK KIRFKPFFPYQTLQGFEEDEEHIHIG GRLKVTLLECSRLLIFGSYDREAN SSVWEEKQRSSIKTGTISLTAVFM AFPGLWYKLLVDLPFWGLEDGGI CPG  951 2301 A 8108 1612 839 EVALFCFEMAAGMYLEHYLDSIE NFQLMRDLDQRTEDLKAEIDKLA SLSSEEKLALLKQIQEAYGKCKEF AMQTYEMVDKHIRRLDTDLARFI ESSDYDSSSSKGKKGRTQKEKK KNSDEEAPKTAQKKLKLVRTSPE GSVHPSDVLDMPVDPNEPTYCLC MIGCDNPDCSIEWFHFACVGLTTM PRCSQERKKK  952 2302 A 8112 595 291 PSVASILARRFSGRALWPPSHSVPG LHGTTLPGGNQRELARQKNMKK RRDDGLSAAARKQRDSTPRDSEN ANEKKEEPK  953 2303 A 8118 1 669 VCAGIRDPCSTPLAKPAAGGAENI LETNILKMTTPNKTPPGADPKQLE GSQAVWSLSSCKPGFGVDQLRDE SDGSQPHLVNIQFRRKTTVKTLCI SYTPSKISVRVGNNFHNLQEIRQL HYPLTDNHKKPTRTFMIQIAVLA THMRQIKIYTPVEESSIGKFPRCTT	ACPEELAF AYLFVKLS EDPLIDFEV RKHTLPNY QQWALTE VHCTLELS
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954 2304 A 8133 66 1015 PPLPPRSFPNLFSRPEPLPEPGRRG	CNIDCDEDA
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AKKDEPKSGEEALIIPPDAVAVDO	
PVGORRAWCWCMCFGLAFMLAG	
LYKYFALQPDDVYYCGIKYIKDD	
APAALYQTIEENIKIFEEEEVEFISV	
DPANIVHDFNKKLTAYLDLNLDK	
SIVMPPRNLLELLINIKAGTYLPQS	YLIHEHMV
ITDRIENIDHLGFFIYRLCHDKETY	
KGIQKREASNCFAIRHFENKFAVE	
955 2305 A 8143 35 1171 VESRSAWHEGEDQIDRLDFIRNQN	
KKKIKEVTEEVANKVSCAMTDEIG	
EFCSEFHPNPDVLKIYKSELNKHII	
ADRCTDEVNALVLQTQQEIIENLK	
DKLHTLIPCKKFDLSYNLNYHKLO	-
FRFSLGWSSLVHRFLGPRNAQRVI	
QLPRSLASTPTAPTTPATPDNASQI	
GLASVTSRTSMGIIIVGGVIWKTIG	
LTMYGALYLYERLSWTTHAKERA YATEKLRMIVSSTSANCSHOVKO	WKLLSVS
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	WKLLSVS AFKQQFVN QIATTFARL LEKIQNNS SSNEES

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DRYTTSRRLDPIPQLKCVGGTAGCDSYTPKVI QCQNKGWDGYDVQWECKTDLDIAYKFGKT VVSCEGYESSEDQYVLRGSCGLEYNLDYTEL GLQKLKESGKQHGFASFSDYYYKWSSADSC NMSGLITIVVLLGIAFVVYKLFLSDGQYSPPP YSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQ NTGHGATSGFGSAFTGQQGYENSGPGFWTGL GTGGILGYLFGSNRAATPFSDSWYYPSYPPSY
957	2307	A	8159	1492	528	PGTWNRAYSPLHGGSGSYSVCSNSDTKTRTA SGYGGTRRR THVVMTGMCYAPHQVLSYINGVTTSKPGVSL VYSMPSRNLSI.RLEGLQEKDSGPYSCSVNVQ DKQGKSRGHSIKTLELNVLVPPAPPSCRLQGV PHVGANVTLSCQSPRSKPAVQYQWDRQLPSF QTFFAPALDVIRGSLSLTNLSSSMAGVYVCKA HNEVGTAQCNVTLEVSTGPGAAVVAGAVVG TLVGLGLLAGLVLLYHRRGKALEEPANDIKE DAIAPRTLPWPKSSDTISKNGTLSSVTSARAL RPPHGPPRPGALTFTPSLSSQALPSPRLPTTDG AHPQPISPIPGGVSSSGLSRMGAVPVMVPAQS QAGSLV
958	2308	A	8161	2340	1192	ELARPKQQSSEKSRNMIRNWLTIFILFPLKLV EKCESSVSLTVPPVVKLENGSSTNVSLTLRPP LNATLVITFEITFRSKNITILELPDEVVVPPGVT NSSFQVTSQNVGQLTVYLHGNHSNQTGPRIR FLVIRSSAISINQVIGWIYFVAWSISFYPQVIM NWRRKSVIGLSFDFVALNLTGFVAYSVFNIGL LWVPYIKEQFLLKYPNGVNPVNSNDVFFSLH AVVLTLIIIVQCCLYERGGQRVSWPAIGFLVL AWLFAFVTMIVAAVGVITWLQFLFCFSYIKL AVTLVKYFPQAYMNFYYKSTEGWSIGNVLL DFTGGSFSLLQMFLQSYNNDQWTLIFGDPTK FGLGVFSIVFDVVFFIQHFCLYRKPGYDQLN
959	2309	A	8163	521	1345	GERAGRRRGRLGVWAQPQPLLPRPVGSRRE MQPPGPPPAYAPTNGDFTFVSSADAEDLSGSI ASPDVKLNLGGDFIKESTATTFLRQRGYGWL LEVEDDDPEDNKPLLEELDIDLKDIYYKIRCV LMPMPSLGFNRQVVRDNPDFWGPLAVVLFFS MISLYGQFRVVSWITTWIFGSLTIFLLARVLG GEVAYGQVLGVIGYSLLPLIVLAPVLLVVGSF EVVSTLIKLFGVFWAAYSAASLLVGEEFKTK KPLLIYPIFLLYIYFLSLYTGV
960	2310	A	8167	1	2921	MTCFKGQKGEQRSHAFEANKDHKAKVPSPN LYSQLNALQFTVDERSILWLNQFLLDLKQSL NQFMAVYKLNDNSKSDEHVDVRVDGLMLK FVIPSEVKSECHQDQPRAISIQSSEMIATNTRH CPNCRHSDLEALFQDFKDCDFFSKTYTSFPKS CDNFNLLHPIFQRHAHEQDTKMHEIYKGNITP QLNKNTLKTSAATDVWAVYFSQFWIDYEGM KSGKGRPISFVDSFPLSIWICQPTRYAESQKEP QTCNQVSLNTSQSESSDLAGRLKRKKLLKEY YSTESEPLTNGGQKPSSSDTFFRFSPSSSEADI HLLVHVHKHVSMQINHYQYLLLLFLHESLILL SENLRKDVEAVTGSPASQTSICIGILLRSAELA LLLHPVDQANTLKSPVSESVSPVVPDYLPTEN GDFLSSKRKQISRDINRIRSYTVNHMSDNRSM SVDLSHIPLKDPLLFKSASDTNLQKGISFMDY LSDKHLGKISEDESSGLVYKSGSGEIGSETSD KKDSFYTDSSSVLNYREDSNILSFDSDGNQNI LSSTLTSKGNETIESIFKAEDLLPEAASLSENL

NO- of NO- of No	SEO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
much conide sequence where the corresponding of the			7			1	
sequence where we will be sequence where the sequence where we will be			noa	1			
Sequence	1						
uence    914   anito first anito acid residue of peptide sequence   pe	cotide	seq-		USSN	location		
nence   914	seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
amino acid reidiude sequence s			1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of peptide sequence   Y=Tyrosine, X=Unknown, *=Sign peodon, /-possible nucleotide delicina, \text{"possible nucleotide delicina, \text{"possible nucleotide delicina, \text{"possible nucleotide insertion}		1			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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ACYKNKVYGWRSGVEKDLDEVLQTHISVYFVN VSKGGVAKEDLISAFGTDDOTEICKQILTKG EVQVSDKERHTQLEQMFRDIATIVADKCVNP ETKRPYTVILIERAMKDIHYSVKTNKSTKQQA LEVIKQLKEKMKIERAHMRI.RPILPVNEGKKI. KEKLKPILKVIESEDYGQQLEVCLIDPGGFREI DELIKKETKGKGSLEVNLKDVEEGDEKFE POLEKKETKKGKSLEVNLKDVEEGDEKFE SVLRRMGKYWKTKQVFKKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKKEDEHILVA SDABLDAKLEVHSVOFIKATGKLEDVTG GLOTTDELTLYGMALVRIVNLISEKKTKFA VPILKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYVLUBULQAKTWOFICHENIKA SPERGIEEEDQEEDEKNIVVDDITTEQKFE PODDGKSTESDVKANGSKGSEVDSSLIKCK ALSHKELYERARELLVSYFEEQFTVLFKFRYI PKAHKA WANFSPREVELALEKGYTCENREA VLDAFLDDGFLVPTFEQLAALQEVEERENVDL NDVLVPKFPSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYLRWTVELIVANTKT GRNARRFSAGQWEARGWRIPKCSASLDWP RMYESCLGSPCMASPQLRHIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLOVGGSEASPIGK SPYTLDSLTWSVKPASSIGGSEAKAQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEGEEDEDDEDDEEDEEDMEVOPFSTGGESPTA ENARLLAQKGAALQGSAWQVSSEDVRWDTF PLGRMPGGTEDPAELMI ENYDTMYLLDQPV LEGRLEPSTCKTDTLGLSCGVGSOCSNNSSSS NFEGLLWSQGQLHGLKTGLQTF PLGRMPGGTEDPAELMI ENYDTMYLLDQPV LEGRLEPSTCKTDTLGLSCGVGSOCSNNSSSS NFEGLLWSQGQLHGLKTGLQTF NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPPKKGGGGIKNPGRSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGSTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGSTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGSTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGSTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGTSTSLKIGTVGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGTSTSLKIGTUGLP NVGRSTFFNVLTINSQASAENFPFCTIDPNESS PSTMPFKKGGGGIKNPGTSTSLKIGTUGLP NVG	961	2311	A	8172	1442	682	<u> </u>
VSKGQVAKKEDLISAFGTDDQTEIĆKQILTKG EQVQSDKERHTQI EMPRIJATIVADKCVNP ETKRPYTVILIERAMKDIHYSVKTINKSTKQQA LEVIKQLKEKMRIERAHMRILRPILPVNEGKIL KEKLKPLIKVIESEDVGQQLEIVCLIDPGGFREI DELIKKETKGKGSLEVLINLKDVEEGDEKFE NISNKAEVSSHPSVISMDSFGGPREIDNGS VILRRMGKKYWKTKQVFIKATGKKEDEHLVA SDAELDAKLEVHSVQETCTELLKIIEKYQLR LNGMKS  4 8181 13 2215 AEGCAERGTEPVVELSMSWESGAGPGLGSQ GMDLVWSAWYGKCVKGKGSLPISAHGIVV AWLSRAEWDQVTVVTLFDDHKLQRYALINI TVWRSRSGNEIPLAKSTADLIRCKLIDVTG GIGTDELRILYGMALVRFVNLISERKTKFAK VPIKCLAGEVNIPVOLITEKKMPHI NDCRRGCYPVLDWLQKTYWCRQLENSLRET WELEEFREGIEEDDEEDEDEDKINVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEVDSHCKK ALSHKELYERARELLVSYEEDFTVLEKFRYI. PKAIKAWNNYSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTTEQLAALQIEYEENVDL NDVLVPKPPSGQWPQLLRGLHSQNFTQALLE RMISELPALGISGIRFTYILKWTVELIVANTKT GRNARRFSAGQWEARGWRLFNCSASLDWP RNYESCLGSPCWASPOLIRIFKAMGQGLPD EEQEKLLRICSTYTQSGERNSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEQ GSVNDVKEERKEEVLPDQVEEEEENDDQE EEEEDDDEDDEEDEMOVPSTOGESTTA ENARLLQKRGALQGSAWQVSSEDVRWDTF PLGRNPGQTEDPAELMI ENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQQQLHGLKTGTLGLF PLGRNPGGTEDPAELMI ENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQQCHGLKTGTLGLF PSTMPPKKGGDGIRGTGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSRP PSTMPPKKGGGGGIRGAFLSHISACDGIFHLTRA FEDDDTITVEGSVDPRIGRIFGSTLKIGTVGLP NVGKSTFFNVLTNSQASAENPFCTIDPNESR VPVPDERTPFLCQVHKPASKIPAELNVVDIAG LVKGAHINGQGLGNAFLSHISACDGIFHLTRA FEDDDTITVEGSVDPRIBEIREELGLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWINKEEVLNKHLELTIS KPMVYLVNLSEKDVJRKKNKWLKIKKEWUD	/01	23	1 **	~ <b>~</b>	1		
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PSTMPPKKGGDGIŘPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD	964	2314	Α	8184	6	1393	
NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD	1		1		1	1	GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR
NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD			1	1		I	PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP
VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD	1		1	1		ŧ	1
LVKGAHNGQGLĞNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD			1			1	
FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD			t	Ī		I	
GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD	1		ļ	1	1	J	-
WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD	ĺ		1	1	1	1	· · · · · · · · · · · · · · · · · · ·
KPMVÝLVNLSEKDYIRKKNKWLIKIKEWVD	1		1	1	}		
			1	1	1	1	
KYDPGALVIPFSGALELKLQELSAEERQKYLE	ŀ	1	ł	1	ì	1	
	1	1	1_	1		L	KYDPGALVIPFSGALELKLQELSAEERQKYLE

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  ANMTQSALPKIIKAGFAALQLEYFFTAGPDEV RAWTIRKGTKAPQAAGKIHTDFEKGFIMAEV MKYEDFKEEGSENAVKAAGKYRQQGRNYIV EDGDIIFFKFNTPQQPKKK
965	2315	A	8195	1437		RSFSLSFSLLSPSEMMALGAAGATRVFVAMV AAALGGHPLLGVSATLNSVLNSNAIKNLPPPL GGAAGHPGSAVSAAPGILYPGGNKYQTIDNY QPYPCAEDEECGTDEYCASPTRGGDAGVQIC LACRKRRKRCMRHAMCCPGNYCKNGICVSS DQNHFRGEIEETTTESFGNDHSTLDGYSRRTT LSSKMYHTKGQEGSVCLRSSDCASGLCCARH FWSKICKPVLKEGQVCTKHRRKGSHGLEIFQ RCYCGEGLSCRIQKDHHQASNSSRLHTCQRH
966	2316	A	8207	416	4082	KFKLIKIMLETLIILLPVVSKFSFVSLSAPQHW SCPEGTLAGNGNSTCVGPAPFLIFSHGNSIFRI DTEGTTNYEQLVVDAGVSVIMDFHYNEKRIY WVDLERQLLQRVFLNGSRQERVCNIEKNVSG MAINWINEEVIWSNQQEGIITVTDMKGNNSHI LLSALKYPANVAVDPVERFIFWSSEVAGSLY RADLDGVGVKALLETSEKITAVSLDVLDKRL FWIQYNREGSNSLICSCDYDGGSVHISKHPTQ HNLFAMSLFGDRIFYSTWKMKTIWIANKHTG KDMVRINI.HSSFVPI.GELKVVHPI.AQPKAED DTWEPEQKLCKLRKGNCSSTVCGQDLQSHLC MCAEGYALSRDRKYCEGNDWKYCEDVNEC AFWNHGCTLGCKNTPGSYYCTCPVGFVLLPD GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL SPVSWECDCFPGYDLQLDEKSCAASGPQPFL LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLNGKRSKITTENISQPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTINTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGGAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ
967	2317	A	8210	3	601	SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM DVEHKMSIRILK

NO: of nucl- otide seq- uence  NO: of nucleotide q- uence  NO: of peptide seq- uence  NO: of peptide seq- uence  NO: of peptide seq- uence  NO: of peptide seq- uence  NO: of peptide seq- uence  NO: of peptide seq- uence  N=Aspartic Acid, E=Glutamic Acid F=Phenylalanine, G=Glycine, H=Hi N=Methionine, N=Asparagine, P=P O=Glutamic Acid F=Phenylalanine, G=Glycine, H=Hi N=Methionine, N=Asparagine, P=P O=Glutamic Acid F=Phenylalanine, G=Glycine, H=Hi N=Methionine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, P=P O=Glutamine, N=Asparagine, N=Asparagine, N=Basparagine, N=Basparagine, N=Basparagine, N=Basparagine, N=Basparagine, N=	stidine,
eotide sequence uence USSN location corresponding to last amino acid residue of peptide sequence vence uence vence	,
seq- uence 09/496 orrespondi ng to first amino acid residue of peptide residue of y=Tyrosine, X=Unknown, *=Stop of	
uence 914 ng to first acid residue Q=Glutamine, R=Arginine, S=Serin amino acid of peptide T=Threonine, V=Valine, W=Trypto residue of sequence Y=Tyrosine, X=Unknown, *=Stop of	roine.
residue of sequence Y=Tyrosine, X=Unknown, *=Stop of	
	ssible
sequence nucleotide insertion	CDVCDDTC
968 2318 A 8211 2 409 ISSCPHTAYEGSMSTLSNFTQTLI YMDNWRQNTTAEQEALQAKVI	
YLMVMIGMFSFIIVAILVSTVKS	
YHQYIVEDWQEKYKSQILNLEE	
AAĞFKMSP	
969 2319 A 8215 1 1938 GMPRSRGGRAAPGPPPPPPPGG	APRWSRWR
VPGRLLLLLPALCCLPGAARA	
RAAVAVARADEAEAPFAGQ	
LLPYDSRASALHSAKALQSAVS'	
VTGVLDQTTIEWMKKPRCGVPI	
NKRYALTGQKWRQKHITYSIHN TRKAIRQAFDVWQKVTPLTFEE	
KEADIMIFFASGFHGDSSPFDGE	
PGPGIGGDTHFDSDEPWTLGNA	
VAVHELGHALGLEHSSDPSAIM	
HNFKLPQDDLQGIQKIYGPPAEP	LEPTRPLPTL
PVRRIHSPSERKHERQPRPPRPPI	
KPNICDGNFNTVALFRGEMFVFI	
RNNRVQEGYPMQIEQFWKGLPA ADGRFVFFKGDKYWVFKEVTV	
ELGSCLPREGIDTALRWEPVGKT	
WRYSEERRATDPGYPKPITVWK	
FISKEGYYTYFYKGRDYWKFDN	
PRNILRDWMGCNQKEVERRKE	RRLPQDDVDI
MVTINDVPGSVNAVAVVIPCILS	
FQFKNKTGPQPVTYYKRPVQEW	
970 2320 A 8216 1235 2223 SRLSLQFYVSFRRTGLFTCKLIVI	
DSLRTNVFVRFQPETIACACIYL. TRPHWFLLFGTTEEEIQEICIETLI	
YELLEKEVEKRKVALQEAKLKA	
ALSTLGGFSPASKPSSPREVKAE	
TVKKEPEDRQQASKSPYNGVRK	
SASRSRSRTRSRSRSHTPRRHYN	
SSRSRSRSRSHSESPRRHHNHGS	
DDLKSSNRHGHKRKKSRSRSQS	
KKHRHERGHHRDRRERSRSFER SRSGHGRHRR	DONHAGANG
971 2321 A 8217 3 3274 DCRLQAAMPTNFTVVPVEAHAL	OGGODETAE
RTEAPGTPEGPEPERPSPGDGNP	
VEVEQESFFEGKNMALFEEEMD	
NKLANYTNLSQGVVEHEEDEES	
MGTFIGVYLPCLQNILGVILFLRI	TWIVGVAG
VLESFLIVAMCCTCTMLTAISMS	
AGGSYYMISRSLGPEFGGAVGLO GAMYILGTIEIFLTYISPGAAIFOA	
AMLHNMRVYGTCTLVLMALVV	
KLALVFLACVVLSILAIYAGVIK	
CLLGNRTLSRRSFDACVKAYGIF	
WGLFCNGSQPSAACDEYFIQNN	
ASGVFLENLWSTYAHAGAFVEK	-
AEESRASTLPYVLTDIAASFTLLV	
IMAGSNRSGDLKDAQKSIPTGTII	
LSCIVLFGACTEGVVLRDKFGEA	
LAWPSPWVIVIGSFFSTCGAGLQ OAIARDGIVPFLOVFGHGKANGI	
VLICETGILIASLDSVAPILSMFFL	
ACAVOTLLRTPNWRPRFKFYHW	
CLALMFICSWYYALSAMLIAGCI	
AEKEWGDGIRGLSLNAARYALI.	
KNWRPQVLVMLNLDAEQAMKF	

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LKAGKGLTIVGSVLEGTYLDKHMEAQRAEE NIRSLMSTEKTKGFCQLVVSSSLRDGMSHLIQ SAGLGGLKHNTVLMAWPASWKQEDNPFSW KNFVDTVRDTTAAHQALLVAKNVDSFPQNQ ERFGGGHIDVWWIVHDGGMLMLLPFLLRQH KVWRKCRMRIFTVAQVDDNSIQMKKDLQMP LYHLRISAEVEVVEMVENDISAFTYERTI.MM EQRSQMLKQMQLSKNEQEREAQLIHDRNTAS HTAAAARTQAPPTPDKVQMTWTREKLIAEK YRSRDTSLSGFKDLFSMKPDQSNVRRMHTAV KLNGVVLNKSQDAQLVLLNMPGPPKNRQGD ENYMEFLEVLTEGLNRVLLVRGGGREVITIYS
972	2322	A	8224	701	246	TSRRVTMKFNPFVTSDRSKNRKRHFNAPSHV RRKIMSSPLSKELRQKYNVRSMPIRKDDEVQ VVRGHYKGQQIGKVVQVYRKKYVIYIERVQ REKANGTTVHVGIHPSKVVITRLKLDKDRKKI LERKAKSRQVGKEKGKYKEELIEKMQE
973	2323	A	8237	279	4610	GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC PRPGPTPAPGAMDKLPPSMRKRLYSLPQQVG AKAWIMDEEDAEEEGAGGRQDPSRRSIRLR PLPSPSPSAAAGGTESRSSALGAADSEGPARG AGKSSTNGDCRRFRGSLASLGSRGGGGGTG SGSSHGHLHDSAEERRLIAEGDASPGEDRTPP GLAAEPERPGASAQPAASPPPPQQPPQPASAS CEQPSVDTAIKVEGGAAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLRMFGSQKA VEREQERVKSAGFWIIHPYSDFRFYWDLTML LLMVGNLIIPVGITFFKDENTTPWIVFNVVSD TFFLIDLVLNFRTGIVVEDNTEIILDPQRIKMK YLKSWFMVDFISSIPVDYIFLIVETRIDSEVYK TARALRIVRFTKILSLLRLLRLSRLIRYIHQWE EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSIIMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRIHD YYEHRYQGKMFDEESILGELSEPLREEIINFNC RKLVASMPLFANADPNFVTSMLTKLRFEVFQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLHKVQHDLNSGVFNYQENEIIQ QIVQHDREMAHCAHRVQAAASATPTPTPVIW TPLIQAPLQAAAATTSVAALTHHPRLPAAIFR PPPGSGLGNLGAGQTPRHLKRLQSLIPSALGS ASPASSPSQVDTPSSSSFHIQQLAGFSAPAGLS PLLPSSSSSPPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSDSPLLTPLPPGARSPQ AAQPSPAPPGARGGGLPEHFLPPPPSSRSPS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGIISPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFFRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL
	~~~		<i>3241</i>			LVPVKDASRICSLTYLLGSHWNNLVVRSPVL G

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM
975	2325	A	8249	62		MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK EEKGKYLPSLEMFRQRFRQFGYHDTPGPREA LSQLRVLCCEWLFREIHTKEQILELLVLEQFLT ILPQELQAWVQEHCPESAEEAVTLLEDLEREL DEPGHQVSTPPNEQKPVWEKISSSGTAKESPS SMQPQPLETSHKYESWGPLYIQESGEEQEFAQ DPRKVRDCRLSTQHEESADEQKGSEAEGLKG DIISVILANKPEASLERQCVNLENEKGTKPPLQ EAGSKKGRESVPTKPTPGERRYICAECGKAFS NSSNLTKHRRTHTGEKPYVCTKCGKAFSHSS NLTLHYRTHLVDRPYDCKCGKAFGQSSDLLK HQRMHTEEAPYQCKDCGKAFSGKGSLIRHYR IHTGEKPYQCNECGKSFSQHAGLSSHQRLHT GEKPYKCKECGKAFNHSSNFNKHHRIHTGEK PYWCHHCGKTFCSKSNLSKHQRVHTGEGEA
976	2326	A	8257	298	7086	GNMACWPQLRLLLWKNLTFRRQTCQLLLE VAWPLFIFLILISVRLSYPPYEQHECHFPNKAM PSAGTLPWVQGIICNANNPCFRYPTPGEAPGV VGNFNKSIVARLFSDARRLLLYSQKDTSMKD MRKVLRTLQQIKKSSSNLKLQDFLVDNETFS GFLYHNLSLPKSTVDKMLRADVILHKVFLQG YQLHLTSLCNGSKSFEMIQLGDQEVSELCGLP REKLAAAERVLRSNMDILKPILRTLNSTSPFPS KELAEATKTLLHSLGTLAQELFSMRSWSDMR QEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEG GGLKIKSLNWYEDNNYKALFGGNGTEEDAE TFYDNSTTPYCNDLMKNLESSPLSRIIWKALK PLLVGKILYTPDTPATRQVMAEVNKTFQELA VFHDLEGMWEELSPKIWTFMENSQEMDLVR MLLDSRDNDHFWEQQLDGLDWTAQDIVAFL AKHPEDVQSSNGSVYTWREAFNETNQAIRTIS RFMECVNLNKLEPIATEVWLINKSMELLDER KFWAGIVFTGITPGSIELPHHVKYKIRMGIDN VERTNKIKDGYWDPGPRADPFEDMRYVWGG FAYLQDVVEQAIRVLTGTEKKTGVYMQQMP YPCYVDDIFLRVMSRSMPLFMTLAWIYSVAV IIKGIVYEKEARLKETMRIMGLDNSILWFSWFI SSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV FLSVFAVVTILQCFLISTLFSRANLAAACGGII YFTLYLPYVLCVAWQDYVGFTLKIFASLLSP VAFGFGCEYFALFEEQGIGVQWDNLFESPVE EDGFNLTTSVSMMLFDTFLYGVMTWYIEAVF PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS NQKRISEICMEEEPTHLKLGVSIQNLVKVYRD GMKVAVDGLALNFYEGQITSFLGHNGAGKT TTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQ NLGVCPQHNVLFDMLTVEEHIWFYARLKGLS GMQRKLSVALAFVGGSKVVILDEPTAGVDP YSRRGIWELLLKYRQGRTIILSTHHMDEADVL GDRIAIISHGKLCCVGSSLFLKNQLGTGYYLT LVKKDVESSLSSCRNSSSTVSYLKKEDSVSQS SSDAGLGSDHESDTLTIDVSAISNLIRKHVSEA RLVEDIGHELTYVLPYEAAKEGAFVELFHEID DRLSDLGISSYGISETTLEEIFLKVAEESGVDA ETSDGTLPARRNRRAFGDKQSCLRPFTEDDA ADPNDSDIDPESRETDLLSGMDGKGSYQVKG WKLTQQQFVALLWKRLLIARRSRKGFFAQIV

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977	2327	A	8260	3	1567	SLHKNQTVVDVAVLTSFLQDEKVKESYV  IPGSTISFSLCFIFPPCVPTMVRKPVVSTISKGG YLQGNVNGRLPSLGNKEPPGQEKVQLKRKV TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGM SLTIWTVCGVLSLFGALSYAELGTTIKKSGGH YTYILEVFGPLPAFVRVWVELLIIRPAATAVIS LAFGRYILEPFFIQCEIPELAIKLITAVGITVVM VLNSMSVSWSARIQIFLTFCKLTAILIIIVPGV MQLIKGQTQNFKDAFSGRDSSITRLPLAFYYG MYAYAGWFYLNFVTEEVENPEKTIPLAICISM AIVTIGYVLTNVAYFTTINAEELLLSNAVAVT FSERLLGNFSLAVPIFVALSCFGSMNGGVFAV SRLFYVASREGHLPEILSMIHVRKHTPLPAVIV LHPLTMIMIFSGDLDSLLNFLSFARWLFIGLA VAGLIYLRYKCPDMHRPFKVPLFIPALFSFTC LFMVALSLYSDPFSTGIGFVITLTGVPAYYLFII WDKKPRWFRIMSEKITRTLQIILEVVPEEDKL
978	2328	A	8261	2	2165	RGGSLRCVLGKLLGQLLCFQSERCVRFPEGLL RHRGCGLLSSRLSAGKPPLRTSFFGSWGVLPP LADAASMSGVRAVRISIESACEKQVHEVGLD GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE HNLHLLIREFHKQTLSSIMMPHPASAPFGHKR

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion MRLSGPQAFDKNEINSLQSSEGLLEKIIKQAK HIFLRSRAAATIDSLASRIEDPQIQAHWSNIND VYESSVKVLITSQGYEQICKSIQLQLNIGVEQI RVVHRDGRVITLSYQEQELQDFLLSQMSQHQ VHAVQQLAKVMGWQVLSFSNHVGLGPIESIG NASAITVASPSGDYAISVRNGPESGSKIMVQF PRNQCKDLPKSDVLQDNKWSHLRGPFKEVQ WNKMEGRNFVYKMELLMSALSPCLL
979	2329	A	8289	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTPSP RDGTMTQGKLSVANKAPGTEGQQQVHGEKK EAPAVPSAPPSYEEATSGEGMKAGAFPPAPTA VPLHPSWAYVDPSSSSSYDNGFPTGDHELFTT FSWDDQKVRRVFVRKVYTILLIQLLVTLAVV ALFTFCDPVKDYVQANPGWYWASYAVFFAT YLTLACCSGPRRHFPWNLILLTVFTLSMAYLT GMLSSYYNTTSVLLCLGITALVCLSVTVFSFQ TKFDFTSCQGVLFVLLMTLFFSGLILAILLPFQ YVPWLHAVYAALGAGVFTLFLALDTQLLMG NRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFG TNRE
980	2330	A	8305	59	857	ASQLPDYSISPPSLPPRISFHPSPTLARVAMAEP SEATQSHSISSSSFGAEPSAPGGGGSPGACPAL GTKSCSSSCAVHDLIFWRDVKKTGFVFGTTLI MLLSLAAFSVISVVSYLILALLSVTISFRIYKSV IQAVQKSEEGHPFKAYLDVDITLSSEAFHNY MNAAMVHINRALKLIIRLFLVEDLVDSLKLA VFMWLMTYVGAVFNGITLLILAELLIFSVPIV YEKYKTQIDHYVGIARDQTKSIVEKIQAKLPG IAKKKAE
981	2331	A	8308	186	1337	TRMSRHEGVSCDACLKGNFRGRRYKCLICYD YDLCASCYESGATITRHTTDHPMQCILTRVD FDLYYGGEAFSVEQPQSFTCPYCGKMGYTET SLQEHVTSEHAETSTEVICPICAALPGGDPNH VTDDFAAHLTLEHRAPRDLDESSGVRIIVRR MFHPGRGLGGPRARRSNMHFTSSSTGGLSSS QSSYSPSNREAMDPIAELLSQLSGVRRSAGGQ LNSSGPSASQLQQLQMQLQLERQHAQAARQ QLETARNATRINTSSVITITIQSTATTNIAN TESSQQTLQNSGFLTRLNDPKMSETERQSM ESERADRSLFVQELLLSTLVREESSSSDEDDR GEMADFGAMGCVDIMPLDVALENLNLKESN KGNEPPPPPL
982	2332	A	8315	1	1004	GSTHASADAWAQWFCTEALVMGAPVWYLV AAALLVGFILFLTRSRGRAASAGQEPLHNEEL AGAGRVAQPGPLEPEEPRAGGRPRRRDLGS RLQAQRRAQRVAWAEADENEEEAVILAQEE EGVEKPAETHLSGKIGAKKLRKLEEKQARKA QREAEFAERERKRLESQREAEWKKEEERLR LEEEQKEEEERKAREEQAQREHEEYLKLKEA FVVEEGVGETMTEEQSQSFLTEFINYIKQSK VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA ELAQASNSLIAWGRESPAQAPA
983	2333	A	8320	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKP DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP CPQPLRSPSLDNPTPFPNLGPSENPLKRLLVPG EFWFFEVTAFYRGRQVFQQTISCPEGLRLVGS

	·		-1 =		r=	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1		•	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide	ì	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
			<u> </u>	· · · · · · · · · · · · · · · · · · ·		EVGDRTLPGWPVTLPDPGMSLTDRGVMSYV
				,		RHVLSCLGGGLALWRAGOWLWAORLGHCH
		1				TYWAVSEELLPNSGHGPDGEVPKDKEGGVF
		ļ			}	DLGPFIVGSLGPPDLITFTEGSGRSPRYALWFC
			1	ŀ		VGESWPQDQPWTKRLVMVKVVPTCLRALVE
		1 /	1		1	MARVGGASSLENTVDLHISNSHPLSLTSDQY
		İ	İ			KAYLQDLVEGMDFQGPGES
984	2334	A	8321	1	1243	ANMAPVEHVVADAGAFLRHAALODIGKNIY
704	2354	J ^ _	0,521	J *	1243	TIREVVTEIRDKATRRRLAVLPYELRFKEPLPE
	i					YVRLVTEFSKKTGDYPSLSATDIQVLALTYQL
		1				EAEFVGVSHLKQEPQKVKVSSSIQHPETPLHIS
	!				†	GFHLPYKPKPPQETEKGHSACEPENLEFSSFM
					1	FWRNPLPNIDHELQELLIDRGEDVPSEEEEEE
		}			İ	NGFEDRKDDSDDDGGGWITPSNIKQIQQELE
		1		[		
	1	i				QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV
	1	1		i		LAVNGMI.IREARSYILRCHGCFKTTSDMSRV
	1	1				FCSHCGNKTLKKVSVTVSDDGTLHMHFSRNP
-			1		1	KVLNPRGLRYSLPTPKGGKYAINPHLTEDQRF
	1		1	į.	ł	PQLRLSQKARQKTNVFAPDYIAGVSPFVENDI
	1			1		SSRSATLQVRDSTLGAGRRRLNPNASRKKFV
			<u> </u>			KKR
985	2335	A	8322	352	529	RRNNIRQFIMKVCISGQARWLTPVVPVLWET
		ŀ				EAGRSLELKSLRPAWATWGNPISTKINK
986	2336	A	8325	89	1172	KMNPTDIADTTLDESIYSNYYLYESIPKPCTKE
		j		ļ	j	GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL
						FKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG
	i	<u> </u>				YYAADQWVFGLGLCKMISWMYLVGFYSGIF
		1	l			FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS
		1				LATWSVAVFASLPGFLFSTCYTERNHTYCKT
	j	J			}	KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCY
			ļ			SMIIRTLQHCKNEKKNKAVKMIFAVVVLFLG
		ļ				FWTPYNIVLFLETLVELEVLQDCTFERYLDYA
		Ì	1			IQATETLAFVHCCLNPIIYFFLGEKFRKYILQL
	Ì	1	ŀ		1	FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS
				ł		TMDHDLHDAL
987	2337	T <sub>A</sub>	8326	3	470	SLSAMRFLAATFLLLALSTAAQAEPVQFKDC
	i	İ				GSVDGVIKEVNVSPCPTQPCQLSKGQSYSVN
					1	VTFTSNIQSKSSKAVVHGILMGVPVPFPIPEPD
		1				GCKSGINCPIQKDKTYSYLNKLPVKSEYPSIK
	1	1		[		LVVEWQLQDDKNQSLFCWEIPVQIVSHL
988	2338	A	8335	1205	323	VIKMALAARLLPOFLHSRSLPCGAVRLRTPA
700	1236	' •	0000	1200		VAEVRLPSATLCYFCRCRLGLGAALFPRSAR
		1			1	ALAASALPAQGSRWPVLSSPGLPAAFASFPAC
	1					PQRSYSTEEKPQQHQKTKMIVLGFSNPINWV
		!		1	1	RTRIKAFLIWAYFDKEFSITEFSEGAKOAFAH
		1	1	:		VSKLLSQCKFDLLEELVAKEVLHALKEKVTS
	ļ	]		1		LPDNHKNALAANIDEIVFTSTGDISIYYDEKG
		1	1			
			1		1	RKFVNILMCFWYLTSANIPSETLRGASVFQVK
					1	LGNQNVETKQLLSASYEFQREFTQGVKPDWT
				,		IARIEHSKLLE .
989	2339	A	8349	67	185	IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL
						IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS
989	2339	A	8349 8361	67	185	IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASFFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ
						IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASFFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL
						IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASFFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ
						IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASFFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL
						IARIEHSKLLE MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF
						IARIEHSKLLE MSGFIHOLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQ ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G-Glycine, H-Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	!	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide		/=possible nucleotide deletion, \=possible
		ļ	<del></del>	sequence		nucleotide insertion
	ţ					LIKKYDQMAIFHCLFWPSLTLLGGALIVGMV
		İ			İ	RLTQHLSLLCEKYSTVVRDEVGGKVPYIEQH
001	0343	<del> </del>	100.00	<u></u>	001	QFKLCIMRRSKGRAEKS
991	2341	A	8369	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVL
	ļ	i	1			EGFLSAEECVAMQQRIGEIVAEMDVPLHCRT
j		1			!	EFSTQEEEQLRAQGSTDYFLSSGDKIRFFFEK
	l	}			1	GVFDEKGNFLVPPEKSINKIGHALHAHDPVFK
		1				SITHSFKVQTLARSLGLQMPVVVQSMYIFKQP
						HFGGEVSPHQDASFLYTEPLGRVLGVWIAVE
	J	}	]		]	DATLENGCLWFIPGSHTSGVSRRMVRAPVGS
				ì	i	APGTSFLGSEPARDNSLFVPTPVQRGALVLIH
		1				GEVVHKSKQNLSDRSRQAYTFHLMEASGTT
992	2242	<u> </u>	8370	1000	l	WSPENWLQPTAELPFPQLYT
992	2342	A	83 /0	906	4	MALSGNCSRYYPREQGSAVPNSFPEVVELNV
	i		1		-	GGQVYFTRIISTLISIPIISLLWKMFSPKRDTAN
			i			DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV
i	ì	!	1		ł	LPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI KQSPDEFCHSDFEDASQGSDTRICPPSSLLPAD
			ł	ļ		RKWGFITVGYRGSCTLGREGQADAKFRRVPR
				İ		ILVCGRISLAKEVFGETLNESRDPDRAPERYTS
				1	1	RFYLKFKHLMGAPASNFILGFWGLGQNQDK
		ł				HPVNIYLQQRSVIRPDLTSKKAGDLKGKGDA
		i				OEVSRRRWLGDPEHL
993	2343	A	8379	1	2794	MRMQRHKNDTMDFGDSGKRIGGGVLCLLHQ
773	2343	^	03/9	*	2//3	SNTSFIKLNNNGFEDIVIVIDPSVPEDEKITEQIE
	-			i	}	DMVTTASTYLFEATEKRFFFKNVSILIPENWK
	ŀ	-	ļ	1		ENPQYKRPKHENHKHADVIVAPPTLPGRDEP
		ĺ	[			YTKOFTECGEKGEYIHFTPDLLLGKKONEYG
			1			PPGKLFVHEWAHLRWGVFDEYNEDQPFYRA
	•		1			KSKKIEATRCSAGISGRNRVYKCQGGSCLSRA
	1	ļ	1.	l	1	CRIDSTTKLYGKDCQFFPDKVQTEKASIMFM
	i	1		1	į	QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRST
	ł					WEVISNSEDFKNTIPMVTPPPPPVFSLLKIRQRI
	ĺ	ĺ	ľ			VCLVLDKSGSMGGKDRLNRMNQAAKHFLLQ
		Į				TVENGSWVGMVHFDSTATIVNKLIQIKSSDER
				•	ł	NTLMAGLPTYPLGGTSICSGIKYAFQVIGELH
		J		}	]	SQLDGSEVLLLTDGEDNTASSCIDEVKQSGAI
		1			1	VHFIALGRAADEAVIEMSKITGGSHFYVSDEA
ı				1	}	QNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
	l	1	ł	l	l	LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPP
						SISLWDPSGTIMENFTVDATSKMAYLSIPGTA
	!			I		KVGTWAYNLQAKANPETLTITVTSRAANSSV
	1			•	į	PPITVNAKMNKDVNSFPSPMIVYAEILQGYVP
,	ł	}	}	}		VLGANVTAFIESQNGHTEVLELLDNGAGADS
				1	[	FKNDGVYSRYFTAYTENGRYSLKVRAHGGA
				Į.		NTARLKLRPPLNRAAYIPGWVVNGEIEANPP
						RPEIDEDTQTTLEDFSRTASGGAFVVSQVPSL
		1	1			PLPDQYPPSQITDLDATVHEDKIILTWTAPGD
		[				NFDVGKVQRYIIRISASILDLRDSFDDALQVN
						TTDLSPKEANSKESFAFKPENISEENATHIFIAI
		l			ĺ	KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPT
						PTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIV
	,	ļ	}	]		NFILSTTI
994	2344	A	8385	231	644	INSSPRTGRDHQELNLHTERDSRSQRAVLKIP
						RONPGIFYWIFLPSRSHSASHGSRORQVSCOG
	1	1				TODEILKMRNTFAELKNSLEALSSRMDQAEE
ļ						
j	]	]				RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL
						RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL PSSWDYRACLS
995	2345	A	8390	194	3421	

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DFLSMKQSPALAPEERCRRAGSPKPVLRADD NNMGNGCSQKLATANLLRFLLLVLIPCICALV LLLEILLSYVGTLQKVYFKSNGSEPLVTDGEI
						QGSDVILTNTIYNQSTVVSTAHPDQHVPAWT TDASLPGDQSHRNTSACMNITHSQCQMLPYH ATLTPLLSVVRNMEMEKFLKFFTYLHRLSCY QHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCE AAKEGCESVLGMVNYSWPDFLRCSQFRNQT ESSNVSRICFSPQQENGKQLLCGRGENFLCAS GICIPGKLQCNGYNDCDDWSDEAHCNCSENL FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC DCNPTTEHRCGDGRCIAMEWVCDGDHDCVD KSDEVNCSCHSQGLVECRNGQCIPSTFQCDG DEDCKDGSDEENCSVIQTSCQEGDQRCLYNP CLDSCGGSSLCDPNNSLNNCSQCEPITLELCM NLPYNSTSYPNYFGHRTQKEASISWESSLFPA LVQTNCYKYLMFFSCTILVPKCDVNTGEHIPP CRALCEHSKERCESVLGIVGLQWPEDTDCSQ FPEENSDNQTCLMPDEYVEECSPSHFKCRSGQ CVLASRRCDGQADCDDDSDEENCGCKERDL WECPSNKQCLKHTVICDGFPDCPDYMDEKN CSFCQDDELECANHACVSRDLWCDGEADCS DSSDEWDCVTLSINVNSSSFLMVHRAATEHH VCADGWQEILSQLACKQMGLGEPSVTKLIQE QEKEPRWLTLHSNWESLNGTTLHELLVNGQS CESRSKISLLCTKQDCGRRPAARMNKRILGGR
						TSRPGRWPWQCSLQSEPSGHICGCVLIAKKW VLTVAHCFEGRENAAVWKVVLGINNLDHPS VFMQTRFVKTIILHPRYSRAVVDYDISIVELSE DISETGYVRPVCLPNPEQWLEPDTYCYITGW GHMGNKMPFKLQEGEVRIISLEHCQSYFDMK TITTRMICAGYESGTVDSCMGDSGGPLVCEK PGGRWTLFGLTSWGSVCFSKVLGPGVYSNVS YFVEWIKRQIYIQTFLLN
996	2346	A	8392	199	3085	KVILSSEMSKTNKSKSGSRSSRSRSASRSRSRS FSKSRSRSRSKTNKSKSGSRSSRSRSRSRSRSRSRS FSKSRSRSRSLSRSRKRRLSSRSRSRSRSPSPAHN RERNHPRVYQNRDFRGHNRGYRRPYYFRGR NRGFYPWGQYNRGGYGNYRSNWQNYRQAY SPRRGSRSRSPKRRSPSPRSRSHSRNSDKSSS DRSRRSSSSRSSSNHSRVESSKRKSAKEKKSSS KDSRPSQAAGDNQGDEVKEQTFSGGTSQDTK ASESSKPWPDATYGTGSASRASAVSELSPRER SPALKSPLQSVVVRRSPRPSPVPKPSPPLSST SQMGSTLPSGAGYQSGTHQGQFDHGSGSLSP SKKSPVGKSPPSTGSTYGSSQKEESAASGGAA YTKRYLEEQKTENGKDKEQKQTNTDKEKIKE KGSFSDTGLGDGKMKSDSFAPKTDSEKPFRG SQSPKRYKLRDDFEKKMADFHKEEMDDQDK DKAKGRKESEFDDEPKFMSKVIGANKNQEEE KSGKWEGLVYAPPGKEKQRKTEELEESFPE RSKKEDRGKRSEGGHRGFVPEKNFRVTAYK AVQEKSSSPPPRKTSESRDKLGAKGDFPTGKS SFSITREAQVNVRMDSFDEDLARPSGLLAQER KLCRDLVHSNKKEQFFRSIFQHIQSAQSQRSP SELFAQHIVTIVHHVKEHHFGSSGMTLHERFT KYLKRGTEQEAAKNKKSPEIHRRIDISPSTFRK HGLAHDEMKSPREPGYKAEGKYKDDPVDLR LDIERRKKHKERDLKRGKSRESVDSRDSSHSR ERSAEKTEKTHKGSKKQKKHRRARDRSRSSS SSSQSSHSYKAEEYTEETEEREESTTGFDKSRL

SEQ II		1 050 5	T > 4 -	1 650	D-dies-	I n 452 1 5	Lawrence Co. Co.
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I I I I I I I I I I I I I I I I I I I	1003	2353	A	8427	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILR

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SLDTENIDEILNNADVALVNFYADWCRFSQM LHPIFEEASDVIKEEFPNENQVVFARVDCDQH SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS KRNIIGYFEQKDSDNYRVFERVANILHDDCAF LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY LGAMTNFDVTYNWIQDKCVPLVREITFENGE ELTEEGLPFLILFHMKEDTESLEIFQNEVARQL ISEKGTINFLHADCDKFRHPLLHIQKTPADCP VIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDL HSGKLHREFHHGPDPTDTAPGEQAQDVASSP PESSFQKLAPSEYRYTLLRDRDEL
1004	2354	A	8432	910	387	GLSRKLRAGFLPGFCRVSPCGSWVVETLVKM ACAAARSPADQDRFICIYPAYLNNKKTIAEGR RIPISKAVENPTATEIQDVCSAVGLNVFLEKN KMYSREWNRDVQYRGRVRVQLKQEDGSLC LVQFPSRKSVMLYAAEMIPKLKTRTQKTGGA DQSLQQGEGSKKGKGKKKK
1005	2355	A	8453	90	530	QSHETKMQSGTHWRVLGLCLLSVGVWGQD GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE ILWQHNDKNIGGDEDDKNIGSDEDHLSLKEF SELEQSGYYVCYPRGSKPEDANFYLYLRARG NPGLONRYHRLFREDHSKGHSO
1006	2356	Λ	8458	3	307	AVQRIRHEMNIFRETGOLSHLAAIVILLLKIW KTRSCAGISGKSQLLFALVFTTRYLDLFTSFIS LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC QLCIFN
1007	2357	A	8459	43	553	GAGAGGDWAAMDKLKKVLSGQDTEDRSGL . SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT VLLWVPRKGLHLFAVFYTFGNIASIGSTIFLM GPVKQLKRMFEPTRLIATIMVLLCFALTLCSA FWWHNKGLALIFCILQSLALTWYSLSFIPFAR DAVKKCFAVCLA
1008	2358	A	8462	487	150	AQDIRSVHSLGQKSTPVKHFRTLSHLHGLPDP PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS DPRWGCVGPSMPTSTCLPGAVEASTTKASLP KCPVDSSLPTPEACFL
1009	2359	A	8465	134	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVP NETIIVLPSNVINFSQAEKPEPTNQGQDSLKKH LHAEIKVIGTIQILCGMMVLSLGIILASASFSPN FTQVTSTLLNSAYPFIGPFFFIISGSLSIATEKRL TKLLVHSSLVGSILSALSALVGFIILSVKQATL NPASLQCELDKNNIPTRSYVSYFYHDSLYTTD CYTAKASLAGTLSLMLICTLLEFCLAVLTAVL RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRRPYPVMRKICQVGPAGLAFILNISPVA HRVALCHLAGCQEQAAWYHTLQILFFLVSAY FFSCPVPEKYFPGSCDIVGHGHQIFHAFLSICI LSQLEAILLDYQGRQEIFLQRHGPLSVHMACL SFFFLAACSAATAALLRHKVKARLTKKDS
1011	2361	A	8478	5	409	TELSQLEKAHPPADMGRRKSKRKPPPKKKMT GTLETQFTCPFCNHEKSCDVKMDRARNTGVI SCTVCLEEFQTPITCILGNLGFFQRVGRGLESG PCSSGPLCALVQGQSRPEEQVPPSDFCGVRRC RAGFQCQ
1012	2362	A	8481	2810	1652	RTSTOKWOSVFNDSQEHLERFYCNPENDRM RMKYGGQEFWADLNAMVVYETTEFDQLRR LSTPPSSNVNSIYHTVWKFFCRDHFGWREYPE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion  SVIRLIEEANSRGLKEVRFMMWNNHYILHNS FFRREIKRRPLFRSCFILLPYLQTLGGVPTQAP PPLEATSSQIICPDGVTSANFYPETWVYMHP SQDFIQVPVSAEDKSYRIIYNLFHKTVPEFKYR ILQILRVQNQFLWEKYKRKKEYMNRKMFGR DRIINERHLPHGTSQDVVDGICKHNFDPRVCG KHATMFGQGSYFAKKASYSHNFSKKSSKGV HFMFLAKVLTGRYTMGSHGMRRPPPVNPGS VTSDLYDSCVDNFFEPQIFVIFNDDQSYPYFVI QYEEVSNTVSI
1013	2363	Α	8488	2	517	IENCRTRLRQAWHEVCGNKMAAPIPQGFSCL SRFLGWWFRQPVLVTQSAAIVPVRTKKRFTP PIYQPKFKTEKEFMQHARKAGLVIPPEKSDRS IHLACTAGIFDAYVPPEGDARISSLSKEGLIER TERMKKTMASQVSIRRIKDYDANFKIKDFPE KAKDIFIEGSPLY
1014	2364	A	8501	363	17	YIRTGYVYICIIYAQLMYTYYIRTAYVYICILY AQLMYTYVLYTHSLCIHMYSIRTAYVYICIIY AQIMYTYVFYTHRLCIHMYSIRTDYVYICILY AQLMYTYVFYTHSYMSDE
1015	2365	A	8504	3	2190	NSSEHFSQAPQRLSFYSWYGSARLFRFRVPPD AVLLRWLLQVSRESGAACTDAEITVHFRSGA PPVINPLGTSFPDDTAVQPSFQVGVPLSTTPRS NASVNVSHPAPGDWFVAAHLPPSSQKIELKG LAPTCAYVFQPELLVTRVVEISIMEPDVPLPQ TLLSHPSYLKVFVPDYTRELLLELRDCVSNGS LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC RLLLPSPPWDRWLQVTAESLVGPLGTVAFSA VAALTACRPRSVTIQPLLQSSQNQSFNASSGL LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL NTGMDSGGSLTISLRANKTEMRNETVVVACV NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR RANLIIPYPETDNWYLSLQLMCPENAEDCEQ AVVHVETILYLVPCLNDCGPYGQCLLLRRHS YLYASCSCKAGWGWSCTDNSTAQTVAQQR AATLLLTLSNLMFLAPIAVSVRFFLVEASVY AYTMFFSTFYHACDQPGEAVLCILSYDTLQY CDFLGSGAAIWVTILCMARLKTVLKYVLFLL GTLVIAMSLQLDRRGMWNMLGPCLFAFVIM ASMWAYRCGHRQCYPTSWQRWAFYLLPG VSMASVGIAIYTSMMTSDNYYYTHSIWHILL AGSAALLLPPPDQPAEPWACSQKFPCHYQIC KNDREELYAVT
1016	2366	A	8511	1	453	KWYPSGPVRIPGRFYYKLPAGHRRCRMAPAK KGGEKKKGRSAINEVVTREYTINIHKRIHGVG FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP NKLYTLVTYVPVTTFKNLQTVNVDEN
1017	2367	A	8513	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINT LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVVGLADLLSKHDSQHKLSEVIT GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP RGTLEDALDAFCQVGQQPLIAVALLGNISSIA FFNFAGISVTKELSATTRMVLDSLRTVVIWAL

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SLALGWEAFHALQILGFLILLIGTALYNGLHR PLLGRLSRGRPLAEESEQERLLGGTRTPINDA S SPFWTEKRRMEKPLFPLVPLHWFGFGYTALV
		1				VSGGIVGYVKTGSVPSLAAGLLFGSLAGLGA YQLYQDPRNVWGFLAATSVTFVGVMGMRS YYYGKFMPVGLIAGASLLMAAKVGVRMLM TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLLLAVLL AAHPDAQAEVRLSVPPLVEVMRGKSVILDCT PTGTHDHYMLEWFLTDRSGARPRLASAEMQ GSELQVTMHDTRGRSPPYQLDSQGRLVLAEA QVGDERDYVCVVRAGAAGTAEAAARLNVF AKPEATEVSPNKGTLSVMEDSAQEIATSNSRN GNPAPKITWYRNGQRLEVPVEMNPEGYMTS RTVREASGLLSLTSTLYLRLRKDDRDASFHC AAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQ FWVGSPSTPAGWVREGDTVQLLCRGDGSPSP EYTLFRLQDEQEEVLNVNLEGNLTLEGVTRG QSGTYGCRVEDYDAADDVQLSKTLELRVAY LDPLELSEGKVLSLPLNSRAVVNCSVHGLPTP ALRWTKDSTPLGDGPMLSLSSITFDSNGTYVC EASLPTVPVLSRTQNFTLLVQGSPELKTAEIEP KADGSWREGDEVTLICSARGHPDPKLSWSQL GGSPAEPIPGRQGWVSSSLTLKVTSALSRDGI SCEASNPHGNKRHVFHFGTVSPQTSQAGVAV MAVAVSVGLLLLVVAVFYCVRRKGGPCCRQ RREKGAP
1020	2370	A	8530	2	1200	PRVRLLRPSRSRSCRGLLSTRAPGPSPFRSLHS SPLLPHAMKSPFYRCQN'ITSVEKGNSAVMGG VLFSTGLLGNLLALGLLARSGLGWCSRRPLR PLPSVFYMLVCGLTVTDLLGKCLLSPVVLAA YAQNRSLRVLAPALDNSLCQAFAFFMSFFGL SSTLQLLAMALECWLSLGHPFFYRRHITLRLG ALVAPVVSAFSLAFCALPFMGFGKFVQYCPG TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV LATVLCNLGAMRNLYAMHRRLQRHPRSCTR DCAEPRADGREASPQPLEELDHLLLLALMTV LFTMCSLPVIYRAYYGAFKDVKEKNRTSEEA EDLRALRFLSVISIVDPWIFIIFRSPVFRIFFHKI FIRPLRYRSRCSNSTNMESSL
1021	2371	A	8536	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPR KHDSGAADLERVTDYAEEKEIQSSNLETAMS VIGDRRSREQKAKQER
1022	2372	A	8537	94	541	RKERRRRRMEAVVFVFSLLDCCALIFLSV YFIITLSDLECDYINARSCCSKLNKWVIPELIG HTIVTVLLLMSLHWFIFLLNLPVATWNIYRYI MVPSGNMGVFDPTEIHNRGQLKSHMKEAMI KLGFHLLCFFMYLYSMILALIND
1023	2373	À	8540	26	431	RMMKCPQALLAIPWLLLSWVSSEDKVVQSPL SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK KAPTFLFMLTSSGIEKKSGRLSSILDKKELSSIL NITATQTGDSAIYLCAVEAQCSLVTCSLYSNS TAEALQL
1024	2374	Α	8544	1731	743	GVRLRÝSPIAVVMVGEAGRDLRRRRAVAVT AEKMAVLAPLIALVYSVPRLSRWLAQPYYLL SALLSAAFLLVRKLPPLCHGLPTQREDGNPCD FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	seq- uence		USSN 09/496 914	location correspondi ng to first amino acid	to last amino acid residue of peptide	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				residue of peptide sequence	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT WIVEFFANWSNDCQSFAPIYADLSLKYNCTG LNFGKVDVGRYTDVSTRYKVSTSPLTKQLPT LILFQGGKEAMRRPQIDKKGRAVSWTFSEEN
						VIREFNLNELYQRAKKLSKAGDNIPEEQPVAS TPTTVSDGENKKDK
1025	2375	A	8546	2194	1707	TVSFHKTMASLKCSTVVCVICLEKPKYRCPA CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS ALPTKTVKPVENKDDDDSIADFLNSDEEEDR VSLQNLKNLGESATLRSLLLNPHLRQLMVNL
						DQGEDKAKLMRAYMQEPLFVEFADCCLGIV EPSQNEES
1026	2376	A	8547	1078	594	VGMELPAVNLKVILLGHWLLTTWGCIVFSGS YAWANFTILALGVWAVAQRDSIDAISMFLGG LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAIL SLLLKPLSCCFVYHMYRERGGELLVHTGFLG
				<u> </u>		SSQDRSAYQTIDSAEAPADPFAVPEGRSQDAR GY
1027	2377	A	8557	1	340	DFLGPASPQEEGGSESSTMTELETÄMGMIIDV FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ SGKDKDAVDKLLKDLDANGDAQVDFSEFIVF VAAITSACHKYFEKAGLK
1028	2378	A	8569	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLL LLLLGSGQGPQQVGAGQTFEYLKREHSLSKP YQGEAPRPCFLRDWELQVHFKIHGQGKKNL HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG
						VFVDTYPNEEKQQERVFPYISAMVNNGSLSY DHERDGRPTELGGCTAIVRNLHYDTFI.VIRY VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG YYFGTSSITGDLSDNHDVISLKLFELTVERTPE
						EEKLHRDVFLPSVDNMKLPEMTAPLPPLSGL ALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK RFY
1029	2379	A	8572	1	578	AAAASHRSRARSRPRRVSSGPAPRRAQSSAG RVASGLDSAPLCTMARALCRLPRRGLWLLLA HHLFMTTACQEANYGALLRELCLTQFQVDM
						EAVGETLWCDWGRTIRSYRELADCTWHMAE KLGCFWPNAEVDRFFLAVHGRYFRSCPISGR AVRDPPGSILYPFIVVPITVTLLVTALVVWQS KRTEGIV
1030	2380	A	8574	1352	372	DSSTVKGGSESRHLCLIPDLKGKARTREASSG SRTCGRRTSLCTSAKSSWTYRSGRLSWQSIKG THLTITQALRQPLHRAPLLPGQLCWSPRPLEK
						NKAMGRPLLLPLLLLLQPPAFLQPGGSTGSGP SYLYGVTQPKHLSASMGGSVEIPFSFYYPWEL AIVPNVRISWRRGHFHGQSFYSTRPPSIHKDY
						VNRLFLNWTEGQESGFLRISNLRKEDQSVYF CRVELDTRRSGRQQLQSIKGTKLTITQAVTTT TTWRPSSTTTIAGLRVTESKGHSESWHLSLDT
						AIRVALAVAVLKTVILGLLCLLLLWWRRRKG SRAPSSDF
1031	2381	A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQL AFDDFQESCAMMWQKYAGSRRSMPLGARIL FHGVFYAGGFAIVYYLIQKFHSRALYYKLAV
						EQLQSHPEAQEALGPPLNIHYLKLIDRENFVDI VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW HLDEVFLELKDGQQIPVFKLSGENGDEVKKE
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR WAAGALGVAGLLCAVLGAVMIVMVPSLIKQ

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	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ł	in	nucleotide	location	F=Phenylalanine, G-Glycine, H=Histidine,
cotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
{	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/
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1034	2384	Α	8597	640	164	VTTSCIPFAFGLGVRASERLAEIDMPYLLKYQ
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1						KTPIPTSLRKREGEYSKVLAJAONFV
1036	2386	A	8606	1	562	PTRAHSFDLCCSPCRRRLLGREEAGEEPTSPV
1				· .		TQYLQPRSPEECKMFACAKLACTPSLIRAGSR
1						VAVDDISASVI SDDEASDEOCOTUMISASVI
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	1					VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG
						VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY
1000						AILGFALSEAMGLFCLMVAFLILFAM
1037	2387	Α	8615	2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
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1	İ	ĺ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		peptide	* * * * * * * * * * * * * * * * * * *	/=possible nucleotide deletion, \=possible
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1038	2388	A	8621	3	1494	RSRMARAPLGVLLLLGLLGRGVGKNEELRLY
1035	2300	1	0021			HHLFNNYDPGSRPVREPEDTVTISLKVTLTNL
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1039	2389	A	8636	1	900	PGRERPGGGGARRRPOHLPALLPSERPDCATL
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						PSLALKPTPGGSQPLPTPA
1040	2390	A	8645	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSF
1040	2390	^	8043	70	1366	HEHRHQSGRCLSTGMAPNLKGRPRKKKPCPQ
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1041	2391	A	8646	113	1492	LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYP
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	1	ĺ	1			SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS
1	1	1	}	l	}	TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM
						VRIMATEPPIINLOPGNFTLDIPASIMMLTOPK
	1	1				NSTVETIVS.MDFVASTSVGLVILGQRLVCSLS
1	1	1		•		LNRFRLALPESNRSNIEVLRFENILSSILHFGVL
		1				PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF
		1		}		
ļ						LLISTDLKYETSSKQQPSFHVWEGLNLISRQW RGKSAP
1042	7202		8672	520	170	
1042	2392	A	00/2	538	170	ARRIARTRESKAAVSQDNVPALQPGKKKKLR
	1	L	1		l	LGGKKKKFKFFRLPKEFKKQLMYSPSNFKKM

NO: of nucl- ectide seq- uence  NO: of nucl- ectide seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucl- seq- uence  NO: of nucleotide location correspondin to last amino acid residue of peptide residue of peptide sequence  NO: of nucleotide location correspondin to last amino acid residue of peptide sequence  NO: of nucleotide location correspondin to last amino acid residue of peptide sequence  N=Tyrosine, X- /=possible nucle nucleotide location  N=Methioniue, y=Tyrosine, X- /=possible nucle nucleotide location correspondin to last amino acid residue of peptide sequence  T=Threonine, V y=Tyrosine, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /=possible nucle nucleotide location T=Insequence, X- /	
nucl- cotide seq- uence USSN o9/496 uence USSN o9/496 uence USSN o9/496 orrespondi ng to first armino acid residue of peptide residue of peptide sequence sequence sequence sequence sequence sequence TSLAGNTVQC LDMITSTDHV  1043 1043 105 106 106 106 106 106 106 106 106 106 106	-Lysine, L-Leucine, N-Asparagine, P-Proline, R-Arginine, S-Scrine, /-Valine, W-Tryptophan, =Unknown, *=Stop codon, ectide deletion, \-possible ttion
eotide seq- uence USSN 09/496 corresponding to last amino acid residue of peptide residue of peptide sequence sequence sequence sequence TSLAGNTVQC LDMITSTDHV  1043 2393 A 8688 359 17 GLKTRAPATF	, N=Asparagine, P=Proline, R=Arginine, S=Scrine, /=Valine, W=Tryptophan, =Unknown, *=Stop codon, ectide deletion, \=possible tion
seq- uence  09/496 914  ng to first amino acid residue of peptide sequence  09/496  914  ng to first amino acid residue of peptide sequence  09/496  10/43  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10/496  10	R=Arginine, S=Serine, /=Valine, W=Tryptophan, =Unknown, *=Stop codon, ectide deletion, \=possible tion
uence  914  ng to first amino acid residue of peptide residue of peptide sequence  914  ng to first amino acid residue of peptide sequence  914  ng to first amino acid residue of peptide sequence  915  T=Threonine, V Y=Tyrosine, X= /=possible nucleotide inser TSLAGNTVQC LDMITSTDHV 1043  2393  A 8688  359  17  GLKTRAPATF	R=Arginine, S=Serine, /=Valine, W=Tryptophan, =Unknown, *=Stop codon, ectide deletion, \=possible tion
amino acid residue of peptide residue of peptide sequence	/=Valine, W=Tryptophan, =Unknown, *=Stop codon, ectide deletion, \=possible tion
residue of peptide sequence Y=Tyrosine, X= /=possible nucleotide inser TSLAGNTVQC LDMITSTDHV 1043 2393 A 8688 359 17 GLKTRAPATP	=Unknown, *=Stop codon, ectide deletion, \=possible tion
peptide	ectide deletion, \=possible
Sequence   nucleotide inser	tion
1043 2393 A 8688 359 17 GLKTRAPATF	
LDMITSTDHV   1043   2393   A   8688   359   17   GLKTRAPATF	CLNKLKYVIYSAQYPAYGNITT
1043 2393 A 8688 359 17 GLKTRAPATP	/LEODFWICFTFYSVKERQI
••••   ••••   ••   ••••   ••••	TFOREVLGPAKODMORRCPRI
	KRRWRDYKRWKSGGFTGESC
	_
	GGLQGDHSELLQWQKRILRTE
	NIFPICSYITGFL
	PITAGHSCSSGGVLQVKSPATQS
	DFNMESDSFEDFWKGEDLSNYS
:	DAAPCEPESLEINKYFVVIIYAL
1 1 1 1	LVMLVILYSRVGRSVTDVYLL
	ALTLPIWAASKVNGWIFGTFLC
KVVSLLKEV	NFYSGILLLACISVDRYLAIVHA
TRTLTQKRYI	LVKFICLSIWGLSLLLALPVLLFR
RTVYSSNVSP	PACYEDMGNNTANWRMLLRIL
PQSFGFIVPLI PQSFGFIVPLI	LIMLFCYGFTLRTLFKAHMGQK
HRAMRVIFAY	VVLIFLLCWLPYNLVLLADTLM
RTQVIQETCE	RRNHIDRALDATEILGILHSCLN
PLIYAFIGQKI	FRHGLLKILAIHGLISKDSLPKDS
RPSFVGSSSG	
l l l l l l l l l l l l l l l l l l l	NRRGAQGGKMHTCCPPVTLEQ
	VMLOTLAFAVTSLVLSCAETIDY
	CEEKDGILTVSCENRGIISLSEIS
	SGNLLNRLYPNEFVNYTGASIL
	ETGAFHGLRGLRRLHLNNNKL
	GLENLEYLQVDYNYISVIEPNAF
	ILNDNLLSSLPNNLFRFVPLTHL
	LPYVGLLQHMDKVVELQLEEN
	LKDWLDSISYSALVGDVVCETP
1	EVSKQELCPRRLISDYEMRPQTP
	PASVNSVATSSSAVYKPPLKPP
	RVRPTSRQPSKDLGYSNYGPSIA
	CCPTACSCNLQISDLGLNVNCQE
	PKPYNPKKMYLTENYIAVVRRT
l ;	LHLGNNRISMIQDRAFGDLTN
	RIERLSPELFYGLQSLQYLFLQY
	FDPVPNLQLLFLNNNLLQAMPS
l l l l l l l l l l l l l l l l l l l	LNLRSNHFTSLPVSGVLDQLKS
	WDCTCDIVGMKLWVEQLKVG
	APKKFAETDMRSIKSELLCPDYS
	SIQVPARTSAVTPAVRLNSTGA
	ASSVPLSVLILSLLLVFIMSVFVA
	RRKKNQSDHTSTNNSDVSSFN
	GGTGGHPHAHVHHRGPALPK
	EYIPHPLGHMCKNPIYRSREGN
SVEDYKDLHI	ELKVTYSSNHHLQQQQQPPPPP
	QLQLQPGEEERRESHHLRSPAYS
VSTIEPREDLI	LSPVQDADRFYRGILEPDKHCST
	PKFPCSPAAYTFSPNYDLRRPH
	SRLREPVLYSPPSAVFVEPNRNE
	VEPDYLEVLEKOTTFSQF
	WYSLALGSGSRGRDHSGSGVGT
	AADYVRSKDFRDYLMSTHFW
	IAAINDMKKSPEIISGRMTFALC
	YKVQPRNWLLFACHATNEVA
QLIQGGRLIKI	
	TLNTDGKVKSFTSPHSNPNLPP
	NWSSHLPPSPATESVGKRGNAK
	PLWNFFAQQL
1048 2398 A 8747 3 5054 PEVTKPSLSQI	PŤAASPĪĠŠSPŠPPVNGGŇNAKŔ

SEQ ID	SEQID	TMA	Lero	· n		
NO: of		Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1104	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
cotide	seq-		USSN	location	corresponding	F-Phenylalanine, G-Glycine, H-Histidine, I-Isolcucine, K-Lysine, L-Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	i	-	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ſ		[		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ì		peptide	-	/=possible nucleotide deletion, \=possible
	1			sequence		nucleotide insertion
						VAVPNGQPPSAARYMPREVPPRFRCQQDHK
	1	1	Ì	1	i	VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN
			i			PNNAQVTGALLQSESGTAPDSTLGGAAASNY
	i	1		į	l	ANSTWGSGASSNNGTSPNPIHIWDKVTVDGS
		1		i i		DMEEWPCIASKDTESSSENTTDNNSASNPGSE
	1	1	1	}	ł	KSTLPGSTTSNKGKGSQCQSASSGNECNLGV
						WKSDPKAKSVQSSNSTTENNNGLGNWRNVS
	1	}	ł	ļ	}	GQDRIGPGSGFSNFNPNSNPSAWPALVQEGTS
	1	}	1	in the second		RKGALETDNSNSSAQVSTVGQTSREQQSKME
	ł	1	ł		}	NAGVNFVVSGREQAQIHNTDGPKNGNTNSL
				]		NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ
	1	1	ļ			STGDRKTGSVGSWGAARGPSGTDTVSGQSNS GNNGNNGKEREDSWKGASVQKSTGSKNDS
		1		;		WDNNNRSTGGSWNFGPQDSNDNKWGEGNK
	]	l	}	1 1		MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN
	İ					SSTGAWDNQKGHPLLENQGNAQAPCWGRSS
	J	1		,		SSTGSEVEGQSTGSNHKAGSSDSHNSGRRSY
	1	ł	1	<b>!</b>		RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG
		J	,	]		QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES
			Ì			AATQTKNSGGWGDAPSQSNQMKSGWGELS
	J	}	]	] ]		ASTEWKDPKNTGGWNDYKNNNSSNWGGGR
		1	1			PDEKTPSSWNENPSKDQGWGGGRQPNQGWS
		1	1			SGKNGWGEEVDQTKNSNWESSASKPVSGWG
			1			EGGQNEIGTWGNGGNASLASKGGWEDCKRS
		į.	1			PAWNETGRQPNSWNKQHQQQQPPQQPPPPQ
	1	ĺ	1	[		PEASGSWGGPPPPPPGNVRPSNSSWSSGPQPA TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG
		ļ				DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP
	i	ĺ	1 1	1		MTSKSASDSKSMQDGWGESDGPVTGARHPS
	1		i l	ľ		WEEEEDGGVWNTTGSQGSASSHNSASWGQG
	1 !		1 1	ĺ	Ì	GKKQMKCSLKGGNNDSWMNPLAKQFSNMG
	1		}	ļ		LLSQTEDNPSSKMDLSVGSLSDKKFDVDKRA
	1 1		í í	Í	ĺ	MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS
			l l		į	GPYFEKGGSHGLFGNSTAQSRGLHTPVQPLN
	ľ		1 1	ľ	i	SSPSLRAQVPPQFISPQVSASMLKQFPNSGLSP
	1 1		1 1	İ	ŀ	GLFNVGPQLSPQQIAMLSQLPQIPQFQLACQL
	1 1		1 1	1	ł	LLQQQQQQLLQNQRKISQAVRQQQEQQLA
	j		1 1	1	İ	RMVSALQQQQQQQQQQRQPGMKHSPSHPVGPK
	}		}	l	ł	PHLDNMVPNALNVGLPDLQTKGPIPGYGSGF
	1 1		} }	1	1	SSGGMDYGMVGGKEAGTESRFKQWTSMME GLPSVATQEANMHKNGAIVAPGKTRGGSPY
	<b>!</b>		1 1		1	NQFDIPGDTLGGHTGPAGDSWLPAKSPPTNK
	<b>!</b>				İ	IGSKSSNASWPPEFQPGVPWKGIQNIDPESDP
i	1 1			}	1	YVTPGSVLGGTATSPIVDTDHOLLRDNTTGS
				ľ	}	NSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK
				J		FPDYKSTWSPDPIGHNPTHLSNKMWKNHISS
				}		RNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRG
j	)	,	j	j	J	WGTQDSRLASASTWSDGGSVRPSYWLVLHN
		ļ		ĺ		LTPQIDGSTLRTICMQHGPLLTFHLNLTOGTA
ļ				1		LIRYSTKQEAAKAQTALHMCVLGNTTILAFF
- 1		ĺ	[	[		ATDDEVSRFLAOAOPPTPAATPSAPAAGWOS
}		[	1	- 1	ì	LETGQNQSDPVGPALNLFGGSTGLGOWSSSA
	- 1	ĺ		ſ	ſ	GGSSGADLAGASLWGPPNYSSSLWGVPTVED
049	2399		9749	700		PHRMGSPAPLLPGDLLGGGSDSI
( 5-0	2377	^	8748	200	1387	VPWKRQDEQLSLQVETLYLDSPAVIHLLSPTF
1		1	1			LPPSSLPPFLQIVDSSSSACTLDSFFPFLAPWDS
ŀ		}	1	1	}	PQDCGFKDHQPLTLQALTVELARWTLMLLLS
		1	,			
	-					TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT
,			ļ		j	TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA PFALSALLYGANNNLVIYLQRYMDPSTYQVL

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ucii.cc	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}	]	7,4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ	1		İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ľ		1	l		sequence	/=possible nucleotide deletion, \=possible
Ì	l	1	ł	peptide		
	ļ	ļ	ļ	sequence		nucleotide insertion
	1		ļ		ļ	SNLKIGSTAVLYCLCLRHRLSVRQGLALLLL
ŀ	ł	İ	!	ł	ł	MAAGACYAAGGLQVPGNTLPSPPPAAAASP
1				1		MPLHITPLGLLLLILYCLISGLSSVYTELLMKR
Į.			İ			QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP
			İ			GLLEGFSGWAALVVLSQALNGLLMSAVMKH
ļ.	1	}	İ	ļ	1	GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
				1		FFLATLLIGLAMRLYYGSR
1050	2400	A	8758	3	1660	WVSSMGFEELLEQVGGFGPFQLRNVALLALP
1030	2.00	1	0,50	1 3		RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
ţ	ì		ì			HODVWLEAHLPREPDGTLSSCLRFAYPQALP
ļ		l l	1			NTTLGEERQSRGELEDEPATVPCSQGWEYDH
1			1	1		
}		1	1		l	SEFSSTIATESQWDLVCEQKGLNRAASTFFFA
1	i	Í	i	<b>{</b>		GVLVGAVAFGYLSDRFGRRRLLLVAYVSTLV
1	1	1	I.	,		LGLASAASVSYVMFAITRTLTGSALAGFTIIV
1	1	1	ĺ	1	1	MPLELEWLDVEHRTVAGVLSSTFWTGGVML
1	1	l	1	ĺ		LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
	]			1	Ì	VPESARWLLTQGHVKEAHRYLLHCARLNGR
+	1			•		PVCEDSFSQEAVSKVAAGERVVRRPSYLDLF
i	1	1	(	ĺ		RTPRLRHISLCCVVVWFGVNFSYYGLSLDVS
1		i	i			GLGLNVYQTQLLFGAVELPSKLLVYLSVRYA
				1	İ	GRRLTOAGTLLGTALAFGTRLLVSSDMKSWS
i				i		TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR
1		1		1	ł	QTGMGLTALVGRLGGSLAPLAALLDGVWLS
1	1	1	i.			LPKLTYGGIALLAAGTALLLPETRQAQLPETI
į	1		1	1		QDVERKSAPTSLQEEEMPMKQVQN
1051	2401	A	8759	515	1625	EIRTPVAVSSAPSGDSEGDEEETTQDEVSSHTS
1031	2401	A	8/39	313	1023	
1		1	1		į	EEDGGVVKVEKELENTEQPVGGNEVVEHEV
1		İ	1		ĺ	TGNLNSDPLLELCQCPLCQLDCGSREQLIAHV
1					į	YQHTAAVVSAKSYMCPVCGRALSSPGSLGR
ł		İ				HLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
		1	1	1		EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYP
J	1	1	i	ŀ		AGILLVCNNCAAYRKLLEAQTPSVRKWALRR
ļ.		1			ļ	QNEPLEVRLQRLERERTAKKSRRDNETPEERE
i		Ì				VRRMRDREAKRLQRMQETDEQRARRLQRDR
Į.		1	1	İ	1	EAMRLKRANETPEKRQARLIREREAKRLKRR
i		]	[			LEKMDMMLRAQFGQDPSAMAALAAEMNFF
1	1	1				QLPVSGVELDSQLLGKMAFEEQNSSSLH
1052	2402	A	8763	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
		1 .,	1 3.33	1100	1 . •	ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
1	1	1	i	ĺ		HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY
1	1	1				
j	1	)	1		]	PATGADVAFSVNHLLGDPMANVAMAYGSSI
1	I	1	1	t	1	ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
l	1	1				YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
1		!		1		RQDLNAPDLYIPTMAFITYVLLAGMALGIQK
	l .		1	1		RFSPEVLGLCASTALVWVVMEVLALLLGLYL
			i			
						ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
						ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
						LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
1053	2403	Ā	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
1053	2403	A	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
1053	2403	Ā	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
1053	2403	Ā	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE
1053	2403	A	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVVYTPW
1053	2403	A	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVYYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK
1053	2403	A	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVYSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER
1053	2403	A	8768	2	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVVYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER NEKKAQIQEMKKREKEEMKKKREMDELRSY
						LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVYYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER NEKKAQIQEMKKREKEEMKKKREMDELRSY SSLMKVENMSSNQDGNDSDEFM
1053	2403	A	8768	344	712	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVVYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER NEKKAQIQEMKKREKEEMKKKREMDELRSY
						LFGSDGYYVALAWTSSALMYFIVRSLRTAAL GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNNVNVYYTPW SNLKKTADMDVGQIGFHRQKDVKIVTVEKK VNEILNRLEKTKVERFPDLAAEKECRDREER NEKKAQIQEMKKREKEEMKKKREMDELRSY SSLMKVENMSSNQDGNDSDEFM

SEQ ID	CEATO	14-4	660	Predicted	Dradiot-1 1	Amino acid sequence (A=Alanine C=Cysteine,
MICh of	SEQ ID NO: of	Met hod	SEQ ID NO:	beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of nucl-	peptide	11100	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	derice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
dence	}		1 /14	amino acid	of peptide	T-Threonine, V=Valine, W=Tryptophan,
			}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	5545555	/-possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
1055	2405	A	8770	430	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK
		1		1		KMLKCVVVGDGAVGKTCLLMSYANDAFPEE
	ļ	l	1			YVPTVFDHYAVTVTVGGKQHLLGLYDTAGQ
					į.	EDYNQLRPLSYPNTDVFLICFSVVNPASYHNV
				Į.		QEEWVPELKDCMPHVPYVLIGTQIDLRDDPK
		1		í	1	TLARLLYMKEKPLTYEHGVKLAKAIGAQCYL
	1				İ	ECSALTQKGLKAVFDEAILTIFHPKKKKKRCS
				]		EGHSCCSII
1056	2406	A	8773	261	332	NPRIQLSGNSCCAGSCRVWLSEQ
1057	2407	A	8778	3	477	PAGIRHEQARGADRMGKCRGLRTARKLRSH
						RRDQKWHDKQYKKAHLGTALKANPFGGAS
	İ				]	HAKGIVLEKVGVEAKQPNSAIRKCVRVQLIK
		1		<b>†</b>	}	NGKKITAFVPNDGCLNFIEENDEVLVAGFGR
	ļ	1	}	ì	İ	KGHAVGDIPGVRFKVVKVANVSLLALYKGK
		ļ <u></u>				KERPRS
1058	2408	A	8808	171	881	PGLSQEPSGSMETVVIVAIGVLATIFLASFAAL
		1			1	VLVCRQRYCRPRDLLQRYDSKPIVDLIGAME
	ļ	1	}	]	}	TQSEPSELELDDVVITNPHIEAILENEDWIEDA
,		1	1		,	SGLMSHCIAILKICHTLTEKLVAMTMGSGAK
	į					MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
				[		DPKLLDARTTALLLSVSHLVLVTRNACHLTG
	Į.					GLDWIDQSLSAAEEHLEVLREAALASEPDKG
1059	2409	A	8809	246	757	LPGPEGFLQEQSAI MRLOGAIFVLLPHLGPILVWLFTRDHMSGWC
1039	2409	^	0009	246	'3'	EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY
	1					LVWKDLGGGLGWPLALPLGLYAVOLTISWT
		1				VLVLFFTVHNPGLALLHLLLLYGLVVSTALI
	l	l	1	ł		WHPINKLAALLLLPYLAWLTVTSALTYHLWR
		1				DSLCPVHQPQPTEKSD
1060	2410	A	8810	304	381	PKLSVYPLQSHHCLSEPFQSLVCCLA
1061	2411	A	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA
	l	)	1			FIFSYITAVTLHHIDPALPYISDTGTVAPEKCLF
				i		0.100.00.00.00.00.00.00.00.00.00.00.00.0
						GAMLNIAAVLCIATIYVRYKQVHALSPEENVI
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET
1062	2412	A	8824	1	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI
1062	2412	A	8824	i	763	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGK VILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGK VILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV
1062	2412	A	8824	1	763 627	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPFKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPFKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTORALH
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGK VILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPFKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL
1063	2413	A	8826	147	627	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGK VILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTORALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTTLSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE
1063	2413	A	8826	147	627	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV
1063	2413	A	8826	147	627	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPFKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTORALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV TAEYIHKAEHEKLMQLTNVSRAKAEDALSE
1063	2413	A	8826	147	627	IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLHMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV

CCC ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	1	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	1	noa	L	beginning		
nucl-	peptide	i	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		į	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		}	ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		i	i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \-possible
		1		sequence		nucleotide insertion
	<del></del>	<del>                                       </del>		sequence	<del></del>	
	, '			ĺ	ĺ	VAKLEKQLLEEKAAMTDAMVPRSSYEKLQS
						SLESEVSVLASKLKESVKEKEKVHSEVVQIRS
	1	1		1	}	EVSQVKREKENIQTLLKSKEQEVNELLQKFQ
				İ		QAQEELAEMKRYSESSSKLEEDKDKKINEMS
ì		1	1	ì	1	KEVTKLKEALNSLSQLSYSTSSSKRQSQQLEA
						LQQQVKQLQNQLAECKKQHQEVISVYRMHL
	i				ł	LYAVOGOMDEDVOKVLKQILTMCKNQSOK
ļ	1	i	1	1	1	
	I	ļ	<u> </u>	ļ. <u>.</u>		K
1065	2415	A	8841	3	663	AAATAASLSPRGCRLRTPSSDVGPSRAPPPSA
	1	1		1		APLPTGRAQMSPSGRLCLLTIVGLILPTRGQTL
1	1	!	1			KDTTSSSSADATIMDIQVPTRAPDAVYTELQP
	1	1	1	1		TSPTPTWPADETPQPQTQTQQLEGTDGPLVT
1	I	1	1			DPETHKSTKAAHPTDDTTTLSERPSPSTDVQT
1	1		1	1	i	
1	1		1	[	1	DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA
	<del> </del>	1	1		\	AVLFITGIIILTSGKCRQLSRLCRNHCR
1066	2416	A _	8853	3806	2204	FVGEQEGGCEAGAGRGAQTYPGEAGERWFG
						RRRRGRVVSRKKMSLKSERRGIHVDQSDLL
1	i	1	1	1	[	CKKGCGYYGNPAWQGFCSKCWREEYHKAR
		1			Ī	QKQIQEDWELAERLQREEEEAFASSQSSQGA
			1			<b>QSLTFSKFEEKKTNEKTRKVTTVKKFFSASSR</b>
				İ		VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE
			1	}	ļ	1
					•	FLKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE
l .	İ			1		EQSECAQDFYHNVAERMQTRGKVPPERVEKI
		1		ŀ		MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI
				İ		QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV
	E	1		i	1	KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI
			i		<b>!</b>	KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI
			1	1	1	QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE
		1		ļ		
	1	Į.	1	1	1	KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES
						WSPDACLGVKQMYKNLDLLSQLNERQERIM
			1			NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI
1			ſ	ļ	Ì	KPPNQPLAAIDSENVENDKLPPPLQPQVYAG
1067	2417	A	8855	1372	1513	SNMREVGCGWLVPVIPAFWEAEVGGSLEARS
			5557		1010	LRQAWATKQDPISKKK
1068	2418	<del>  </del>	8856	1530	1583	PCRPGMECNSMISVHCNL
		A				<u> </u>
1069	2419	A	8857	1530	1583	PCRPGMECNSMISVHCNL
1070	2420	A	8866	293	1675	PYPQGGYPQGPYPQEGYPQGPYPQGGYPQGP
1	l	ŀ	1		1	YPQSPFPPNPYGQPQVFPGQDPDSPQHGNYQ
l .	i		1	]		EEGPPSYYDNQDFPATNWDDKSIRQAFIRKVF
	1	1	1	I		LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV
	1	Į.	1	1		WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL
!	1		1	1	1	VALSVLTASLSYMVGMIASFYNTEAVIMAVG
1	1	İ	1	1	1	
ł	ŀ		1	ì		ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM
I	1		1	I		VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA
	1	1	[	I		VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI
i	1	1	[	(	[	FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP
1	1	1	1	}	1	WHGSASCTSPLSCPQAQPREKDASLQPSCMY
ł	1	1	1	I	1	TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC
	I	ŀ	1	I		HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ
J	1	ł	1	Į.	1	
	ł	1	1	1	[	EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS
	<u> </u>	L	<u> </u>	L	L	GDMRSGGLIPVLSPE
1071	2421	A	8868	2	358	ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH
l		l	1	1	1	DDKMGSNTFFKRNDCRYVMISCKADMAYDN
Ī	1	İ	1	ſ	ĺ	VRHPFMI*SI\KLIMEETYLNIIKAVYDRPTASII
	1	1	1	ļ		LNGEKLKVFPVRSGT*OGCSVWP
1000	1 2425	<del> </del>	10055	12		
1072	2422	A	8870	33	658	MESVLSKYEDQITIFTDYLEEYPDTDELVWIL
		l				GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI
1	1	1	1	[		GGTGPSSDAGWGCMLRCGQMMLAQALICRH
l	1	1	1	1		LGRDWSWEKQKEQPKEYQRILQCFLDRKDC
	1	1	1	1		

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Decision			ŀ		1		
			1 .104			1	
Sequence			ļ				
United   September   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United   United		. •					
amino acid residue of peptide residue of peptide residue of peptide sequence		uerice	ļ				
Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Sequence   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Pep	uence	1	l	914			
peptide		ļ			t .		
		1			B .	sequence	
CYSHIQMAQMGYGEKSIGEWYLGPNTVAG   GV*KNLAUFDEWNSLGLVYYSMDNPSGSIA   GV*KNLAUFDEWNSLGLVYYSMDNPSGSIA   GV*KNLAUFDEWNSLGLVYYSMDNPSGSIA   GV*KNLAUFDEWNSLGLVYYSMDNPSGSIA   GV*KNLAUFDEWNSLGLVYSMDNPSGSIA   GV*KNLAUFDEWNSLGLVYSMDNPSGSIA   FFFKLCKVLPLSADTAGLTGP    DFSV*GDVDEWTCPTCLQLUTEPLSLNCGGRL   GV*CVCTA*IKESVIISGG*SSPVCHTTFQPANL   RTSRYLPTSISKLGGPEPOGE    1074	j						
1073   2423   A   8879   146   412   DFSV*GDVDIEVTCPICLQLLTEPLSLNCGGLL		<u> </u>		ļ <u></u> .	sequence	<u></u>	
1073   2423   A			i	1			
1073		!		l			
*QVCITA*IKESVILSGG*SSSPVCHTI*FQPANL RISRYLP*PISIKLGPDEPGG*   1074   2424   A	1	1	ŀ				RFPKKLCRVLPL\SADTAGLTGP
1074   2424   A   8884   67   435	1073	2423	Α	8879	146	412	DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
1074				i .		t	*OVCITA*IKESVIISGG*SSSPVCHTTFOPANL
1074		Ì	!			}	RTSRYLPT*SIKSLGPDEPOEG
KEISFODYICHTFOODCWADRSPLHAAAHG   RILALKTLIQGWNYNLDAYSSLHEACL   GPYACAKPY WKMPRHGGTVTOPPLLMV   1075   2425   A   8896   1294   248   RSGDRNGLTHQLGGLSGSRNGSYRSRSSRS   RSEPSAPPGIPPASASSSVYYGSVSRPYGSDSK   SREEPSAPPGIPPASASSSVYYGSVSRPYGSDK   PWPSLLDKERESLROCKELGAPE   VWGLSPRNTEPPDSDEHTFVEDEERKSKRSKRSKRSKRKKK   KYSDEDSDSDSDEDTSDSDEDTMSREAKKAKKK   KYSDEDSDSDSDETDSDDNKRAKKAKKK   KYSDEDSDSDSDETDSDDNKRAKKAKKK   KYSDEDSDSDSDETDSDSDDNKRAKKAKKK   EKKKKHRSKKYKKRSKRSKRSKRSKRKKKKKKSKSKRSKRIKK   KYSDEDSDSDSDETDSDSDSTMRAKKAKKK   EKKKKHRSKKYKKRSKSKRSKRSKSKRSSSSSKES   QEFFLENFWADRTHALPGEGAAMAEYVKAGKRI   PRRGEIGLTR*RNCHHLNOVM*V*VVSRIHRR   MEAVRTAKREPESTVLMRREPLHPFNFRET   KERE   GRSTEAEKPAFDERTGKGRKLPRAGEFHG*E   KERE   GRSTEAEKPAFDERTGKGRKLPRAGEFHG*E   VYTUSSREVKAESSGKRGCPSPSPSEVR   VSTSAMVDPKGSIPRPSRYPVDSVLSRGKE   LLQKAIRNOK**CTVQD,GGVIEGFLSKE   VSTYNSKREVKAESSGKRGCPSPSPSEVR   VSTSAMVDPKGSIPRPSRYPVDSVLSRGKE   LLQKAIRNOK**CTVQD,GSHCILVGFR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYIQEL WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGAYKYICH WRKKOGVIKFLOWSPR   AKIGA	1074	2424	A	8884	67	435	
RILALKTLIAQGYNVNILWTLDRVSSLHEACL	10.14	~	1	0001	٠,	.55	
*GPVACAKPY WKMYPRHGITVTGPILMV	1					}	
1075	1			1			
SRERPSAPRGIPPASASSSVYYGSYSRPYGSDK   PWPSLLDKERFERIRGICAPE	1055	0.105		2006	1004	2.10	
PWPSILDKEREESIQKRISERERIGEIGAPE	1075	2425	I A	8896	1294	248	
VWGLSPKNPPDSDEHTPVEDEPKKSTTSAS   TSEEKKKKSSRKKKKKKSSKRKIK   KY9EDSDSDSDENDRRAAKKAKK   EKKKKKRSKKYKKKSSKRJKIK   KY9EDSDSDSDESDEDNRRAAKKAKK   EKKKKHSKKYKKRSKSSRKJKS   EKKKKHSKKYKKRSKSSRKJKS   OEPHLENPWLDRTKAEPSDLIGPEAPKILTS   ODDKPLNYGHALLPGEGAAMAEYVKAGKRI   PRRGEIGLTR*RNCHHLNAQVM**VVSRIRR   MEAVRTAKREPESTVLMRREPLHPFNPRRET   KERE		1		į		İ	
TSEEEKKKKSSKRKIKK   KYSEDSDSDSDSDEDDNRRAKKAKKK   KYSEDSDSDSDSDEDDNRRAKKAKKK   EKKKHRSKYKKKRSKKSRKESDSSSKES   QEFLENFWKDRTKAEEPSDLIGPEAPKILTS   QDDKPLNYGHALLPGEGAAMAEYVKAGKRI   PRRGEIGLTR*RNCHHLNAQVM**VYSRIRR   MRAVRTAKKEPESTUMREPELIFPPRRETI   KERE	1	ì	ļ			}	
KYSEDSDSDSETDSSDEDNKRRAKKKK   EKKKHRSKKYKKSESSSSSSESES    CEFFLENPWKDRTKAEEPSDLIGPEAPKTLTS     ODKPLNYGHALLPGEGAAMASYVKAGKRI     PRRGEIGLTR*RNCHHLMAQVM**VVSRIRR     MEAVRTAKREPESTVLMRREPLHFFNPRRET     KERE			ŀ	j .			
	i		i	ļ	!		
QEEFLENPWKDRTKAEEPSDLIGPEAPKITTS   QDDKPLNYGHALPGEGAAMAEYVKAGKI   PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR   MEAVRTAKREPESTVLMRREPLHPFNPRRET   KERE				i		1	KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
ODDKPLNYGHALLPGEGAAMAEYVKAGKRI   PRRGEIGLTR*RNCHILNAQVM**VVSRIRR   MEAVRTAKREPESTYLMRREPLHPFNPRRET   KERE	ļ			ļ		}	EKKKKHRSKKYKKKRSKKSRKESSDSSSKES
PRRGEIGLTR*RNCHHLNAQVM**VVSRIRR	1					1	QEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
MEAVRTAKREPESTVLMRREPHPFNPRRET   KERE		ŀ	ļ	ļ			QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
MEAVRTAKREPESTVLMRREPHPFNPRRET   KERE		ŀ	1	ļ	}	}	PRRGEIGLTR*RNCHHLNAOVM**VVSRHRR
1076		1	}				
1076	•						
**POPPRESFQVSRKMPEEIPPGARKHPFSGKS FYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKE VSYIVSSREYKAESSGKSHRGCPSPSPSEVR VETSAMVDPKGSHPRSRRYPDSVPLSRGKE LLQKAIRNOK**CTVQQLSHCRLYGEKTTAK RSQREHVQQQSQEHGKWPDLKGPR 1077 2427 A 8901 352 3 AKIGAYKYIQELWRKKQSDVMHFLLRVRCW QYPALHRAGTEWQLSALHRAPRSTQPDKAC RLGYKAKQGYIIYRICVRRGGWKCPVPKAVT 'YGKPVHHGVN*LKFAQSLQSVAEEQ 1078 2428 A 8905 536 781 ACPAENREVPEMAAGQAPHAGPGAGPGQPA PALPFAATTGSRGQALCRGGRRRQHLHGPLH RPPQAPALHAGCQLAPHPT 1079 2429 A 8912 121 376 NLIWKLCVTERRLVILDNYDLASE/YEANKYI CNRIIGFKPGQDKYFILGLPTGSTPL-CYPKLI EYNKNGHLSKYVKTESMDEY 1080 2430 A 8920 381 1788 SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG GHSLFSCEPITLRMCQDLPYNTTFMPNLLNHY DQQTAALAMEPFHPMVNLDCSRDFRFFLCAL YAPICMEYGRVTLPCRRLCQRAYSECSKLME MFGVPWPGMECSRFPDCDEFYPRLVDLNLA GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY SFLHVRDCSPPCPNMYFRREBLSFARYFIGLIS IICLSATLFIFVTFLDVTRFTYPERPIKCYAV WHMMYSLIFFUGFLLEDRVACNASIPAGYKA STVYLGSHNKACTMLFMILYFTTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVGAPLCLYVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIGERC 1081 2431 A 8922 56 420 EERIKMSTGPDVKATVGDISSDORINVAQGE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVPCSVRHGLALILQLCNFSIYTQQMN LSIAPJAMVNNTAPPSQPNASTERPST	1076	2426	Δ	8899	146	789	
FYLDLPAGKNLOPLTGAIQQLGGVIEGPLSKE VSYIVSSRREVKAESSGKSHRGCPSPSPSEVR VETSAMVDPKGSIPRPSRKPVDSVPLSRGKE LLQKARINQK**CTVQQLSHCRLYYGEKTTAK RSQREHVQQOSQEHGK WPDLKGPR  1077 2427 A 8901 352 3 AKIGAYKYIQELWRKQSDVMHFLLRVRCW QYPALHRAGTEWQLSALHRAPRSTQPDKAC RLGYKAGQYIIYRICVRRGGWKCPVPKAVT YGKPVHHGVN*LKFAQSLQSVAEEQ  1078 2428 A 8905 536 781 ACPAENREVPEMAAGQAPHAGPGAGPQQPA PALPFAATPGSRGQALCRGGRRQHLHGPLH RP*QAAPALHAGCQLAPHPPT  1079 2429 A 8912 121 376 NLIWKLCVTERRLVILDNYDLASE/YEANKYI CNRIQPKPGQDKYPTIGLPTGSTPL*CYPPKLI EYNKNGHLSFKYVKTFSMDEY  1080 2430 A 8920 381 1788 SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG GHSLFSCEPITLRMCQDLPYNTTFMPNLUNHY DQQTAALAMEPFHPMVNLDCSRDFRPFLCAL YAPICMEYGRVTIPCRRLCQRAYSECSKLME MFGVPWPEDMECSRPPDCDETYPRLVDLNLA GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY SFLHVRDCSPPCPNMYRREBLSFARYFIGLIS IICLSATLFTFVTFLIDVTRFRYPERPIKCYAV WHMMVSLIFTUGFLLEDRVACNANSIPAQYKA STVTQGSHKACTMLFMILYFTFTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKLIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSIL,YVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVFCSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1010	2420	l ' <b>`</b>	""	140		
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YAPICMEYGRVTLPCRRLCQRAYSECSKLME MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS IICLSATLFTIFVITFLIDVTRFRYPERPIKCYAV WHMMVSLIFFIGFLLEDRVACNA\SIPAQYKA STVTQGSHNKACTMLFMILYFFTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1			1			
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GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY SFLHVRDCSPPCPNMYFRREBLSFARYFIGLIS IICLSATLFTFVTFLDVTRFRYPERPIKCYAV WHMMVSLIFFIGFLLEDRVACNA\SIPAQYKA STVTQGSHNKACTMLFMILYFFTMAGSVWW VILTITWFLAAVPK\WGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIGERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	]	J	J	] .			
SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS IICLSATLFITVIFLIDVTRFRYPERPIKCYAV WHMMVSLIFFIGFLLEDRVACNA\SIPAQYKA STVTQGSHNKACIMLFMILYFITMAGSVWW VILTITWFLAAVPK WGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST		l		1			
IICLSATLFTFVTFLIDVTRFRYPERPIKCYAV WHMMVSLIFFIGFLLEDRVACNA\SIPAQYKA STVTQGSHNKACTMLFMILYFFTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1	l	l				
WHMMVSLIFFIGFLLEDRVACNA\SIPAQYKA STVTQGSHNKACIMLFMILYFFTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1	l	1	1 1			
STVTQGSHNKACTMLFMILYFFTMAGSVWW VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST		!		ļ i			
VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST		į		}			WHMMVSLIFF\IGFLLEDRVACNA\SIPAQYKA
VILTITWFLAAVPKWGSEAIEKKALLFHASA WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST		Ì	1	[		;	STVTQGSHNKACTMLFMILYFFTMAGSVWW
VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVFCSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	]	ļ		}			VILTITWFLAAVPKWGSEAIEKKALLFHASA
VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVFCSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST				[			WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST				j 1			VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
VVIGCYFYEQAYRGIWETTWIQERC  1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST		} ,	l	}			
1081 2431 A 8922 56 420 EERTKMSTGPDVKATVGDISSDGNLNVAQEE CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST			Ì	[			
CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1081	2431	Δ	8022	56	420	
TLANFVF\CSVRHGLALILQLCNFSIYTQQMN LSIAIPAMVNNTAPPSQPNASTERPST	1001	2451	^	0,222	50	720	
LSIAIPAMVNNTAPPSQPNASTERPST		l		j l	:		
				1 1			
1082 2432 A 8923 355 1079 PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV	1000	0.425	<u> </u>			1050	
	1082	2432	A	8923	355	1079	PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M-Methionine, N-Asparagine, P-Proline,
uence	3,3,5,5		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
5555	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
<b>l</b> :		<u> </u>	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
[		ŀ	1	peptide	Sequence	/=possible nucleotide deletion, \=possible
1		ļ	ì	sequence		nucleotide insertion
				Sequence	<del>-</del>	GPFSKKDQYDVKAPAMFNIRNTGK/TLVART
			ļ	ł	1	OGTOIASDGLKGLLFEVSLADLONDEVAFRK
		]	]	]		FKLITEDVODKNCLTNFYGMDLTCDKICSMV
<u> </u>		ļ	1			EKWSTMIEAHVDVKTTDGYFFHLFCVGFTKK
!		Ì	1	l		HNNQILKTSYA*HQQS/RQIQKKMMEIMT*EV
1			1	İ	}	OTNDLKEVVNKLIPDNIGKDTEKV/CPIYPLH
1 1		ĺ	ĺ	i	•	DVFIRKVKMLENPGFER\MELRGGGSSS
1083	2433	A	8948	28	385	LTWPOPHIPSCPAMSEETLOSKLAAAKKKLP
1003	2433	\ \hat{\chi}	0,70	20	1 303	WGAVQGSRAMSDLLLLLLDLTLLLLLMLLGF
	ļ		1			AGYSGQLAGVAVSAGSPPI/RYKFHVEPYGET
}			1			GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084	2434	A	8950	156	318	HYTPINTDTIENSENNKCW*GY*E\VGLIHHW
1004	2454	Α.	8930	130	310	WGGKRVOPFWKRVWOKRTLNLRV
1085	2435	A	8956	16	413	HMGQLGYFIQCWWECKRLISF\WKTI*QSPAK
1083	2433	l A	0930	10	413	*TIYTSYDTAIPIS/GI/YPKRMSSKCHOETCAR
		ł				MFILAPFTATIKGKOLTCPLVEERIDY\MWYS
'	,	İ	ŀ	l .		HKYYIKVKRNL+VTITH\TWVNLNILMFEIILW
<b>!</b>	ł		i		ļ	YSHKYY
1086	2436	A -	8962	868	1026	H*KILQVGRAQRAHXSRL*SQLLRRLRHESHL
1086	2430	A	8902	000	1026	NPGARGCSEARLHRCTPAWTT
1007	2437		0005		330	LHVKHLGHFOLVFSEVICHCILMPVS*ELORL
1087	2437	A	8985	58	330	
1		1	1	1	]	*ERSVCAFHVCIQTYVCLQVYACMCVYYICM
1000	2420	<b></b> _	0000	204	404	FVYSVYGCGLCTCVCMDVYICVCVQEFL
1088	2438	A	8989	394	404	N*KWILHVNVRIQSIFF/IKRNQK/INSHELKLD
	1	1				KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA
					İ	KYTVKRIKIHPTDLEKMLRNHLSDKD*YS/GV YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE
i i		l	1			VISMENKHKKIFSTS
1089	2439	A	8991	60	329	MALTPESPSSFPGLAATGSSVPEPPGGPNATL
1099	2439	A	8991	00	329	NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV
	1	[		<u> </u>		GVEDNAYTLEVNSRYMRAVGIM*IHL
1090	2440	<b>-</b>	8996	2	351	SNITITLT*MKKYDNTFCW*GCGQIG/T/LIYC
1090	2440	A	0990	4	331	WQESKFIQAFWSKIQQYLA*ISIHILFDPAFLFL
						GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR
] .	•	1		1		
1001	2441		0007	07	152	LLIAALFIIVQYWKQSKDHYI
1091	2441	A	8997	97	456	YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT
		1	1	1		LVSSRFKISKVIVVGDLSVGKTCLINR*GGAG
[		1		J _		AELGRVGPSLARWAGSRSQHLVPSQ\VCKDS
1092	2442	A	8999	548	811	FDKNYKAPIGADFEMERFEVLGIPF SSFIKRHILIFEDDWHQTTCCHHPHHP\F*RCQ
1092	2442	^	עצינס	348	011	FHIFYVSVONSISPSLSVSSSHPDRPDHEVHOH
				I		RAAHHOHGOGPLGHGLVARVG
1002	7442		0002	3	2745	
1093	2443	A	9002	³	2745	ALLGLQQPAQSLILSRSSVMGVRGLQGFVGS
<u> </u>			1	[		TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD
! ;		1	1	1		AMCCLRYWYTPESWICGGQWREYFSALRDF
1		1	1	İ		VKTFTAAGIKLIFFFDGMVEQDKRDEWVKRR
į i		ĺ	1	i	İ	LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA
		1	1	1		VFTRFALKTLGQETLCSLQEADYEVASYGLQ
[		!	İ	1		HNCLGILGEDTDYLIYDTCPYFSISELCLESLD
}			1	1	}	TVMLCREKLCESLGLCVADLPLLACLLGNDII
		1		1		PEGMFESFRYKCLSSYTSVKENFDKKGNIILA
		1		1		VSDHISKVLYLYQGEKKLEEILPL/VTKQSSFL
]		1	1	1		*RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP
		ļ	1	1		RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP
1		Ì	l	[		GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG
1		1		1		PESRREVPMCSDPEPRQEVPMCTGPEPRQEVP
i	I	ı	1	I	I	MCTGPEARQEVPMCTDSEPRQEVPMCTDSEP
		l				DODUM GITTOEPH OPIN GITTOPEN OPIN GI
			]			RQEVPMYTGSEPRQEVPMYTGPESRQEVPMY TGPESRQEVLIRTDPESRQEIMCTGHESKQEV

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline. Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \text{\text{\colored}}possible nucleotide insertion  PICTDPISKQEDSMCTHAENQKLPVATDFEFK
						LEALMCTNPEIKQEDPTNVGPEVKQQVTMVS DTEILKVARTHHVQAESYLVYNIMSSGEIECS NTLEDELDQALPSQAFIYRPIRQRVYSLLLED CQDVTSTCLAVKEWFVYPGNPLRHPDLVRPL QMTIPGGTPSLKILWLNQEPEIQVRRLDTLLA CFNLSSSREELQAVESPFQALCCLLIYLFVQV DTLCLEDLHAFIAQALCLQGKSTSQLVNLQP DYINPRAVQLGSLLVRGLTTLVLVNSACGFP WKTSDFMPWNVFDGKLFHQKYLQSEKGYA VEVL/CRTK*ISAHQIPQPEGSRLQGLHEGEQT HHWPSPLGLTPRREVGKTGLQLPQDGLWV
1094	2444	A	9021	97	834	AREACRAKTDFPGRRFRLWPSCCCRVIVGAE T*HMAEPVSPLKHFVLAKKAITAIFDQLLEFV TEGSHFVEATYKNPELDRIATEDDLVEMQGY KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSVI NAMLWDKVLPSGIGHITNCFLSVEGTDGDKA YLMTEGSDEKKSVKTVNQLAHALHMDKDLK AGCLVRVFWPKAKCALLRDDLVLVDGPGTD VTTELDSWIDKFCTKSSTREITNSGSDT
1095	2445	A	9022	1	537	LVLNSRVEDFVPPEGAGRTLPFALRPLAACW LLHRRARRSSALCPRPRSWGVSGGEGAGARE P*ITSSSCCLSAA/SHLSIQSPNMAGARRRIRPQ LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV FAYGQT\GAGKTYTMGTGFD
1096	2446	A	9029	1	285	FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL GQHSETPSLKKKVLAGYSGMCL*SQVLRRLRQ EDCLSPGGGNCRES*SCPYTPAWITERDPV
1097	2447	Α	9032	716	357	ARSTGFWGEILWCGFLKRSLALSPRVKCSGAI LAHCNFRHAGFPPLSCLSLPNRWEYRRPPARP GKFFLVFLVETGFQC/G*DGLDLLTSRSACLG LPKCWDYRREPAASIIFQTTFFINSK
1098	2448	A	9038	230	652	KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ G*AALDHLKVFDRIPLPYDKKKQMAVSATLE VVRPKP*RKFAYLGHWAQKVDWKYQAMTA TMGEKRKVYYQKICYQKK
1099	2449	A	9043	185	372	IIFYSHQQCMRVIWQGCGDIETLIHCW*E*KII HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP RKIKTCPQNSCTSMLINAIHNDQKWKKINI
1100	2450	A	9045	763	584	RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF
1101	2451	A	9050	275	2	LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS+VAGITDMCRYTQLILFHAS
1102	2452	A	9053	449	1224	KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV
1103	2453	A	9058	403	3	GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIIKSPRFPIIKMTDITKCW*GC\GA AGMQI/H/CW\WCVNVGKFWEMS*YYLLKLSI ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA

NO of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No of   No o	00010	SEO ID	Met	CEÓ	Deadistad	Predicted end	Amino sold servense (AmAlonine Co-Contains
Deptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Pept	SEQ ID		1	SEQ	Predicted	1	Amino acid sequence (A-Alanine C-Cysteine,
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Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Pept			İ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ĺ	1	residue of		
	ļ	1	]				
1104   2454   A   9064   75   393			1				
1104		ļ <u> </u>	ļ		sequence		
RRNROTHSTESNKLKARGHSGYVM-LIH-NSV							
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RSILLONGSGYYILSI-QYDVFFFNYFFRDR	1105	2455		0065	366	778	<u> </u>
AWPCCPGWSAAWLTIVILAHYRRGLERSCC	1103	2433	^	3003	300	۱٬٬۰	
LSLSSSWDHRRVPPCPANF*YFSMGFTAFPRL							
VLNS*TQGI	i				1		
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11107   2457   A   9086   580   18							VLNS*TQGI
IIITCDPAPLLGICED	1106	2456	A	9083	673	816	ESGSLIH*WWENKPAQPLWWEI*QHVOKLPT
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AFSQSSVLWAHKQQKTSLSLVIRRELQIKU	1107	2457	A	9086	580	18	<del></del>
VRENELPIRLAKILKLDNYKCWQG/SGSNMSL   HEWEYNNEHIWNSVTFPRK VEHVYITYA   PEISVR*IHGGLPTLV*IQETHTSVFRGAPSVIP   ETRICRPTKESNKLLHIYTMMEHYGDENK   108   2458   A 9093   540   1   GGNDCSVTPTTEFGRKEIT*KRKF*EKTDRLP   GA/PPSRTPPTPYPCHIGDRLIPSRPLPAGPA   SAFPPAERSGGHRASL*RARWSAAVPRRSA   GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP   DSRPAAPGSRLIPDFGLDS*PASTRTSSVD*GG   QRPPPPSGDSLS*PPGCCRY   GA/PASCHLPDFGLDS*PASTRTSSVD*GG   QRPPPPSGDSLS*PPGCCRY   GA/PASCHLPDFGLDS*PASTRTSSVD*GG   QRPPPPSGDSLS*PPGCCRY   GA/PASCHLPDFGLDS*VUFFQLR   GA/PASCHLPDFGLDS*VUFFQLR   GA/PASCHLPDFGLDS*VUFFQLR   GA/PASCHLPDFASGELWDRIRLT   CSRPFFFAVGMFF*VDFLAAFSGELWDRIRLT   CSRPFFFAVGMFF*VDFLAAFSGELWDRIRLT   CSRPFFFAVGMFF*VDFLAAFSGELWDRIRLT   CSRPFFFAVGMFF*VDFLAAFSGELWDRIPLT   GROWNERLT   CSRPFFFAVGMFF*VDFLAAFSGELWDRYFYF   SALLSSVL*NQGGRNVLEAREAAKHPTI*RQS   LLRKQRNKKMIP   SFLSVRLECNGAIMAHCALPLPG   RRRGGGSRPRRTPPPABGPGPS*FGMDVFFYF   AAAGDPASLDPAQCLQYYGYSKFGNNNNYM   NAMEANNAFFAASEQTFHTIFSLGDEEFEIPPIT   PPPESDPALGMPDVLLPFQALSDPLPSQGSEFF   PQFPPQSLDLPSTITSRNL*VEGDGVLHSSGLHM   DSHTQVSQYRQDPSLIMRPSST*PPDAARSG   VMPPAQLTTINQSQLSAQLGINLGGASMPHT   SPSPPASKSATPSSSINEEDADEANRAIGEK   RAAPDSGKKPKTPKK   SCLSLPSSWDYSHLYPPRANFFVLLVETGFLH   VGQAGHEPLTSGDPPASSQSAGTTGVSHQA   WFSFFFSRDTVLLCSGWSRTSGLKQSACLS   LLKCWDY   SLLKCWDY   SLLKCWDY   SLLKCWDY   SPRMRRSGT/ATLALPLSPQGTVRTAVEFQWM   TQTQSLSPLLGSSDPPAPS*VLGITGQRYHACLII   YLYVQTVPQRV   VHOLTQQDGSPFTAAFGAG   UNIVERVED   VHOLTQQDGSPFTAAFGAG   UNIVERSIDEGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPPAGGAG   QPSPNGRNLYLPLFR   SASHEPAEHDGGADSLSASOPPRPAGGAG   QPSPNGRNLYLPHPAFAGGGGTP*GSA   GAGGPYGSPSAGACGAACGRPRPPPAASSA   GAGGPYGSPSAGACGAACGRPRPPPAASSA   GAGGPYGSPSAGACGAACGRPRPPPAASSA   GAGGPYGSPSAGACGAACGRPRPPAAFAGGGGTP*GSA   GAGGPYGSPSAGACGAA	,	~~,	1 11	7000	1 300		1
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GAPPSRTPTTPYPCPHGDRLLPPSRPLPAGPA   SAFPPAERSRGHRRASL*RARWSAAVPRRSA   GSASEPVQSRWRLPVGSDSPPAVPVRVCPAP   DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG   QRPPPSGDBLSPPGCCRY	ļ	ł	ŀ	}	ł	ł	ETR\CRPTKESINKLLHIYTMEHYGDENK
GAPPSRTPTTPYPCPHGDRLLPPSRPLPAGPA   SAFPPAERSRGHRRASL*RARWSAAVPRRSA   GSASEPVQSRWRLPVGSDSPPAVPVRVCPAP   DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG   QRPPPSGDBLSPPGCCRY	1108	2458	A	9093	540	1	GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
SAFPAERSGÜRRASL*RARWSAAVPRRSA   GSASPYQSRWLRLPVGSDSPPAVPVRVCPAP   DSRRAAPGSRI*POPGLDSPASPTSPSVD*GG   QRPPPPSGDSLSPPGCRY   HESYHVVPNILCNPV_APTSGAHSIG*KWPSWL   GAVAHSCNPSTLVGRGGRITRGQELR   HESYHVVPNILCNPV_APTSGAHSIG*KWPSWL   GAVAHSCNPSTLVGRGGRITRGQELR   GAVAHSCNPSTLVGRGGRITRGQELR   CSRPFTNILGSFGLAFLRVCSSLDSLDDSVVGP   SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS   LLRKQRNKRMAIP   SFLSVRLECNGAIMAHCALPLPG   RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP   AAAGDPASLDFAQCLGYYGYSKFGNNNYM   NMAEANNAFFAASEGTFHTPSLGDEEFEIPPIT   PPPESDPALGMPDVLLPFQALSDPLPSGGSFT   PQFFPQSLDLPSITISRNLVEQDGVLHSSGLHM   DQSHTISRNLVEQDGVLHSSGLHM   DQSHTISRNLVEQDGVLHSSGLHM   DQSHTISRNLVEQDGVLHSSGLHM   DQSHTISRNLVEQDGVLHSSGLHM   VSPSPPASKSATPSPSSSINEEDADEANRAIGEK   RAAPDSGKKKTPKK   RAAPDSGKKKTPKK   SCLSLPSWDYRHVPPRPANFFVLLVETGFLH   VGQAGHEPLTSGDPPASSAQSAGTIGVSHQA   WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS   LLKCWDY   LLKCWDY   LLKCWDY   LLCCWDY   LLYVQTVPQRV   STILFSPPAPS*VLGITGQRYHACLII   YLYVQTVPQRV   TQTGSLSPLASPW*RLGT   SPRMRRSGT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSPMRRSGT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSPMRRSGT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSQFNRRSGT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSQFNRRSGT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSQFNRSGRT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGSSASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSQFNRSGRT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGGLSGASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSQFNRSGRT/ATLNLPLSPQGTVRTAVEPQVM   TQTGSLSFLLGGLSGASLDCGFSMAPGLDLISVE   WRLQHKGRGRGDLHPDHHLSVPSSADHPA   QPSGFNYSTRPHDPAFFHADEAAGRGGRGLQ   PAAPHALPAGLPHGPPAPAPAEGGGTP*GSA   GAGGP*GSPAGRACGAACGRPPPPRPAASSA   GAGGP*GSPAGRACGAACGRPPPPRPAASSA   GAGGP*GSPAGRACGAACGRPPPPRPAASSA   GAGGP*GSPAGRACGAACGRPPPPRAASSA   GAGGP*GSPAGRACAACGACGRPPPPRAASSA   GAGGP*				1		_	
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DSRPAAPĞSRLPDPGLDSPAPSRTPSSSVD*GG	1	1		1	1	}	<b>1</b>
1109   2459   A   9099   1255   1425   HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL GAVAHSCNPSTLVGRGGRITRGQELR     1110	l						
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1110	1109	2459	A	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
CSRPFTRIOSFGLAFLRVCSSLDSLDDSVVGP   SALLSSYL/NQGGRNVLEAREAAKHPTI*RQS   LIRKQRNKRMAIP							GAVAHSCNPSTLVGRGGRITRGQELR
CSRPFTRIOSFGLAFLRVCSSLDSLDDSVVGP   SALLSSYL/NQGGRNVLEAREAAKHPTI*RQS   LIRKQRNKRMAIP	1110	2460	A	9103	242	70	EEOFFFFAVGMFP*VDFLAPASGELWDRLRLT
SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS   LIKKQRNKRMAIP		- '''	1			' "	
LLRKQRNKRMAIP   1111   2461	ļ	1	ŀ	ł	ł		
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1112 2462 A 9113 100 910 RRRGGGSRPRTTPVPAPGPGPSFGMDVRFYP AAAGDPASLDFAQCLGYYGYSKFGNNNYM NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT PQFPPQSLDLPSITISRNLVEQDGVLHSSGLHM DQSHTQVSQYRQDPSLIMRPSST*PDAARSG VMPPAQLTTINQSQLSAQLGLNLGGASMPHT SPSPPASKSATPSPSSSINEEDADEANRAIGEK RAAPDSGKRPKTPKK  1113 2463 A 9120 3452 3051 FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH VGQAGHEPLTSGDPPASASQSAGITGVSHQA WPSFFFSRDTVLLCCSGWSRTSGLKQSACLS LLKCWDY  1114 2464 A 9122 152 377 NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII YLYVQTVPQRV  1115 2465 A 9124 553 981 QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE WRLQHKGRGRGDLHLPDHHLSVPSSADHPA QQPSQFNGRNLYFLPLFR  1116 2466 A 9135 48 410 SASIEEPAEHDGGADSLSASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPAPAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA							
AAAGDPASLDFAQCLGYYGYSKFGNNNNYM NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT PQFPPQSLDLPSITISRNLVEQDGVLHSSGLHM DQSHTQVSQYRQDPSLIMRPSST*PDAARSG VMPPAQLTTINQSQLSAQLGLNLGGASMPHT SPSPPASKSATPSPSSSINEEDADEANRAIGEK RAAPDSGKKPKTPKK  1113 2463 A 9120 3452 3051 FLRPSFALVPQAGVQWCALSWLQPPSPFFK*F SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH VGQAGHEPLTSGDPPASASQSAGITGVSHQA WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS LLKCWDY  1114 2464 A 9122 152 377 NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS SLHP*PPGSSDPPAPPS*VLGITGQRYHACLII YLYVQTVPQRV  1115 2465 A 9124 553 981 QRPLLRQQLGSWPTCRSLEGDLASPW*RLPG SPMRRSGT/ATLNLPLSPQGTVRTAVEPQVM TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE WRLQHKGRGRGDLHLPDHHLSVPSSADHPA QQPSQFNGRNLYFLPLFR  1116 2466 A 9135 48 410 SASHEPAEHDGGADSLSASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPAPAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		1	1				
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WRLQHKGRGRGDLHLPDHHLSVPSSADHPA QQPSQFNGRNLYFLPLFR  1116 2466 A 9135 48 410 SASHEPAEHDGGADSLSASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPAPAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		I	[	Į.	1		
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1116 2466 A 9135 48 410 SASHEPAEHDGGADSLSASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		i		l	· ·		
1116 2466 A 9135 48 410 SASHEPAEHDGGADSLSASQPPRPAGRPAGA QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		1					
QHVHVPPWTDVLAGQDRRAPTAGDGAPWP APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA	1116	2466	A	9135	48 .	410	
APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		} - · · · -	1	1			
PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA				1			
GAGGP*GSPAGRACGAAGCRPRPPRPAASSA		ł		1			
		I			İ		
*NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS		1			'		
		<u>L.</u>	L	<u></u>	L	L	*NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  CPARTSVQGGTWTC*APAGRPAGLGGWEAE RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS KSGHWAKECLOPRIPPRPCPICVGPHWKSDCP TCPGAVPRAPGTLPQGSLTDSFPDLLSLVAED *CCLMASEASWTIT\ELWVTLTVEGKSVP/CL NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTPQLWCQLGQYSFMHYFLVIPTCPVPLLG* GILTKLSAFLTIPRLQPHLIAALSPSS
1118	2468	A	9154	471	2	AAGQVVVEVTSHLYLCITSDAAGLRLLPPAES ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTELKQII*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIFQIA
1119	2469	A	9155	2	3187	ACPRLARRRRVYSLRRRRGWLRARWSRGQ NNMAARRITQETFDAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSVLRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGIEIIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERILLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQGYLRG\ WKARRAYTGTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPPPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYRKKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESPEVMPEEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV
1120 1121	2470 2471	A	9163 9166	272	207 523	PPRACRPCPRACPCPPT*KCSQPVSWPC PMSSLQGCFYTFKCIIFKGIFLLLISNI.JAF**EK V/CSHITDSLKFIGKGWVGMVTHACNPGTLG
1122	2472	С	9170	442	236	G*GGWIA*VREFETSLGNM MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*
1123	2473	A	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1124	2474	A	9173	3	374	GPSPSLLVLLPQEPGGTGTPVRAGAGAGMWL WEDQGGLLGPFSFLMLMLLLETRNPVNACLL TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA IAHRGGRHDPPENTLGAIR/OGS**WSNRR
1125	2475	A	9179	704	188	ESSSGLLFQCFQGIHVQKLTLQARPTLFSWWL CSKPPKETGELENAESGGDGGRRGGKQDNV AWWRRM\QKG\DFPWDDEDFPQSGPFGGQA LPMGFFYLYFRDPGREITWKHFVQYYLARGL VDRLEVVNKQSVRVIPAPGTSSEVRGEFKAE YCRHKFISCKNVVFYFFQ
1126	2476	Α	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPN
1127	2477	A	9185	1	321	LTGQLGSILLRVFSKSRAGLGARKLKAYRTM EYMAESTDRSPGHILCCECGVPISPNPAQY\CV ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY LTFFSTIS
	2478	A	9186	183	847	VLKFLLLQTMDEQSQGMQGPPVPQFQPQKAL RPDMGYNTLANFRIEKKIGRGQ\FSEVYRAAC L\LDGVPVALKKVQIFDLMDAKARADCIKEID LLKQLNHPNVIKYYASFIEDNELNIVLELADA GDLSRMIKHFKKQKRLIPERTVWKYFVQLCS ALEHMHSRRVMHRDIKPANVFITATGVVKLG DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD NG
1129	2479	A	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT RATT\KIRVVATITRARIEDMRHSATALTRPD ATTAQIPKLPVTTVCNRRANPGIPPSVL
1130	2480	٨	9194	131	487	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV LALLGYLAVRPFLPKKKQQKDSLINLKIQKEN PKVVNEINIEDLCLTKAAYCRCWRSKTFPAC DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE PLAFLRALELLFAIFAFATCGGYSGGLRLSVD CVNKTESNLSIDIAFAYPFRLHQVTFEGPTCE GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIQLTTK TQPVEATDDAFWDQFWADTATSVQDVFALV PAAEIRAVREESPSNLATLCYKAVEKLVQGA ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD WRGFFWSTVPGAGRGGQGEEDDEHARPLAE SLLLAIADLLFCPDFTVQSHRRSTVDSAEDVH SLDSCEYIWEAGVGFAHSPQPNYIHDMNRME LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY NHLY
1133	2483	A	9208	1165	1463	GPRARVQGFSGADIVKFMALGSMYLVLTLIV AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS NVYFIV
1134	2484	A	9210	66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK RADGAAPAGEGEGVTLQGNITLLKGVAVIVV AIMGSGIFVIPTGVLKEAGSPGLALVVWAAC GVFSIVGALCYAELGTTISKSGGDYAYMLDV YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL LKPLFPTCPVPEEAAKLVACLCVLLLTAVNC YSVKAATRVQDAFAAAKLLALALIILLGFVQI GKGDVSNLDPNFSFEGTKLDVGNIVLALYSG LFAYGGWNYLNFVTEEMINPYRNLPLAIIISLP

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1135	2483	A	9216	40	410	DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV MQETLRNLASIGEKWKDQNIEDQYKNPRNNL RSLLGERVDENTEENHCGETSSQIPDDTLNK
1136	2486	A	9223	3	983	RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG DLVFAKMKGYPHWPARIDDIADGAVKPPPN KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGK PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSD SEAPEANPADGSDADEDDEG'RGVMAVTAVT ATAASDRMESDSDSDKSSDNSGLKRKTPALK MSVSKRARKASSDLDQASVSPSEEENSESSSE SEKTSDQDFTPEKKAAVRAPRGPLGGRKKK APSASDSDSKADSDGAKPEPVAMARSASSSS SSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRK PKPERPPSSSSSD
1137	2487	A	9229	21	239	LFPRLECRDPVTVNCTLNLPGSKNAPTTASQV GSTWNYRGGLPHPTNFFVKTGFRCSQAGLKL RGSREPPAWA
1138	2488	A	9231	207	443	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL EGIVWHETEEGVLVVNVTWRNKTYVGTLLD CTKHDWAPPRFCESPTSDLEMRGGRGRGKR ARSAAAAPGSEASFTESRGLQNKNRGGANGK GRRGSLNASGRRTPPNCAAEDIKASPSSTNKR KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK YKHINGLRYHQAHAHLDPENKLEFEPDSEDK ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA SPGAGNPPGTPKGKRELMSNGPGSIIGAKAGK NSGKKKGLNNELNNLPVISNMTAALDSCSAA DGSLAAEMPKLEAEGLIDKKNI.GDKEKGKK ANNCKTDKNPSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR KLKDKEGKETGSPKMDAKLGKLEDSKGASK DLPGHFLKDHLNKNEGLANGLSESQESRMAS IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/AS
		_		_		VTAAVSGLLVGYELGIISGALLQIKTLLALSC HEQEMGVSSLVIGALL
1140	2490	Α	9238	248	328	MAQGNNYGQTSNGVADESPNMLVYRKV
1141	2491	A	9242	2	535	FVEAAVKMLGSLVLRRKALAPRLLLRLRSP TLRGHGGASGRNVTTGSLGEPQWLRVATGG RPGTSPALFSGRGAATGGRQGGRFDTKCLAA ATWGRLPGPEETLPGQDSWNGVPSRAGLGM\ WPWAAALVVHCYSKSPSNKDAALLEAARAQ \NMQEVSRNRCALLHSAAVQEYGYON
1142	2492	A	9245	157	466	HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTC CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF GICKEYSRQ
1143	2493	A	9247	264	115	GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDG
L		L		L	l	ARDSTSIRMGPEIPPP

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1144	2494	A	9260	1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGP SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE AMEESDRPCEISEIDDNPKISENPRRSPTHEKN TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM ERRR
1145	2495	A	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGRF PGLRSPACDPTVGVDFFSRLLEIEPGKRIKLLL WDTAGQERFISIT
1146	2496	A	9277	592	814	MFTYLEGREGIKSQPKMEPHSVT\RLECSGMI SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA WLIFAFLVETGF
1147	2497	A	9279	1255	2	FRRGRRGEEEKEEEEEEEGWVNGMENSHPP HHHHQPPPQPGPSGERRNHHWRSYKLMIDP ALKKGHHKLYRYDGQHFSLAMSSNRPVEIVE DPRVVGIWTKNKE\LELSVPKFKIDEFYVDQV PPKQVTFAKLNDNIRENFLRDMCKKYGEVEE VEILYNPKTKKHLGIAKVVFATVRGAKDAVQ HLHSTSVMGNIIHVELDTKGETRMRFYEL\LV TGRYTPQTLPVGELDAVSPIVNETLQLSDALK RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDTA YSSCRLDTPNSYG/QGTPLTPRLGTFFSQDSSY SSRQPIPSYLFSQDPAVTFKARRHESKFTDAY NRRHEHHYVHNSPAVTAVAGATAAFRGSSD LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPP PAQATPAPGFR
1148	2498	A	9302	1026	6	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY ADPQNLTDVSIFLLLEVSGDPELQPVLAGLFL SMCLVTVLGNLLIILAISPDSHLHTPMYFFFSN LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVAI CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSQL HSWIVLQFTIIKNVEISNFVCDPSQLLKFACSD SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL GNLIIILDVSPDSHLPTPMYFFLSNLSLPDIGFT STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAIF GGMEERHAPECDGL
1149	2499	Α	9303	1	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE FRLVAADRSMGRYMLFGVINLICTGFLLMWC SSINSIALINSYTYLTIFDLFSLMTCLISYWVTL RKPSPVYSFGFERLEVLAVFASTVLAQLGALF ILKESAERFLEQPEIHTGRLLVGTFVALCFNLF TMLSIRNKPFAYVSEAASTSWLQEHVADLSR SLCGIIPGLSSIFLPRMNPFVLIDLAGAFALCIT YMLIEI
1150	2500	Ā	9308	797	693	DRSTSVTRAGVQWCSLGSLQPRTPGLLRSSCL SLP
1151	2501	A	9309	205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG SKTAAPPCQWSRMASEGPNIPCPGARHSDKQ FLICTI
1152	2502	A	9314	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRR PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/I PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL GTNVSLRAA
1153	2503	A	9315	392	1	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPSP PADDLVKAGRDRKDPQVR/ERRLRPNPGRLG GPR\PRPARARS/CHQPRLTRVCPRSPPPEARA PAPAAPARGRGAPKRNRPRTDTRAPRGSSAR PGNS

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mucheotide seq-	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Sequence			hod				
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minto acid residue of sequence   from the period   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pep		uence		-			
Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part   Part	uence		ļ	914			
			i				
1154   2504   A   9321   331   433   MPC/QAOYOTPAPSPOPRDHSASDPLTPEPIK   PT				ĺ	1	sequence	
1154				ļ			
1155   2505   A   9324   180   275   MEEPQSDPSVEPPLSQETFSDLWKILSENNVL     1156   2506   A   9326   383   619   MISPSKTEGDPLPIPPEGOREVRGFGGGPV     1157   2507   A   9327   152   292   YERGRSQGGGSIPAGAQPGGRAIGAGWQS     1158   2508   A   9328   I   430   QELKGQAPPHLASPSPAPSTAGLGCNIRVD     1158   2508   A   9328   I   430   QELKGQAPPHLASPSPAPSTAGLGCNIRVD     1159   2509   A   9334   108   383   KGRQVAGINGNQUKKRHESMCPVSLIVONTUGER     1159   2509   A   9334   108   383   KGRQVAGINGNQUKKRHESMCPVSLIVONTUGER     1160   2510   A   9338   2   430   FVGRPGLSGAGGGVAGTAGWAS     1161   2511   A   9341   I   390   NSRVDEPVAFGLELAGREV     1161   2511   A   9341   I   390   NSRVDEPVAFGLELAGREV     1162   2512   A   9343   84   837   QGRFRAFGWQRDFLQGGWASTLEKI     1162   2512   A   9343   84   837   QGRFRAFGWQRDFLQGGWASTLEKI     1163   2513   A   9346   967   616   DSLALSPRICEGOSTAGAGCGGK     1164   2514   A   9347   3   1099   SSPFTCAGTSAGALGHTHAT     1165   2515   A   9347   3   1099   SSPFTCAGTSAGATAGTWAT     1166   2516   A   9362   547   991   DVISIGPPLIR SURVEY     1167   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1168   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1169   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1160   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1161   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1162   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1163   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1164   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1165   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1166   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1166   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1166   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1167   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1168   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1169   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1169   2516   A   9363   201   387   PPILRWFYPSGRFRIP     1169   2516   A   9363   201   387   PPILRWFYPSG		L	<u> </u>	<u> </u>			
1155	1154	2504	Α	9321	331	433	
1156	<u> </u>			[ <u></u>			
EAAQRHCRASVSLIRMRPGQGSSRPARVPL   RGPDSHRIREPPSPP   RGPDSHRIREPPSPP   SEPDSHRIREPPSPP   YERGRSQGGSHPAGAQPGGRAIGAGWGS   REPLWEGLGRSGSPLPG   YERGRSQGGSHPAGAQPGGRAIGAGWGS   KEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPLWEGLGRSGSPLPG   SEPGLWGGSSPLSVITTIERRYSLKS   SESGLLVSCPIJGNLVVVVVSYPRGRRRP/	1155						
1157   2507   A   9327   152   292   YERRIRSEQGGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAQPGGRAIGAGWQS   KEPLWEGLQRSGSIPAGAGAGWQS   KEPLWEGLQRSGSIPAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1156	2506	Α	9326	383	619	
1157		1	)	]		)	EAAQRHCRASVSILRMRRPGQGSSRPARVPL
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	1157	2507	A	9327	152	292	YERRGRSQGGGSHPAGAQPGGRAIGAGWQS
1158		ļ			1		
Lisktfsyssalamlogerrclyvtidsrcf    VCMCPLTFiQALMVSQVISSVITTIERRYSLKS    SESGILVSCFDIGNLVVVVFVSYPRGRRRRP    RVAAVGGLDLEGGEM    RVAAVGGLDLEGGEM    1160   2510   A 9334   108   383	1158	2508	A	9328	1	430	
1159   2509   A   9334   108   383   SESGILVSCPIOIGN LVYVPVSYRGRRRP/ RVAAVGGLIDLEGGEMI   REGION/ROMONICAREKHESMCPYSLTONTYR   LMEAGLPQKQAERADELFEAGLVIYVKLDER   VINALVSSVGLQWFKESDLSHIRLLEISFR	1100	1		1	-		
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LMEAGLPOKQÁRRADELFAGLIYIYÁLDER	1150	2500	Δ	0334	108	383	
VINALVSSVĞLQWFKESDLSHLRILEISFR	1139	2509	^	3334	108	363	
1160	į.	i					
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DHTDQELREEIHKANVERVHDUSQEATIEKI RTKWIPLV/RWGDHA/EGPVGIKSYLPSGRSM EAELPIMSQLTEITCVEC	1100	2310	A	9336	4	430	
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VAGASVGAGVWARNPRYRTEGEACVEFKA MLIAVGIHLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNII.QFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1		1	[	Ì	!	HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL
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VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILQFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRTTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRKGGNHWWF AIRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS					1		
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SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTTEVLLVHRLDGHNITFS YVSIFVPLWLSLLTLMATTFRRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLTQKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFFSSEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1	1	1	1	1	}	
VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATIFRRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS		1	1	I	1	Į.	
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LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1						
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VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD 1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFFSEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1165	2515	Δ	9362	547	001	
CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1,103	(1,1,2	^	3302	, ,,,	, , , , , , , , , , , , , , , , , , ,	
TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS				1			
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1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	]	j			l	)	
GAISAHLAHCNLCLPGSSDSPASAFQVAS	1166	2616	-	10262	201	207	
	1100	2516	I A	9303	201	38/	
110/ 251/ A 9368 7/0/ 108/ AVLTPCLSPCSPSRIPRPSRPYPGRRSLSHTPP	116=		<del> </del>	0262	707	1000	
	1167	2517	<u> </u>	3308	1/0/	1087	AVLIPCESPOSPSKIPKP/SKPYPGKKSESHIPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
		[	-	peptide sequence		nucleotide insertion
	<del> </del>	┼	<del> </del>	sequence	<del></del>	PRPLILYAPAP\RPAGTAFIPHSHPPPPDLLRPT
		Ì	] .			ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
				ļ		PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
1168	2518	A	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
		1	}	}	ļ	PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
				!		LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
	ł			İ	i	QQSILAGLVVVATTGMIGSPLECLFGELGGRA
		1				DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL
		<u> </u>	-		110	FNAMQASSEH
1169	2519	A	9377	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
		1				NSARRMEAMASGSNWLSGVNVVLVMAYWS LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH
		i		i		NAPKOLKEEIDILLSRVHNIKYEP\HLLADDDA
1170	2520	A	9378	302	1303	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
••••	2520	] ^	13.0	302	1303	ILLLTICAAGIGGTFQFGYNLSIINAPTLHIQEF
				i		TNETWOARTGEPLPDHLVLLMWSLIVSLYPL
	-	1	1		<b> </b>	GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
		}			1	AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
						SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
		i				LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
		j	}	1	1	ERAACQGCRARRPWELFQHRALRRQVTSLV
		1			!	VLGSAMELCGNDSVYAYASSVFRKAGVPEA KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
	1	1	1	i	ì	WGGTPRSFALNQFTLQKKKK
1171	2521	A	9381	2	412	RGPASAQEDERARTAPLERVRARGRMTTSSA
••••	1	^ •	7301	<del>-</del>	! ·	LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE
	(		1			TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV
		j	J	ļ	•	EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
		<u> </u>				SKRLFFWMQEP
1172	2522	A	9384	20	355	GWNGRSTEASPAAEAPHVPHKET KAAMGTQ
		1	1		ŀ	CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
						LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL ASFNEVGNTALIVLESY
1173	2523	A	9393	430	87	LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
11/3	2323	^	7373	450	°′	QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
			į.			KIFVLFDFNIMFETPFYII*FIFLFSONLKRIRQV
		ĺ		[	ĺ	IRPPISFSKINNGP
1174	2524	A	9397	77	374	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
		1	1			RLVKLALLQLLRAFYGIKVKGVRVHRDCGTP
		ĺ		(	ĺ	ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
	L	L	25.22			LGML
1175	2525	A	9399	66	397	HESSRADRDKMDTRGSTYTDADPVNKSGGT
						AKMNKWSKGKVRDKLNNLVLFDTATYDKL
	1	ļ	1	}		CKEVPNYKLITLAVVSERLKIPGSLARAALIIE LLSRGLI*LVIQHIAQVIY
1176	2526	A	9408	2	299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
1170	2320	^	7400	~	233	GERGYAONGDF*DAOLDDYSFSCYSHAOVN
	ł	1	1	1	}	GAPNSLTRAYDDP*VKISGLECQKVGALVEV
			1			KCLNL
1177	2527	A	9416	2	402	CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
		ł			ł	YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
		}		i		FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
	l	<u> </u>	<u>i</u> i			DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1178	2528	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
				ļ		ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL
1105	1	<u> </u>	0.55	1450		ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
1179	2529	A	9420	1450	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG
		1				GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA WWRAP
	L	L	L	L	L	TH TICH

NO. of   NO. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
					1		D=Aspartic Acid F=Glutamic Acid
Deskin   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation   Decation			1100	1			F=Phenylalanine G=Glycine H=Histidine
1180	1		l				I=Isoleucine K=I vsine 1=I eucine
180	1						
minto acid residue   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence		dence		7			
Fesidue of peptide   Sequence   Y=Tyrosine, X=Unknown, "Stop codon, pepsisible nucleotide deletion, t-posible   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequenc	uence			714			
peptide   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence   soquence	Į.	1				,	V=Typesine V=Ll-known *=Step soden
	į	ĺ	ľ			sequence	
1180	ł	ł	l	l		ł	
SRFSRTSTRYPYENDEPARQKLTGVLHAPLLK			<b>L</b>	l			
1181   2531   A   9436   2   274	1180	2530	A	9422	176	375	
1181	İ	İ		1			•
IARTILDRITGIPHOYCFVE*ADWATADKCVH   YNOKPLPGATPLLSIQLHQLAHLOS   1182   2532   A   9442   3   240   VDKCSSKSIVLSEYCPHCMCSI.STDPKPFGQI   SMIIK*MGAGGGEKISAMGKADVHRELYLGI   LYPTEDVKLTFRARH   1183   2533   A   9444   384   3   LXDFQPWALIDWPLPCCCTPLLIFLVLECFTR   KGCSGWAPWI.SI.QCOHFGRPRWADHLRSGV   RDQPGQYSKTTFLPKIQKLAGHSGAHL*SYLL   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWKNRI.NPGGRSCSEFRWHHICTRGWAT   ERMRWGGRSCWSTSICHGPGWAT   ERMRWGGRSCWSTSICHGPGWAT   ERMRWGGRSCWSTSICHGPGRLGWAT   ERMRWGGRSCWSTSICHGPGRLGWAT   ERMRWGGRSCWSTSICHGPGRLGWAT   ERMRWGGRSCWSTSICHGPGRLGWAT   ERMRWGGRSCWSTSICHGPGLAG   ERMRWGGRSCWSTSICHGPGLAG   ERMRWGGRSCWSTSICHGPGLAG   ERMRWGGLGCGSTGGGRAK   A   S483   463   86   VTVGLTLLIRGAPRFTAG*PPSGGGPPLAPLL   PROHICTLOTHRILIPEAPVKV*KT*RLFGLR   GASSCRRRCPVLAARKAGCLGSTSKPSTTENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRENG   ERKSLARCCSLUHRGGCSSPSTSTRE			1	l			
II82   2532   A   9442   3   240   VDKCSKSKIVLSFYCPHCKUS.STDPKPFGQL SMILK*MGAGDEKISAMGKARVDHRELYLGL LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFRARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYKLIFARH   LYPTEDYK	1181	2531	Α	9436	2	274	
1182	]	Ì	Į .	J	1	]	
SMILK*MGAGDEKISAMGKARYDHRELYLGL				l			IYNGKPLPGATPLLSLQLHQLAHLGS
LYPTEDYKLTFRARH	1182	2532	Α	9442	3	240	VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL
1183	1		]				SMILK*MGAGDEKISAMGKARVDHRELYLGL
RGSGWAPWLSLQCQHFGRPRADHLRSGV   RDQFGQYSKTTFLPKIQKLAGHSGAHL*S*ILL   ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT   ERG   ERGFKSLMPKIPLQYIYYVRVRTTWSFCLPLDG   RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV   HTCNFSTLGGRAGWIV*AQEFET   RCPMWQGQASRMDPAKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWCWALKAKDREASTCCSLA   WWWGWCWCWALKAKDREASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKACASTACKACA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCAKACACAA   WWGWCAKACACAA   WWGWCAKACACAA   WWGWCAKACACAAA   WWGWCAKACAAAANTCAASTCCSLA   WWGWCAKACAAAANTCAASTCCSLA   WWGWCAKACAAAANTCAATACACAAAATACACACAAAATACACACAAAATACACACAAAAAA		ŀ	ĺ			1	
RGSGWAPWLSLQCQHFGRPRADHLRSGV   RDQFGQYSKTTFLPKIQKLAGHSGAHL*S*ILL   ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT   ERG   ERGFKSLMPKIPLQYIYYVRVRTTWSFCLPLDG   RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV   HTCNFSTLGGRAGWIV*AQEFET   RCPMWQGQASRMDPAKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWYALKAKDREASTCCSLA   WWWGWCWCWALKAKDREASTCCSLA   WWWGWCWCWALKAKDREASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKACASTACKACA   WWGWCWCAKAKDRAASTCCSLA   WWGWCWCAKAKDRAASTCCSLA   WWGWCAKACACAA   WWGWCAKACACAA   WWGWCAKACACAA   WWGWCAKACACAAA   WWGWCAKACAAAANTCAASTCCSLA   WWGWCAKACAAAANTCAASTCCSLA   WWGWCAKACAAAANTCAATACACAAAATACACACAAAATACACACAAAATACACACAAAAAA	1183	2533	A	9444	384	3	LKDFQPWALHDWPLFCCCTFLLFLVLECFTR
RDQPGQYSKTTFLPKIQKLAGHISGAHL*S*LL	1 - 1 -		1				KGCSGWAPWLSLOCOHFGRPRWADHLRSGV
				1		1	
ERG	1			1			
1184	1	ł		1			
RRLMLS*YSK-!T*KYNLIPSYSMTLPPOMV   HTCNSYTLGGRAGWIV*AQEFET	1104	2524	<del>l</del> a	0462	301	655	
HITCNPSTLGGRAGWIV*AQEFET	1104	2554	Ι ^ .	7402	371	055	
1185	1		Į.		1		
	1106	2525	<b>.</b>	04/2	316	-	
	1185	2535	A	9467	213	300	
WSAVVQFWLTAASNSCFSLLSSWDYRCA	Į.						
1186	I		ł				
1187				<u> </u>		_	
1187	1186	2536	A	9468	275	452	
SSRGAEPCLSNCHISPAPRKQRMGDSDQ*STP   NPASPHPEAPQEPWDSASGSVGSFSLGRAK   ASS*VPGKGRGPRQGSELLAETILELFLALAN   S							
NPASPHPEAPOEPWDSASGSVGSFSLGRGAK   ASS*VPGKGRGPRQSELLAETILELFLALAN   S	1187	2537	Α	9469	388	3	
ASS*VPGKGGGPRQGSELLAETILELFLALAN   S   S	1	1	1				
1188		1		1	<b>!</b>		NPASPHPEAPQEPWDSASGSVGSFSLGRGAK
1188		į		i			ASS*VPGKGRGPRQGSELLAETILELFLALAN
GRLMANPEALKILSAITQPMVEEALAGLYRAC	1	1	l	1	į	1	
PFYLTNNLAGMKKGLCLGSTEQAHTIGI	1188	2538	Α	9471	124	397	TMDKKNRHGNSLDMASEIHMTGPMCLIENTT
1189	1	Ì	1			i	GRLMANPEALKILSAITQPMVEEALAGLYRAC
PSLLKIQKISWAWWRAPVVPATWEAEAEEW R			1	1		ļ	*FYLTNNLAGMKKGLCLGSTEQAHTIGI
PSLLKIQKISWAWWRAPVVPATWEAEAEEW   R	1189	2539	A	9480	584	769	GHVQSQHFGRPRRADHLRSGDRDHPG*HDET
R						1	PSLLKIOKISWAWWRAPVVPATWEAEAEEW
PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR GASSCRRRCNPVLAARKAGSPRSHSTRENC RRSRCPDTAHRRRRGRRRNPSCVRSPRWR 1191 2541 A 9489 1 LADALCLSAAATGAVRPGARAQPSTRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEELTAVNVK LEELTAVNVK CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEENTS LAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM 1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ 1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVYPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	1	l	ļ	}	1	
PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR GASSCRRRCNPVLAARKAGSPRSHSTRENC RRSRCPDTAHRRRRGRRRNPSCVRSPRWR 1191 2541 A 9489 1 LADALCLSAAATGAVRPGARAQPSTRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEELTAVNVK LEELTAVNVK CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEENTS LAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM 1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ 1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVYPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1190	2540	A	9483	463	86	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL
GAŠSCRRRCNPVLAARKAGSPRSHSTRENC RRSRCPDTAHRRRRGRRRNPSCVRSPRWR  1191 2541 A 9489 1 411 LADALCLSAAATGAVRPGARAQPSTRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEEELTAVNVK  1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM 1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTAMIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	:-	1	1		1	
RRSRCPDTAHRRRRGRRNPSCVRSPRWR  1191 2541 A 9489 1 LADALCLSAAATGAVRPGARAÓPSTRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEEBLTAVNVK  1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEENTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EXAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP		1					
1191 2541 A 9489 1 411 LADALCLSAAATGAVRPGARAQPSTRRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEELTAVNVK  1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EXAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP		1	ł			i	
SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEEELTAVNVK  1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1191	2541	A	9480	1	411	
ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEEELTAVNVK  1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEENTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EXAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	****	2541	^`	7,107	^	·••	
MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ   KEEELTAVNVK	!	1		1	1	1	
KEEBLTAVNVK	1	1	1	1	I	1	
1192 2542 A 9497 389 161 VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEENTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	1	1	1	1	1	
CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS  1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVVNN*S*TYVYPCDKIILLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKJ RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASEŠAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPINIL*  PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1102	2542	1	0407	290	161	
KDTYSDHEEINTS	1192	2542	A .	747/	309	101	
1193 2543 A 9509 186 1 IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLGLYPTEM 1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSSASLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKJ RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ 1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL*PLHLLHD*EXAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	Ì	1		ļ	1	1	
FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM  1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	I	ļ.,	0.00	106	<del></del>	
1194 2544 A 9512 58 433 PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1193	2543	A	9509	186	1	
LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP			L	L	<u> </u>	ļ	FGK1FVNVN*S*1YVYPCDKIILLLGLYPTEM
SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1194	2544	A	9512	58	433	
RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ  1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHILLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	J		1		}	]	
1195 2545 A 9515 595 1223 GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP			1			1	
AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1			1	1	1	
AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1195	2545	A	9515	595	1223	
PCPLCIARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	1		1	1	1	
LPRCSCAPLRSASAPQVS*CV*AVNLLPIINL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1		1	1	1	1	
PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	1	1	1	1	1	
APGSGPCGATARPSRGGRAGGSRARRPIPPGP	1	1	1	1	1	i	
					1	1	
				1	}	1	
	L	L	L	J	<u> </u>	L	G LIGHT SOCKIT MASON

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide		/=possible nucleotide deletion, \=possible
L			0.0	sequence		nucleotide insertion
1196	2546	A	9518	229	468	RSPTATPAPHAMGPGAPFARGGRPLPLLGAM
1		ļ			ļ	AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA GYIGALFPMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG
1137	2547	^	7521	20)	1	HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE
1			1			APNWKYKYGY*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSIVTLNISGPNO*NKRHRVAEWI
					Į	VKQEPNICHL*ETHFPFRDTYRLKEREQKKRK
1	1	J			}	SSYS
1199	2549	Α	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA
						V*QRGDGKNPGVTHLNRPVGTX
1200	2550	A	9548	186	1	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI
						KAIYDKWTSDIMLNLQKL*AFFLRVIVRQI
1201	2551	A	9549	591	2	SSVVEFPRGPRSSLPPLDSTFPCGSSPNWTGGC
i	1					GSCPSGE*LVSPGSEQRKKYSNSNVIMHETSQ
					1	YHVQHLATFIMDKSEAITSVDDAIRKLVQLSS
í		İ		ĺ		KEKIWTQEMLLQVNDQSLRLLDIESQEELEDF PLPTVQRSQTVLNQLRYPSVLLLVCQDSEQSK
1						PDVHFFHCDEVEAELVHEYMESALTDCRLGK
i .			1		Ì	AMRP
1202	2552	A	9552	428	1	KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK
1			***-			LDCERPPOGPLPSLPELAKTSYSDLTGLATED
					ŀ	*WGPGMDAPATTIASSKTRVTLMVAGRPVFF
ì	1	İ	1	İ	İ	LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV
						SKPRATPPLFCSLHTF
1203	2553	A	9568	517	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG
1	İ	ŀ				EKEKRRREKGEREERKMRHRERKGESGQRD
1204	2554	A	9573	83	415	TMENWRVERLTEKER
1204	2554	A	93/3	83	413	EDKRLRLVDGDSRCAGRV*IYHDGFWGTICD DGWDLSDAHVVCQKLGCGVAFNATVSAHFG
1		i	ľ			EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ
						HDCRHKEDAGVICSEFTALR
1205	2555	A	9577	64	424	ARGSCPTRPRTANGRMGETKDAPQMLVTFK
					i -	DVAVTFFREEWRQLVLVHRTLYR*GMLETC
					İ	GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE
						VSHSPCAGDMRELFTREATLTPHPYNNGA
1206	2556	Α	9584	38	476	TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL
		Ì				SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV
	}				}	NPQPLSTPSWQIETKYSTKVLTGNWMEERRK
		]		'		GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL
1207	2557	A	9586	2	412	LRSSPAALLRALCITTVTGTALALRSRVATTN
1207	2331	^	0000	_	714	PDGCRNVLRPKYYRLCDKAESWGIALETVPT
		1	[			GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP
		]	1			THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL
	]	ł	1			FGILFSICFS
1208	2558	Α	9597	122	3	IKNYWPGMVAHACNPSPLGGRGRWIA*AQK
		<u></u>				FADAWADAW
1209	2559	A	9611	148	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK
1		[	1	i	1	GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ
						RIRDHDLLDKRKTVTALKAGEDRAILLGLAM
]	1	ļ				MVCSIMM*FLLGITLLRSYMQSVWTRESQCT
1212	3660		0619	204		LLNASITETFNC
1210	2560	A	9618	384	2	SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI
	İ	ļ				KVQVKNNDLGLQATINNEANWIAHQDDFNW
	1	1				LLAELNTCQRQETADS***WSPKNSHVGKDS
						GELSAK
1211	2561	Α	9620	316	610	QKHPGGGQLGRSPQEDSRFHNKASSGVSRVR

SEQ ID SEQ ID Met SEQ Predicted Predicted end Amino acid sequence (A= NO: of NO: of hod ID NO: beginning nucleotide D=Aspartic Acid, E=Glutt	
nucl- peptide in nucleotide location F=Phenylalanine, G=Glyc	
eotide seq- USSN location corresponding I=Isoleucine, K=Lysine, I	
seq- uence 09/496 correspondi to last amino M=Methionine, N=Aspara	
uence 914 ng to first acid residue Q=Glutamine, R=Arginine	
arnino acid of peptide T=Threonine, V=Valine,	
residue of sequence Y=Tyrosine, X=Unknown	i, *=Stop codon,
peptide /=possible nucleotide dele	tion, \=possible
sequence nucleotide insertion	•
LGRAWWLTPVIPTLWI	EAKAGGSPE*D*AGRG
GSRL*SQHFGRPRRVD	HLRSAVQDQPGQHGE
TPSLLKIQKIN*VWGRF	LL*SSYSEAEAGESL
1212 2562 A 9623 297 344 QFPVDGDYQKIEKITQI	LFQAQNLSLCLAMTR
TREL*KGGGKGRHE*A	VVPFLKKGGYGVKAP
AILNTSNCT*CF*ETKM	ILSDDPKACVFEVSSA
DL*NTSFGVIR	
1213 2563 A 9624 2 356 AELSLASTACGRNTSG	DSLPDYDRAPISSPLA
TSGTILSAISCLWDLPT	PVLRVGLSCQPSMSSQ
LYFHRDDMALEGVSRI	
1214 2564 A 9634 776 912 SLSRWVRAKL*VPYNC	ENCLNPRGGGCSEPR
SHYCTPAWATEKDS	
1215 2565 A 9636 220 426 KPGNFAVSSEY*DITSG	
EENFGEKLHDIGFGNG	FLDKT*KAQATKAKI
DK	
1216 2566 A 9637 391 76 CFLEDGCTQAS*AEEA	
RERRSIRFKMKNHSPDI	
NHLPETERNLLEHGLM	YIRLNAAFCSLVAHS
LFGFILKAT	
1217 2567 A 9655 2008 2432 LHCKMGALETQTHPCS	
EEHHLQPVQVLQTLLH	
PAPPTPTPWRSRQSGKO	
GALGGRGGRALGGSRY	
VLMSAQEPWAIKEEHV	
MLDFEGEDTFHGDMAI NFEAQRALANIAADQA	
NVPPKVTVL	EALEINIDMOSD I TEIF
1219 2569 A 9662 3 284 PDWTEKRKMQDTGSIL	PIHWEGEGVAALVA
YGGIIGYVKAGSVPSLA	
LSQDPRNVWVFLATSG	
KI	
1220 2570 A 9669 200 699 LLLTGYIQTLQNQQLSO	GNOOEMOAVDNLTSA
PGNTSI.CTRDYKITOVI	
GLAMRIFFQIRSKSNFII	
PFKILSDAKLGTGPLRT	
SISFLGLITIDRYQKTTR	
K	
1221 2571 A 9676 164 562 KERDSSTFSAAMTTMQ	GMEQAMPGAGPGVP
QLGNMAVIHSHL, WKG	
VQILTALMSLSMGITMI	MCMASNTYGSNPISV
YIGYTIWGSVMFIISGSI	LSIAAGIRTTKGLVRG
SLGMNITSS	
1222 2572 A 9688 43 412 VAKMVKCCSAIGCASR	
PTDENIKRKWVLAMKF	
DVLCSRHFKKTDFDRS.	
PYHLQGKREKLHCRKN	
1223 2573 A 9696 308 564 RTSMGILYSEPICQAAY	
DSSYANVQDGFNGDTF	
LKKECLCQPQKPERENI	
1224 2574 A 9700 3 632 DAWASGGELGSLFDHI	
GRRPRAVKVYTINLESC	
ELVERFALYGAIEQYNA	
	DEQSFFGGLLHVCYA
PEFETVEETRKKLQMRI	
	RQDFHSEMSGFCKA

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
4000		1	**.	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			i	peptide	Sequence	/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
1005	2505	<del> </del>	0710		177	L
1225	2575	A	9710	1	163	RSGCVLRMTEWETGAPAVAETPDIKLFGKWS
100		<u> </u>	0010		400	TDDVHINDISLQDYIAGVRLILL
1226	2576	Α	9713	82	492	QGLPSFLPAFGPSGSWLGPAPTLGSSCNTVDT
		ŀ	1			ICHGYSEIRPLFYLSFCDLLLGLCWLTETLLYG
	l			Ì		ASVANKDIICYNLQAVGQIFYISSFLYTVNYI
					ĺ	WYLYTELRMKHTQSGQSTSPLVIDYTCRVCQ
		ĺ				MAFVFSSLI
1227	2577	A	9720	3	416	GKWKRTQVPLLGEECADMDLARKEFLRGNG
ļ					1	LAAGKMNISIDLDTNYAELVLNVGRVTLGEN
1			1		ļ	NRKKMKDCQLRKQQNENVSRAVCALLNSGG
ļ	<b>!</b>	1	1	!		GVIKAEVENKGYSYKKDGIGLDLENSFSNML
	1			Ì		PFVPNFLDFMQNGNYF
1228	2578	A	9723	278	411	EASSSNTVASNVADKTDPHSMNSRVFIGNLN
1220	23/9	1 ^	9123	270	411	TLVLQKSDVEAVF
1000	2570	<b>-</b>	0206	121	902	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDY
1229	2579	Α	9725	121	902	LEAMSGEENENT DE 1Q15151DDQ5QQ51D1
	ì		1			GGSGGPYSKQYAGYDYSQQGRFVPPDMMQP
t	l	ł	1	ĺ	1	QQPYTGQIYQPTQAYTPASPQPFYGNNFEDEP
			1	<b>;</b>		PLLEELGINFDHIWQKTLTVLHPLKVADGSIM
Ì			į			NETDLAGPMVFCLAFGATLLLAGKIQFGYVY
ſ		ĺ	!	ĺ		GISAIGCLGMFCLLNLMSMTGVSFGCVASVL
į.		1			t	GYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
	[	ļ		1	1	WCSFSASKIFISALAMEGQQLLVAYPCALLYG
				i		VFALISVF
1230	2580	Α	9739	11	247	TFVLNMNTPKEEFODWPIVRIAAHLPDLIVYG
			1	}		HFSPERPFMDYFDGVLMFVDISGKCKRDVCL.
	[			1	1	MWMSNRLAWEFTCRA
1231	2581	A	9744	37	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPP
	2301		1	-	1	ACRIMPTTVDDVLEHGGEFHFFQKQMFFLLA
						LLSATFAPIYVGIVFLGFTPDHRCRSPGVAELS
				ŀ	1	LRCGWSPAEELNYTVPGPGPAGEASPRQCRR
ł	l	ì		1	1	YEVDWNQSTFDCVDPLASLDTNRSRLPLGPC
			1		1	RDGWYYETPGSSIVTEFNLVCANSWMLDLFQ
]		j	Ī		1	SSVNVGFFIGSMSIGYIADRFGRKLCLLTTVLI
Ė			1			
		ļ				NAAAGVLMAISPTYTWMLIFRLIQGLVSKAG
ł			1			WLIGYILITEFVGRRYRRTVGIFYQVAYTVGL
1						LVLAGVAYALPHWRWLQFTVALPNFFFLLY
f	ŀ	ſ	1	1		YWCIPESPRWLISQNKNAEAMRIIKHIAKKNG
		<u> </u>	<u> </u>	<u> </u>		KSLPASL
1232	2582	A	9753	164	517	PGPGMQGPPPITPTSWSLPPWRAYVAAAVLC
I	İ		1		İ	YINLLNYMNWFIIAGVLLDIQEVFQISDNHAG
ŀ	1		]		1	LLQTVFVSCLLLSAPVFGYLGDRHSRKATMS
	l	l	1			FGILLWSGAGLSSSFISPRYSWLF
1233	2583	A	9757	25	419	LPAPWTERVRKSEGLVGTCLGDPMASPRTVT
1					[	IVALSVALGLFFVFMGTIKLTPRLSKDAYSEM
l	1		1		1	KRAYKSYVRALPLLKKMGINSILLRKSIGALE
)	1		Į	l	1	VACGIVMTLVPGRPKDVANFFLLLLVLAVLF
1	1		1	}		FHOLV
1234	2584	A	9765	71	456	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP
1254	2304	1 ^	*,55	l ' <b>'</b>	1 750	CSRCGYGVYPAEKISCIDQIWHKACFHCEVC
ŀ	l .				1	
1	ĺ	I		1	ŀ	KMMLSVNNFVSHQKKPYCHAHNPKNNTFTS
I	1	i	1			VYHTPLNLNVRTFPEAISGIHDQEDGEQCKSV
	L	<u></u>	Ļ		l	FHWD
1235	2585	Α	9767	52	559	TRSGAMSVDKAELCGSLLTWLQTFHVPSPCA
1	1	i	1	1		SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI
I	1		1			SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP
		J		l		ARHMSWVMGRKRDRCLVINHLFIHSSMEYSP
1		ļ				CARPGHSARNNTDKNLPHTAIILVTSNTYTTI
	!	1				KINFQAGRSGSCL
1236	2586	A	9770	352	608	FRGEALTVRFLTKRFIGEYASNFESIYKKHLC
		<u> </u>			1_000	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

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muche enide   center   USSN     coation   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   co	SEQ ID	SEQ ID	Mct	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deat			noa	l .			
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1237   2587   A   9793   266   315   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES   STATES							1 =
amino acid residue of sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence		uence	}				
Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic   Periodic	uence			914			
		1					
	1		t			sequence	
LERKOLINIELTYPECSQTOKAKPSLTSELHWA   DGPVIVVDISINESSFARAKAL     1237   2587   A 9793   266   515   NILABIYEPPERLELDSOSNPKAFALTILLE     1238   2588   A 9802   537   967   ELGAGRSDREAMALVERISVEDEAVDKIN   FRUCKLAFYEROKOWLSKISTYRALLDSOSNPKAFALTILLE     1239   2589   A 9805   105   540   PEDCOKLAFYEROKOWLSKISTYRALLDSOSDE     1239   2589   A 9805   105   540   PEDCOKLAFYEROKOWLSKISTYRALLDSOSDE     1240   2590   A 9819   3   305   PEDGOKLAFYEROKOWLSKISTYRALLDSOSDE     1240   2590   A 9819   3   305   PEDGOKLAFYEROKOWLSKISTYRISCSGDT     1241   2591   A 9834   841   1209   DIKFLITKGIONIEGIDIREÇK     1242   2592   A 9843   3   305   PEDGOKLAFYEROKOWLSKASTYRALLDSOSDE     1244   2594   A 9845   3   305   PEDGOKLAFYEROKOWLSKASTYRALLDSOSDE     1242   2592   A 9843   3   305   PEDGOKLAFYEROKOWLSKASTYRALLDSOSDE     1244   2594   A 9846   198   411   PEDGOKLAFYEROKOWLSKASTYRALDSOSDE     1245   2593   A 9846   198   411   PERGOKLAFYEROKOWLSKASTENDEN     1244   2594   A 9848   116   650   PEOGOKLAFYEROKOWLSKASTENDEN     1245   2595   A 9849   373   1620   PEOGOKLAFYEROKOWLSKASTENDEN     1246   2596   A 9849   373   1620   PEOGOKLAFOR     1246   2596   A 9850   114   464   PEOGAGRS     1247   2597   A 9851   2   327   PERMISKIMARUS     1248   2598   A 9850   114   464   PEOGAGRS     1249   2599   A 9851   2   327   PERMISKIMAN     1240   2597   A 9851   2   327   PERMISKIMAN     1241   2597   A 9851   2   327   PERMISKIMAN     1242   2598   A 9850   114   464   PEOGAGRS     1244   2594   A 9848   116   PEOGAGRS     1245   2595   A 9850   114   464   PEOGAGR     1246   2596   A 9850   114   464   PEOGAGR     1247   2597   A 9851   2   327   PERMISKIMAN     1248   PEOGAGR     1249   PEOGAGR     1240   PEOGAGR     1240   PEOGAGR     1241   PEOGAGR     1242   PEOGAGR     1243   PEOGAGR     1244   PEOGAGR     1245   PEOGAGR     1246   PEOGAGR     1247   PEOGAGR     1248   PEOGAGR     1249   PEOGAGR     1240   PEOGAGR     1240   PEOGAGR     1241   PEOGAGR     1242   PEOGAGR     1244   PEOGAGR     1245   PEOGAGR     1246   PEOGAGR     1			1		peptide		
	l	ĺ	1	1	sequence		nucleotide insertion
1237   2587   A   9793   266   515   NILAHYPFFRIPLICINSQNNPKAPALTICHH QKIKNFQLLPVLYSICHTPR							LERKQLNLEIYDPCSQTQKAKFSLTSELHWA
2588	1	ļ	ŀ		i		DGFVIVYDISDRSSFAFAKALI
2588	1237	2587	A	9793	266	515	NILAIIYEPERLELLRDSOSNPKAFALTLCHH
1238	1231	2307	′ •	1 7 7 3	200		
1238				1			
FRICKIKAPYRROKOWI.SKKSTYRALLDSVT   TDEDSTREJNIRASKY PLEYGIEGNIPILK   NEETPL KPREVPDVLTSKPSTVRLISCSGDT   GSLII.ADGEGDLKC   SSLII.ADGEGDLKC   SSLII.ADGEGDLKC   PGDPARWTRAGAVGAHLPASGLDJFÖDLKK   NEETPL KPREVPDVLTSKPSTVRLISCSGDT   SSLII.ADGEGDLKC   PGDPARWTRAGAVGAHLPASGLDJFÖDLKK   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL   SSLII.ADGEGVAL	1038	2500	<del>                                     </del>	0000	627	067	
TDEDSTREQINEASK-VPLLAEI/GGERIERLK   NREFTPL.RPREVPDVLTSKFSTVRLISCS.GDT   GSILI.ADGK.GDI.K.C	1238	2366	Α	9802	337	907	
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DIKKLTKGGDNRGDURGSYK		1		1	1		GSESPIVVVLSGSMEPAFHRGDLLFLTNFRED
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1240	•	ĺ	1	Į.	†	ſ	( "
POPLDPAMIL WMQGFVLEAVACQDNDDYLR	1240	2500	ΙΔ -	0810	3	305	
1241   2591   A   9834   841   1209   SPARGKSNRTDVMITAPKNKKMTENLAAPEA LDSSTHSSSTATQSRAKMNTPAPTPSTVPAPPR GGSGPPPCAPHDRVSSVLQCDTQAMDHKTE SSHSVVEFLFKRTKTPSPFPAAVRENRN     1242   2592   A   9843   3   589   TISGGPATEPPASLLSSASSDDFCKEKTEDRYS LGSSLDSGMRTPLCRICFQOPEQGELLSPCRC DGSVKCTHQPCLIKWISERGCWSCELCYTKY HVIAISTKNPLQWAISLTVIEKVQVAAAILGS LFILIASISWLIWSTFSPSARWQRQDLLFQICVG MYGFMDVMIVAVDSEDMVQAAKEVGKRW DIPP     1243   2593   A   9846   198   411   WRISHHAGKMPVMKGLLAPQNTFLDTIATRF DGTHSNFILANAQVAKGFPIVYCSDGFCELAG FARTEVMQ     1244   2594   A   9848   116   650   PICGFLYLCSAMASESSPLLAYRLLGEEGVAL PANGAGGFGGASARKLSTIGVVVYVISMF SIVVPLRIFFVGHAGLLQALAMILVAYFILA LTVLSVCAIATNGAVQGGAYCILQRRWTG VWPVLPAREVMISRTLQFEVGGSIGLMFYLA NVCGCAVSLLGVESVLDVFGA     1245   2595   A   9849   573   1620   KSKCRFFEGLSEGFGFMKEALSSSQVQEAE AMIDEPQGQAGSLTVVVISEHSSLLPQDMM SYIGFKRTAVRGIMHREAFNIGRRIVQVAQ AMSLTEDVLAAALADHLPEDKWSAEKRPL KSSLGYEITFSLLNPDPKSHDVYWDIEGAVRR YVQPFLNALGAAGNFSVDSQILYYAALGVNP RFDSASSSYTUDMHSLFHVINPVESRLGSSAA SLYPVLNFILIYVPELAHSPL YIQDKDGAPVAT NAFHSPRWGGIMYNNDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWLONDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQCPAWM QDGLSPCFFFTLVPSTRMALGTLALVLALPCK REERPAGADSLSWGAGPRISSYV     1247   2597   A   9851   2   327   FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF HQFPITDTIQRSKWIRAVNRVDPSSKKWIRCPSVSVS	12.40	23,0	1.7	1 3013	,	303	
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1241   2591			l	1	1		
LDSSTHSSSTATQSRAKMNTPAPTPSTVPAIPR   GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE     SHSVVEFLFKRTKTPSPFHPAVRENRN     1242   2592   A   9843   3   589   TISCGPATEPPASLLSASSDDFCKEKTEDRYS     LGSSLDSGMRTPLCRICTQGPEQGELLSPCK     DGSVKCTHOPCLIKWISERGCWSCELCYYKY     HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS     LFLIASISWLIWSTFSPSARWQRQDLLFQICYG     MYGFMDVMIVAVDSEDMVQAAKEVGKRWS     DIPP     DGFHSNFILANAQVAKGFPIVYCSDGFCELAG     FARTEVMQ     FARTEVMQ     PICGFLYLCSAMASESSPLLAYRLLGEGVAL     PANGAGGPGGASARKLSTFLGVVVPTVLSMF     SIVVFLRIGFVVGHAGLLQALAMILVAYFILA     LTVLSVCAIATNGAVQGGAYCILQHRWTG     VWPVLPAREVMISRTLGPEVGSIGLMFYLA     NVCGCAVSLLGLVESVLDVFGA     A   9849   573   1620   KSKCRFFEGI.SEGFGPMRKEALSSGSVQEAE     AMIDEPQEQAEGSLTVYVISEHSSLLPQDMM     SYIGPKTAVVRGIMHREAFNIGRRIVQVAQ     AMSLTEDVLAAALADHLPEDKWSAEKRPL     KSSLGYBITFSLLNPDPKSHDVYWDIEGAVRA     VVOPFLNALGAAGNFSVDSQILYYAMLGVNR     RFDSASSSYYLDMHSLPHVINPVESRI.GSSAA     SLYPVLNFILYVPELAHSPLYIQDKDGAPVAT     NAFHSPRWGIMYNVDSKTYNASVLPVRV     EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL     LSGPTSEGLMTWELDRLLWARSVENLATATT     TLTSLA     TLTSLA     TLTSLA     PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS     A   9850   114   464   PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS     A   RSLGRRRIAMVTVGNYCEAEGPVGPAWM     QGLSPCFFFTLVPSTRMLGTLALVLALPCK     RREPPAGADSLSWGAGPRISSYV     1247   2597   A   9851   2   327   FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF     HQPFTDTIGRSKWIRAVIRVDPRSKKWIWIPGP     GALLCSKHFQESDFESYGIRRKLKKGAVPSVS	L	<u> </u>	<u> </u>				
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DGSVKCTHOPCLIK WISERGCWSCELCYYKY	1242	2592	A	9843	3	589	TISCGPATEPPASLLSSASSDDFCKEKTEDRYS
DGSVKCTHOPCLIK WISERGCWSCELCYYKY			- "				LGSSLDSGMRTPLCRICFOGPEOGELLSPCRC
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LFLIASISWLIWSTFSPSARWQRQDLLFQICYG		Į.				ļ	
1243   2593   A   9846   198   411   WRISHHAGKMPVMKGLLAPQNTFLDTIATRF DGTHSNFILANAQVAKGFPIVYCSDGFCELAG FARTEVMQ     1244   2594   A   9848   116   650   PICGFLYLCSAMASESSPLLAYRLLGEEGVAL PANGAGGPGGASARKLSTFLGVVVPTVLSMF SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA LTVLSVCAIATNGAVQGGAYCILQHRWTG VWPVLPAREVMISRTLGPEVGGSIGILMFYLA NVCGCAVSLLGLVESVLDVFGA     1245   2595   A   9849   573   1620   KSKCRFFEGISEGFGPMRKEALSSGSVQEAE AMLDEPQGAEGSLTVYVISEHSSLLPQDMM SYIGPKRTAVVRGIMHREAFNIIGRRIVQVAQ AMSLTEDVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLLNPDPKSHLDVYWDIEGAVRR YVQPFLNALGAAGNFSVDSQILYYAMLGVNP RFDSASSSYYLDMHSLPHVINPVESRLGSSAA SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT NAFHSPRWGGIMVYNVDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGIMTWELDRLLWARSVENLATATT TLTSLA     1246   2596   A   9850   114   464   PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM QDGLSPCFFFTLVPSTRMALGTLALVLALPCK RRERPAGADSLSWGAGPRISSYV     1247   2597   A   9851   2   327   FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF	ĺ	1	i	1	1	1	
1243   2593   A   9846   198   411   WRISHHAGKMPVMKGLLAPQNTFLDTIATRF DGTHSNFILANAQVAKGFIVYCSDGFCELAG FARTEVMQ     1244   2594   A   9848   116   650   PICGFLYLCSAMASESSPLLAYRLLGEEGVAL PANGAGPGGASARKLSTFLGVVVPTVLSMF SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA LTVLSVCAIATNGAVQGGGAYCILQHRWTG VWPVLPAREVMISRTLGPEVGGSIGLMFYLA NVCGCAVSLLGLVESVLDVFGA   NVCGCAVSLLGLVESVLDVFGA   NVCGCAVSLLGLVESVLDVFGA   KSKCRFPEGLSEGFGPMRKĒALSSGSVQEAE AMLDEPQEQAEGSLTVVVISEHSSLLPQDMM SYIGPKRTAVVRGIMHREAFNIGRRIVQVAQ AMSLTEDVLAAALADHLPEDKWSAEKRRPL KSSLGYEIFFSLLNPDPKSHDVYWDIEGAVRR YVQPFLNALGAAGNFSVDSQILYYAMLGVNP RFDSASSSYYLDMHSLPHVNPVESRLGSSAA SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT NAFHSPRWGGIMYNVDSKTYNASVLPVRV EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL LSGPTSEGLMTWELDRLLWARSVENLATATT TLTSLA     1246   2596   A   9850   114   464   PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM QDGGSPCFFTLVPSTRMALGITLALVLALPCK RRERPAGADSLSWGAGPRISSYV     1247   2597   A   9851   2   327   FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF HQFPTDTIQRSKWIRAVNRVDPRSKKIWIPGP GAILCSKHFQESDFESYGIRRKLKKGAVPSVS	1			i			
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FARTEVMQ   PICGFLYLCSAMASESSPLLAYRLLGEEGVAL   PANGAGGPGGASARKLSTFLGVVVPTVLSMF   SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA   LTVLSVCAIATNGAVQGGGAYCILQHRWTG   VWPVLPAREVMISRTLGPEVGGSIGMFYLA   NVCGCAVSLLGLVESVLDVFGA	1243	2593	A	9846	198	411	
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq- uence		USSN 09/496	location correspondi	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	пенсе		914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Í		-	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	peptide	sequence	/=possible nucleotide deletion, \=possible
	-			sequence		nucleotide insertion
1248	2598	A	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE
1248	2398	A	9633	30	***	FRGITVVELIKKEGSTLGLTISGGTDKDGKPR
				)	ļ	VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR
	1					LRHDEITLLKNYGERVVLEVEYELPPPGGCP
		j				WT
1249	2599	A -	9856	2	1265	LPPPRPSRHRRGRAGTRASAAAAAGPTVSAV
1249	2599	A	9836	2	1203	
		Ì	1	1	}	RAPVRGQDSGAGTPQGRLAGRGAHLSRVGA
		1			!	SGSGVAAGPAARHAPRRRCADAGEAVGASC
	1	!			Į.	GRCAVALLSGVCTLVSTHVCVGSGCPGAAGT
i	1					PMGAGDAGASAESAVTTAPQEPPARPLQAGS
ĺ	1	1	1	1	1	GAGPAPGRAMRSTTLLALLALVLLYLVSGAL
			i			VFRALEQPHEQQAQRELGEVREKFLRAHPCV
					1	SDQELGLLIKEVADALGGGADPETNSTSNSSH
		1			1	SAWDLGSAFFFSGTIITTIGGGGDWHVGGGK
ľ	ì	i	ł	1	İ	ELPHGGRCRETEGSQVAPRLPASPLCPGYGN
		i				VALRTDAGRLFCIFYALVGIPLFGII.LAGVGD
}		Į.				RLGSSLRHGIGHIEAIFLKWHVPPELVRVLSA
	1	İ		Ì	1	MLFLLIGCLLFVLTPTFVFCYMEDWSKLEAIY
		<u> </u>	<b></b>			FVIVTLTTVGFGDYVA
1250	2600	Α	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRNDF
}				1	1	EWVYTDQPHTQRRKEILAKYPAIKALMRPDP
		1	3	1		RLKWAVLVLVLVQMLACWLVRGLAWRWLL
1			ı		ĺ	FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR
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ļ		1		ļ		WLVLQPFFYSLRPLCVHPKAVTRMEVLNTLV
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1251	2601	Α	9875	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSR
İ		ł	1	1	ì	LESYRPDTDLSREDTGCNLQHISDRENIDDLN
		1				MEFNPSDHPRASTIFLSKSQTDVREKRKSLFIN
}	Į.					HHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTI
	1				!	KCVALAIYYHIKNRDPDGRMLLDIFDENLHPL
					İ	SKSEVPPDYDKHNPEQKQIYRFVRTLFSAAQL
j		}				TAECAIVTLVYLERLLTYAEIDICPANWKRIV
	1	1			l	LGAILLASKVWDDQAVWNVDYCQILKDITVE
	-					DMNELERQFLELLQFNINVPSSVYAKYYFDL
					ļ	RSLAEANNLSFPLEPLSRERAHKLEAISRLCED
10	2602	<u> </u>	0000	ļ	777	KYKDLRRSARKRSASADNLTLPRWSPAIIS
1252	2602	A	9879	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT
						KAVGIKMGSLSTANVEFCLDVFKELNSNNIG
	1					DNIFFSSLSLLYALSMVLLGARGETEEQLEKV
1055	2665	<u> </u>	10000	100	l	WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
1253	2603	Α	9880	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC
						NFTHATFVLIGIPGLEKAHFWVGFPLLSMYVA
			1			AMFGNC
1254	2604	A	9881	19	494	VISFQIITDTIMDSSTAHSPVFLVFPPEITASEYE
	1	1	ŀ			STELSATTFSTQSPLQKLFARKMKILGTIQILF
			l			GIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG
		]			}	SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSA
						LGAIAGIILLTFEFHPRSKLHL
1255	2605	A	9896	72	386	RPGREQRDCFQAPPLGLGGRQTDMMHHPLT
	1		1	1	ŀ	GATCVGLPNVGMCPQLSGALTFMYLQQGNQ
	İ	]	J	ŀ	J	EATVAPDTMAQPYASAQFAPPQNGIPGEYTA
						PHPHPAPEYTGQTT
1256	2606	A	9902	95	399	SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG
-	1	l	1			DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK
		1		i		PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH
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1257	2607	A	9905	374	459	EHLKSTPNRLGVVAHTCNPSTLGGRGGW
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	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID		hod			nucleotide	
NO: of	NO: of peptide	liod	ID NO:	beginning nucleotide	location	D-Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G-Glycine, H=Histidine,
		ĺ	USSN	location		l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496	correspondi	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	пенсе		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
-			ļ	residue of	sequence.	Y=Tyrosine, X=Unknown, *=Stop codon,
				-	sequence.	
			l	peptide		nucleotide insertion
1050	2608	Ā	9911	sequence 364	1974	AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
1258	2006	^	9911	364	] 1974	QRRGPSCGASGDPQCVGSPHPQRARPLLARP GARLLPGHLPSPRPPRLPTGQPPAAAFRGPVR
						PQGGGHIHPLPTPGGRPCFAVSEGSGSALLLS
				ļ	1	YLGECGSSSYVTGAACISPVLRCREWFEAGLP
						WPYERGFLLHQKIALSRYATALEDTVDTSRL
)					]	FRSRSLREFEEALFCHTKSFPISWDAYWDRND
						PLRDVDEAAVPVLCICSADDPVCGPPDHTLTT
j				}	ļ	ELFHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
ĺ			i			HEVILESFRALTEFFRTEERIKGLSRHRASFLG
ļ		1		}		GRRRGGALQRREVSSSSNLEEIFNWKRSYTRL
					1	MAAAAGAAAAPGSREPQDRPECGAGHPGPR
			İ	!		YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR
Į						ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
}		ł	ł	ł	{	PMVKSSASGQGASGSYNHVREEMLIKAGGA
		1		ļ.	1	MSRRVVRQSKFRHVFGQAAKADQAYEDIRV
		ł	Į	ł	i	SKVTWDSSFCAVNPKFLAIIVEAGGGGAFIVL
						PLAK
1259	2609	Α	9919	693	935	GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
}				i	·	TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
		L		h		PPRPGRSHRKRKLVSTK
1260	2610	A	9921	455	1082	QRSCLCSAIEKDGGDVKALYRRSQALEKLGR
.		1	1	l		LDQAVLDLQRCVSLEPKNKVFQEALRNIGGQ
ŀ						IQEKVRYMSSTDAKVEQMFQILLDPEEKGTE
		1	ļ		ì	KKQKASQNLVVLAREDAGAEKIFRSNGVQLL
ŀ			1			QRLLDMGETDLMLAALRTLVGICSEHQSRTV
ſ		[	Í	ĺ		ATLSILGTRRVVSILGVESQAVSLAACHLLQV
1061		<b> </b>	0000	<u> </u>	420	MFDALKEGVKKGFRGKEGAIIV
1261	2611	A	9928	1	438	GFRGAEAPGAAQAPKKKKPRPTEGGPGAGSG
		i				RGKDPYRGPTLLHQPKPPKDEFLSSLESYEIAF
- (			ľ	[		PTRVDHNGALLAFSPPPPQRQRRGTGATAES
i			1			RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
1262	2612		0031	1.00	436	WTREGLAWQRADRPHCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
1						PPRLPFCLQELQGRHALHTFSLERTCSYQDFL
12/2	2612		0022		400	WADEGRLLHVGAQDLATWHTLSPLGLW
1263	2613	A	9938	247	488	RMSATSVDQRPKGQGNKVSVQNGSIHQKDG
}			}	I		CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
1364	2614		0041		077	YAPSIGFPYSLGEAAWSQL
1264	2614	A	9941	61	277	ESIGLTALGPRRRPWEHRWSDPITLKMKGWG
		ļ		1		WLALLLGALLGTAWARRSQDLHCGACKAVR
1365	2616		0056	l	622	RRVRQFNIYDY
1265	2615	Α	9956	2	522	FVASEVSKMPVPASWPHPPGPFLLLTLLLGLT
			<b>\</b>	!		EVAGEEELQMIQPEKLLLVTVGKTATLHCTV
(			1	]	1	TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP
İ				1		RVTTVSDLTKRNNMDFSIRISSITPADVGTYY
ĺ						CVKFRKGSPDHVEFKSGAGTELSVRGEYSVG
1266	2616		10000	242	207	FLSQVWWWLSSHPFMN
1266	2616	A	10002	243	387	PKNNACHLLFTAVCQPRCKHGECIGPNKCKC
	200	ļ.,	1000	-		HPGYAGKTCNQGRKTV
1267	2617	A	10004	36	707	LPAPASTWSVARETMASSSVPPATVSAATAG
1	į			i i		PGPGFGFASKTKKKHFVQQKVKVFRAADPLV
l						GVFLWGVAHSINELSQVPPPVMLLPDDFKAS
1				}		SKIKVNNHLFHRENLPSHFKFKEYCPQVFRNL
1						RDRFGIDDQDYLVSLTRNPPSESEGSDGRFLIS
J						YDRTLVIKEVSSEDIADMHSNLSNYHQVRPLS
			1	1	l	SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP
10.0			40000	<del></del>		ODOLEDI WEDOLEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LEGO DE LE
1268	2618	A	10005	2	209 ·	GEGYELFVPSNGVPAVCHMVGRRPHRAVLSP SQDELEHSLGESAAQGAAGVVLWVSWENTR

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Scrine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion TKVSLGLA
1269	2619	A	10010	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHD LQLRNLSVADHSKTQVQKKENKSLKRDTKAI IDTGLKKTTQCPKLEDSEKEYVLDPKPPPLTL AQKLGLIGPPPPPLSSDEWEKVKQRSLLQGDS VQPCPICKEEFELRPQVFSIRG
1270	2620	A	10011	2	588	RVDDFVRPLPPGLMSRSRASIHRGSIPAMSYA PFRDVRGPSTHRTQYVHSPYDRPGWNPRFCII SGNQLLMLDEDEIHPLLIRDRRSESSRNKLLR RTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK QYSMEGAPAAPFRPSQGFLSRRLKSSIKRTKS QPKLDRTSSFRQILPRFRSADHDRYRGWSMW DEIDV
1271	2621	A	10013	209	363	LPAPPNLSPRLSFGFQFPGGNDNYLTITGPSHP FLSGAEVSOSCRRRGGRA
1272	2622	A	10014	7	388	SAVTISWKWRSVMGIQTSPALLASLGAGLVT LLGLAVGSYLVRRSRRPQVTLLDPNEKDLLR LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTPVT SDEDQGYVDIDIKVYLKGVHPTFPEGGKMSH
1273	2623	A	10016		3750	MAARTLGRGVGRLLGSLRGLSGQPARPPCGV SAPRRAASGPSGSAPAVAAAAAQPGSYPALS AQAAREPAAFWGPLARDTLVWDTPYHTVW DCDFSTGKIGWFLGGQLNVSVNCLDQHVRKS PESVALIWERDEPGTEVRITYRELLETTCRLA NTI.KRHGVHRGDRVAIYMPVSPLAVAAMLA CARIGAVHTVIFAGFSAESLAGRINDAKCKVV ITFNQGLRGGRVVELKKIVDEAVKHCPTVQH VLVAHRTDNKVHMGDLDVPLEQEMAKEDP VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT QAGYLLYAALTHKLVFDHQPGDIFGCVADIG WITGHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVERLKINQFYGAPTAVRLLLKYGD AWVKKYDRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLVDTWWQT
12/4	2624	A	10017	1	3750	FRPQGTPRSPASHVLTMSAPDEGRRDPPKPKG KTLGSFFGSLPGFSSARNLVANAHSSARARPA ADPTGAPAAEAAQPQAQVAAHPEQTAPWTE KELQPSEKMVSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGLDTTRSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTTRSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTSKAVLTG TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV LTGTKDTVTTGVMGAVNLAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVARGSIQTGV DTSKTVLTGTKDTVCSGVTGAMNVAKGTIQT GVDTSKTVLTGTKDTVCSGVTGAMNVAKGT IQTGVDTSKTVLTGTKDTVCSGVTGAMNVA KGTIQTGVDTTKTVLTGTKNTVCSGVTGAVN LAKEAIQGGLDTTKSWVMGTKDTMSTGLTG AANVAKGAMQTGLNTTQNIATGTKDTVCSG VTGAMNLARGTIQTGVDTTKIVLTGTKDTVC SGVTGAANVAKGAVQGGLDTTKSVLTGTKD AVSTGLTGAVNVAKGTVQTGVDTTKTVLTG TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV VIGTKDTMSTGLTGAANVAKGAVQTGVDTA KTVLTGTKDTVTTGLVGAVNVAKGTVQTGM DTTKTVLTGTKDTIYSGVTSAVNVAKGAVQT GLKTTQNIATGTKNTTFGSGVTSAVNVAKGAA QTGVDTAKTVLTGTKDTVCSGVTGAAN

SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	(	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
}	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ļ	1	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	ļ			peptide		/=possible nucleotide deletion, \=possible
	ļ			sequence	L	nucleotide insertion
ſ	{	(		İ	ĺ	VAKGAIQGGLDTTKSVLTGTKDAVSTGLTGA
l	l	ì	(	1		VKLAKGTVQTGMDTTKTVLTGTKDAVCSGV
}						TGAANVAKGAVQMGVDTAKTVLTGTKDTV
ŀ	1	}		!	!	CSGVTGAANVAKGAVQTGLKTTQNIATGTK NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT
l	1				}	GTKDAVSTGLTGAVNLAKGTVQTGVDTSKT
					ļ	VLTGTKDTVCSGVTGAVNVAKGTVQTGVDT
		1			İ	AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG
{	(	ĺ	[	1	Í	VDASKAVLMGTKDTVFSGVTGAMSMAKGA
ľ		1	Ì	1	ĺ	VOGGLDTTKTVLTGTKDAVSAGLMGSGNVA
Į.						TGATHTGLSTFONWLPSTPATSWGGLTSSRT
Į	1	ļ	ļ	l	}	TDNGGEQTALSPQEAPFSGISTPPDVLSVGPEP
		]	}	1	]	AWEAAATTKGLATDVATFTQGAAPGREDTG
1		ļ		Í		LLATTHGPEEAPRLAMLQNELEGLGDIFHPM
1		l	1	}		NAEEQAQLAASQPGPKVLSAEQGSYFVRLGD
				İ	İ	LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL
}	ł	<u> </u>		ł		QDCFRL
1275	2625	A	10025	124	415	TILARKKEKTCPCKKEIGRNSRSGMYSRKAM
				1		YKRKYSAANTKVEKKKKEKVLAPVTKPVGG
		1				DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHG
				<u> </u>		KKPFS
1276	2626	A	10030	3	507	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMS
i		ł			ļ	ASRPQSPTTPWCLPRRYMKHKRDDGPEKQED
ł		l	1		}	EAVDVTPVMTCVFVVMCCSMLVLLYYFYDL
}	!	1	1	ļ	1	LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK
1	l			1		CRIPNNSLPYFHKRPQARMLLLALFCVAVSV VWGVFRNEDQ
1277	2627	A	10035	51	869	YSRFTVPLPATMASSEVARHLLFQSHMATKT
12//	2027	^	10033	1 31	007	TCMSSQGSDDEQIKRENIRSLTMSGHVGFESL
	-	1		1		PDQLVNRSIQQGFCFNILCVGETGIGKSTLIDT
ļ						LFNTNFEDYESSHFCPNVKLKAQTYELQESN
ł	1	ł		}	}	VQLKLTIVNTVGFGDQINKEERQLGRSQSTEN
[	į	l	ļ	1	}	PQKYRSEQHPVEPKKCTSFWKGALGKWAGIE
ļ		}	1			SSGQSAQQPYLPINSPPHRLADVADVHLFSSV
İ					l .	LSGAFGCYHLDVTVNEFKKQQNRDEQEGYS
						KGDQEQGSWKHGADPLRGGEM
1278	2628	Α	10036	3	457	RAFDVRRKKSLRPCCPRDFHAGCLTVSGPST
			ļ	1		VMGAVGESLSVQCRYEEKYKTFNKYWCRQP
	ł	1	ì	!	[	CLPIWHEMVETGGSEGVVRSDQVIITDHPGDL
	ŀ	ł	i	1	[	TFTVTLENLTADDAGKYRCGIATILQEDGLSG
1070	3/22	<del> </del>	10030	1214	425	FLPDPFFQVQVLVSSASSTENSVKTP
1279	2629	A	10039	214	435	NDSLVPMSSWRSCARAPSSESAWRRSAATRR
	1	1	1	-		SRKCLRTKRKRWSSGKGTQMQSTLSETPRRA
1290	2620	<del> </del>	10042	2	344	QMPCMWWYPFWG
1280	2630	A	10043	4	344	RATWHNAGKEREAVQLMAGAEKRVKASHS FLRGLFGGNTRIEEACEMYTRAANMFKMAK
		}	į .	1	}	l
		1			]	NWSAAGNAFCQAAKLHMQLQSKHDSATSFV
1281	2631	<del> </del>	10080	620	818	DAGNAYKKADPQGKTARHVACYLCV VIYKLDSSLFSYFIYFFIFETESHFLPLMKWTG
1201	2031	A	10090	020	010	PIMAHCSLKILASRNSADSAFLSAGDTSLSHST
1282	2632	Ā	10084	3	1640	SASIIIRGDKRASGEVGIAPSSRHILIGEPSAKY
1202	2032	1 ^	10004	1	1040	NGTAIISLVRGPGILGEVTVFWRIFPPSVGEFA
		1	1	Į.		ETSGKLTMRDEOSAVIVVIOALNDDIPEEKSF
	1		1	j		YEFOLTAVSEGGVLSESSSTANITVVASDSPY
j		!			]	GRFAFSHEOLRVSEAORVNITIIRSSGDFGHVR
				[		LWYKTMSGTAEAGLDFVPAAGELLFEAGEM
1	1	l	ļ			RKSLHVEILDDDYPEGPEEFSLTITKVELQGR
}	İ	1	1			GYDFTIQENGLQIDQPPEIGNISIVRIIIMKNDN
1	!	1	ļ	<b>{</b>		AEGHEFDPKYTAFEVEEDVGLIMIPVVRLHGT
·	<b></b>			<u> </u>		

NO. of No. of nociceoted models of the properties of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the nocice of the n	SEO ID	SEQ ID	Met	SEQ	Predicted	T Donations	
Decidide   Seq						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
1280   10092   290   728   10092   290   728   1285   2635   A   10100   1   574   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374	1	1	,				D-Aspartic Acid, E-Giutamic Acid,
Uence	1	1					I-Isolaucine K-Lucine I - Isolaucine,
1286   2636   A   10100   1   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374   374							
amino acid residue of sequence   for peptide residue of sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence   for peptide sequence		]	J				
Peptide sequence			ļ.				T=Threonine, V=Valine, W=Tryptophan
peptide   peptide   peptide   prossible nucleotide deteiton,   possible nucleotide insertion   publicated   publicated   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publication   publi					residue of		Y=Tyrosine, X=Unknown, *=Stop codon.
YGYYTADFISCSSSASPIGOTYLILIGSTYIC					peptide		
HGONLSFINSIDDNESSEPPIELLITGATOS		<u> </u>			sequence		
AVI.GRILVSRIIJAKSDSPFGVIRFILOSSKISIA   NPNSTMIS.IV. IRETGGLIGEQVNWETVGFN   SQEALLPQNRDIADPYSGLFYFGGGGGVRTII   LTITYPHEEIEVEFFTIKI.H. IV. IRETGGLIGEGKLIDSRAK   DVTLTTQFGDPNGVVQFAPETLSKKTYSEPL   ALEOPLLITEFYRRVGTTGGEGGKLIDSRAK   DVTLTTQFGDPNGVVQFAPETLSKKTYSEPL   ALEOPLLITEFYRRVGTTGGEGGKLIDSRAK   DVTLTTQFGDPNGVVQFAPETLSKKTYSEPL   ALEOPLLITEFYRRVGTTGGEGKLIDSRAK   DVTLTTQFGDPNGVVQFAPETLSKKTYSEPL   ALEOPLLITEFYRRVGTTGGEGGKLIDSRAK   DVTLTTQFGDPNGVVQFAPETLSKKTYSEPL   ALEOPLLITEFYRRVGTTGGEGGKLIDKAKTYSEPL   ALEOPLLITEFYRRVGTTGGFGALTAVHTQTGYPAM   ALEOPLLITEFYRRVGTTGGFGALTAVHTQTGTPAM   HLXRS   TSPSPRAMASALIYVSKFKSFVILVVTPLILI.P   LVILMPAKFVRCAYVIILMAJYWCTEVIPLAV   TSLMPVLFPI-FQILDSRQVGYMKDTNML   FLGGLIVAVAVERWITHKRIALRITLLWVGA   KPARIMLIGFRGVTALLSMWITATTAMWV   FLGGLIVAVAVERWITHKRIALRITLLWVGA   KPARIMLIGAMGVTALLSMWITATTAMWV   FLGGLIVAVAVERWITHKRIALRITLLWVGA   KPARIMLIGQMEATSAATEAGLELVDKGKAKE   LP   AAAATTISFKGTSPSKYVKIKNVGGALYYTT   MQTLTKQDTMLKAMTSGRNEVLTDSEGWIL   IDROCKHFGTTUTLYJLDGAQTAVYTOL   DROCKHFGTTUTLYJLDGAQTAVYTOL   AAAATTISFKGTSPSKYVKIKNVGGALYYTT   MQTLTKQDTMLKAMTSGRNEVLTDSEGWIL   DROCKHFGTTUTLYJLRDGAQTUTLGGFGTQ   GRSKDTDLMTFUTLYJLLGGFGTQ   GRSKDTDLMTFUTSVRRSWWREGHGPGCVRR   VLPPSAHOMDDYTYVSVTGCIVDFQYLEVI   HSA   RSRMGBKPIWEQIGSSFQHTQGRTRTRISG   QRGSDAAGTMGCCTGRCSLICLCALQLVSAL   ERQIFDFLGGWAPLGMFTHVYGLFGTGY   VLPPSAHOMDDYTYVSVTGCIVDFQYLEVI   HSA   RSRMGBKPIWEQIGSSFQHTYQLLFINDMTTQL   AT8   MEEEDESSRGKTESGEDRGDGPPDRDPTLSPS   AT8   A 10107   AT8   MEEEDESSRGKTESGEDRGDGPPDRDPTLSPS   A 10113   237   438   LLSRMPSTNRAGSLKDKPALPEDALEFKEDPEKLFT   DLREIGHGSFGAAYFARDVTROWDRGSSRCHGL   RWRRCSSRGATYARDVTROWDRGSSRCHGL   RWRRCSSRGATYARDVTROWDRGSRCHGL   RWRRCSSRGATYARDVTROWDRGSRCHGL   RWRCCSSRGAGGATYGPPDTVVSKUNGN   PGGQLGFELKGGAGAGGGPTTOTAVLMATD   SGGSKLUSKESKLEVAVIGEN   PGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	}		1				YGYVTADFISQSSSASPGGVDYILHGSTVTFQ
NPNSTMILST.VIERTGGGEGOVNETI   SQRALLPONNDIADPYSGLIGEGOVNETI   LTTYPHERIEVEFTFIIK.HI,VKGEAKLDSRAK     DVTLTUGEFGPPPNGVVQPAPETLSKKTYSEPL     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTFGEIM     ALEGPLLITFYNRVKGTYLILIP     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGPLAND     ALEGR							HGQNLSFINISIIDDNESEFEEPIEILLTGATGG
SQRALLPQNRDIADPYSGLFYFGGGGGGVRTII   LTYPHBEIBUNETPTIKICHI, VKGGAKLDSNAK   DVTLTTUGEFGDPNGUVOGAPETLSKKTYSEPL   ALEGPLLITEPTRYKNGTGERSKLDSNAK   DVTLTTUGEFGDPNGUVOGAPETLSKKTYSEPL   ALEGPLLITEPTRYKNGTGERSKLDSNAK   DVTLTTUGEFGDPNGUVOGAPETLSKKTYSEPL   ALEGPLLITEPTRYKNGTGERSKLDSNAK   DVTLTTUGEFGDPNGUVOGAPETLSKKTYSEPL   ALEGPLLITEPTRYKNGTGERSKLDFTANGLFT   VSPSHLPNLYGFSALHAVHLHQWTGYPAM   HLXRS   PSPSHAMASALIVVSKFKSFVILVVTPLILLT   LVILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVOQYAMDTNML   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVOQYAMDTNML   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVOQYAMDTNML   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVOQYAMDTNML   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVOQYAMDTNML   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   TSLMPVLLEPTLGULDSRQVAYVITAMWSITATAMM   FLUILMPAKFVRCAYVIILMAJFWCTEVPLAV   ALAGATITSFKGTSPSSKYVKLINVGGALTYTT   MQTITKQDTMILKAMFSGRAVVLTDSGGWIL   DRCGKHGTILNYILRDGAVPLPESKEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   ALAGAYVLVQGUPEQOAAQV   PSRSHEBELL   PSRSHQBVYQLFTONDRTQL   PSRSHEBELL   PSRSHQBVYQLFTONDRTQL   PSRSHEBELL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVXQLFTONDRTQL   PSRSHQBVYQLFTONDRTQL   PSRSHQBVXQLFTONDRTQL   PSRSHQBVXQLFTON	[	ſ	[	[	[	[	AVLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIA
LTTYPHEEIVETTIIKI,H_IVKGEAKLDSRAK	ł						
1283   2633   A   10088   316   516   MGSKTLPAPVPIHPSLQLTNYSFLQANGLPT	ł		1	Į		1	SQEALLPQNRDIADPVSGLFYFGEGEGGVRTII
1283   2633   A   10088   316   316   316   MGSKTLPAPPHIPSI.QLTNYSFLQAVNGLPT		[	[	ĺ	ĺ	ĺ	
1283						ļ	
1284	1283	2633	A	10088	316	516	MCSKTI BADVDILDSI OI TRIVSEI OAVRICI DT
1284		1	``	10000	1 3.0	310	VPSDHI PNI VGESAI HAVUI HOWTI GVDAM
1284		1			ļ		HLXRS
LVILMPAKFYRCAYYIILMAIYWCTEVIPLAY   TSIMPYLIPFICIDISTYCVOJYMKOTTNML   FLIGGLIVAVAVERWAITHKRIALRTILLWVGA   KPARLMLIGFMGVYALLSMWISNTATTAMMV   PIVEALLQQMEATSAATEAGLELVDKGKAKE   LP   LP   LP   LP   LP   LP   LP   L	1284	2634	A	10091	2	569	
TSLMPVLLFPLEQILDSRQVCVQYMKDTNML	ĺ		İ				LVILMPAKFVRCAYVIILMAIYWCTEVIPLAV
FLGGLIVAVAVERWINLIKRIALRITLLWVGA   RPARLMI GFMOVTALLSMWISNTATTAMMV   PIVEAIL QQMEATSAATEAGLELVDKGKAKE   LP			1.				TSLMPVLLFPLFQILDSRQVCVQYMKDTNMI.
PIVEALI QOMEATSAATEAGLELVDKGKAKE		Į	ì	1			FLGGLIVAVAVERWNLHKRIALRTLLWVGA
LP	l	1	ľ	1			KPARLMLGFMGVTALLSMWISNTATTAMMV
1285							PIVEAILQQMEATSAATEAGLELVDKGKAKE
AAATRTTSFKGTSPSSKYVKLINVGGALYYTT   MQILTKQDIMLKAMFSGRMEVLTDSEGWIL   DRCCKHFGTILNYLRDGAVPLFBSRBIEELL   AEAKYYLVQGLVEEQQAALQV   RPRGRGAWAGPGGDYSGVRRQQRRTTISGS   QRGSDAAGTMGCCTGRCSLCLCALQLVSAL   ERQIFDFLGFQWAPILGNFHIIVVVIGLFGTIQ   YRPRYMVYTYWTALWVTWNVFIIGFALG   GLSKDTDLMTFNISVHRSWREHGPGCVRR   YLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI   HSA   10107   1   478   MEEDESRGKTEESGEDRGGFPDRDTLSPS   AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL   RWRRCRSPRSEPRSQESGGTDTATVLDMATD   SFLAGLVSVLDPPDTWVPSRLDLRFGESEDM   LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG   KT   LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT   DLREIGHGSFGAAYFARDVRTNEVVAIKKMS   YSG   SGAKAXSAVLPPGPPCSSILLSPPAPLTPRSPG   TEATRPTAMSKSLKKKSHWTSKVHESVIGRN   PEGQLGFELKGGAENGGPYLGEVRGKVAY   ENGSKLVSEELLLEVNETPVAGLTRDVLAVI   KHCKDPLRIKCVKQGESSGLLSVLPGGTAR   GAGQ   GAGQ   T191   2641   A   10116   128   591   RTIRETERSALSCSVLKSEPLFGLOPQASQOR   RRRLPGRRQVQVQESGGSGLRAWVLAMASV   VSILSIFLAPFKHLSPGITNTEDDDTLSTSSAE   VKENRNVGNLAARPPPSGDRARGARR   VFRVGERIRGHRCPDPLCLLDMLFLSFHAG   SVEETERGAAPVGRORGFRRSKRKDK   VSILSIFLAPFKHLSPGITNTEDDDTLSTSSAE   VKENRNVGNLAARPPPSGDRARGAGGCGCSAR   VFRVGERIRGHRCPDPLCLLDMLFLSFHAG   SVEETERGAAVVLVIQSLPKNGSFQPTNEMM   LKFYSFYKQATEGPCKLSRRFGFWDPIGRYKW   DAWSSLGDMTKEEAMMAYVEEMKIIETMP	1205	2625	ļ	10000			L
1286	1283	2033	A	10092	290	728	
DDRCGKHFGTLLNYLRDGAVPLPESRREIEELL   AEAKYYLVQGLVEECQAALQV			ļ	]			
1286						•	MQILIKQDIMLKAMFSGRMEVLTDSEGWIL
1286	1	1	ł	1			
QRGSDAAGTMGCCTGRCSLICLCALQLVSAL ERQEFOFLGFOWAPILGNFHHIIVVILGLFGTIQ YRPRYIMVTVWTVALWVTWNTLICIFGTIQ YRPRYIMVTVWTVALWVTWNTLICIFGTIQ YRPRYIMVTVWTVALWVTWNTLICIFGTIQ GLSKDTDLMTFNISVHRSWWREHGPGCVRR VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI HSA  1287 2637 A 10103 252 376 RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQL GAIYVSFQL  1288 2638 A 10107 I 478 MEEEDESRGKTEESGEDRGDGPPDRDPTLSPS AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRCRSPRSEPRSQESGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT  1289 2639 A 10113 237 438 LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  1290 2640 A 10114 367 856 RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRYTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPYAGLTIRDVLAVI KHCKDPLRIKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRVVGNLAARPPSGDRARGGATR VPRVGERLRGHRCPDFLCLLDMIFLSFHAG SWESWCCCCCUPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMMAYVEEMKKIETMP	1286	2636	Α	10100	1	574	
ERQIFDFLGFQWAPILGNFLHIIVVILGLFGTIQ		1	1	10100	•		ORGSDA AGTMGCCTGRCSLICLCALOLVSAL
VRPRYIMVYTVWTALLWYTWNVFIICFYLEVG	ļ	1	l	}			EROIFDFI GFOWAPII GNEL HILVVII GI FGTIO
Common							YRPRYIMVYTVWTALWVTWNVFIICFYLEVG
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CATYVSFQL							HSA
1288   2638   A   10107   1   478   MEEEDESRGKTEESGEDRGDGPPDRDTLSPS AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRRCRSPRSEPRSQESGGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT   LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG     1290   2640   A   10114   367   856   RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGGFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ   RTIGETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR   QRRFFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQCHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSCGPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIETMP	1287	2637	Α	10103	252	376	
AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRRCRSPRSEPRSQESGGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT  LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  LESRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  LESRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  TEATRPTAMSK SLKKKSHWTSK VHES VIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESGGLLSVLPGGGTAR GAGQ  RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292  2642 A 10121 1 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVVQSLFPGFWDPICRYKW DAWSSLGDMTKEEAMIAYVEEMKKIETMP	1200	2620		10107	-,		
RWRRCRSPRSEPRSQESGGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT  1289 2639 A 10113 237 438 LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  1290 2640 A 10114 367 856 RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSK SLKKKSHWTSK VHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292 2642 A 10121 1 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRRGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1200	2038	A	10107	1	478	
SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM   LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG   KT				ļ	,		
LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT  1289 2639 A 10113 237 438 LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG  1290 2640 A 10114 367 856 RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRRSKKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292 2642 A 10121 I 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP		]			ļ	,	
1289   2639   A   10113   237   438   LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT					i		
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1290 2640 A 10114 367 856 RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERSALSCSVLKSEPLPGLOPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR  1292 2642 A 10121 1 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	$\nabla$				1		DLREIGHGSFGAAYFARDVRTNEVVAIKKMS
TEATRPTAMSK SLKKKSHWTSK VHES VIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292 2642 A 10121 I 749 QRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP							YSG .
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PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ  1291 2641 A 10116 128 591 RTIRETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPSGDRARGGATR  1292 2642 A 10121 I 749 QRRFFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLDMLFLSFHAG SWESWCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP			j	ľ	ł		TEATRPTAMSKSLKKKSHWTSKVHESVIGRN
SHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ				ļ	ļ		PEGQLGFELKGGAENGOFPYLGEVKPGKVAY
1291 2641 A 10116 128 591 RTIRETERRSALSCSVLKSEPLPGLOPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292 2642 A 10121 1 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP		[			j		ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI
1291 2641 A 10116 128 591 RTIRETERSALSCSVLKSEPLPGLOPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR 1292 2642 A 10121 I 749 QRRRFRAGLWGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	[		ĺ		ĺ	[	
RRRLPGRRQVQVQEGGGSCLRAWVLAMASV LGSGRGSGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR  1292 2642 A 10121 I 749 QRRFFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1201	2641		10112	130	601	
LGSGRGSGLSSQLKCKSKRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR  1292 2642 A 10121 I 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1471	2041	^	10110	126	186	RIKELERKSALSUSVLKSEPLPGLQPQASQQR
VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR  1292 2642 A 10121 I 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	ĺ	Į	1	ĺ	Í	Í	L GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
VKENRNVGNLAARPPPSGDRARGGATR  1292 2642 A 10121 I 749 QRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	ļ	ł	1				VSII STEI APEKUI OPOITATEDDDAT OTOS:
1292 2642 A 10121 1 749 QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDGGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1			-		1	VKENRNVGNI AADDDDSGDDADGGATD
VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1292	2642	A	10121	<del></del>	740	ODDDED AGI WGGUGI TOGI DDNGGGGGGAN
SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP					-	1-77	VPRVGERI RGHRCPDPI CTTT DIATE CETTA
RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	Į	1					SWESWCCCCLIPADR PWDR GOLIWOI CMADT
LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	1	ł	1	ł	ŀ		RSVHETRFEAAVKVIOSLPKNGSFOPTNEMA
DAWSSLGDMTKEEAMIAYVEEMKKIIETMP	ŀ		ļ		j	ļ	LKFYSFYKOATEGPCKLSRPGFWDPIGRYKW
	ļ		ļ	-		1	DAWSSLGDMTKEEAMIAYVEEMKKIIETMP
					}		

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C-Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R-Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LGNVLTSTPNAKTVNGKAESSDSGAESEEEE AC
1293	2643	A	10124	2	989	PLMSLVRVVEFVAASSAQKTPSRLENYYMVC KADEKFNQLVHFLRNHKQEKHLVFFRYSGL CGRGIRDSARMCSTCACVEYYGKALEVLVK GVKIMCIHGKMKYKRNKIFMEFRKLQSGILV CTDVMARGIDIPEVNWVLQYDPPSNASAFVH RCGRTARIGHGGSALVFLLPMEESYINFLAIN QKCPLQEMKPQRNTADLLPKLKSMALADRA VFEKGMKAFVSYVQAYAKHECNLIFRLKDL DFASLARGFALLRMPKMPELRGKQFPDFVPV DVNTDTIPFKDKIREKQRQKLLEQQRREKTEN EGRRKFIKNKAWSKQKAKKK
1294	2644	A	10129	91	1042	VTMYKDCIESTGDYFLLCDAEGPWGIILESLA ILGIVVTILLLLAFLFLMRKIQDCSQWNVLPTQ LLFLLSVLGLFGLAFAFIIELNQQTAPVRYFLF GVLFALCFSCLLAHASNLVKLVRGCVSFSWT TILCIAIGCSLLQIIIATEYVTLIMTRGMMFVN MTPCQLNVDFVVLLVYVLFLMALTFFVSKAT FCGPCENWKQHGRLIFITVLFSIIWVVWISML LRGNPQFQRQPQWDDPVVCIALVTNAWVFL LLYIVPELCILYRSCRQECPLQGNACPVTAYQ HSFQVENQELSRDKWKVLLNSDFLSHSGA
1295	2645	A	10133	376	518	RPRVVTHNSQWCFLPQDHPGWLPGQSGAPG GRGAPRQEGPGSSWRQV
1296	2646	A	10135	3	551	EWSLDPFMGIMSGQVGDLSPSQEKSLAQFRE NIQDVLSALPNPDDYFLLRWLQARSFDLQKS EDMLRKHMEFRKQQDLANILAWQPPEVVRL YNANGICGHDGEGSPVWYHIVGSQDPKGLLL SASKQELLRDSFRSCELLLRECELQSQKLGKR VEKIIAIFGLEGLGLRDLWKPGIELLQE
1297	2647	A	10138	48	407	MVSSCCGSVCSDQGCGQDLCQETCCRPSCCE TTCCRTTCCRPSCCVSSCCRPQCCQSVCCQPT CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCC QPVCCQPTCCRPSCCETTCCHPXCC
1298	2648	A	10156	94	453	GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG QEMYLRFDQTTRRSPYRMSRILARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP INIVAVKNDHDFLEKDLGEPLCRRLNT
1299	2649	A	10161	1	393	PRFSELVDGRGRVSARFGGSPSKAATVRSQPT ASAQLENMEEAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV
1300	2650	A	10162	98	391	AKIASLERIMPANYTCTRPDGDNTDFRYFIYA VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF VPV
1301	2651	A	10165	1	7545	PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV IMEGVQEETDTRDVKRQVERSEICTEEPQKQ

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ŀ	USSN	location	corresponding	I=Isoleucine, K≈Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ŀ		ļ		peptide		/=possible nucleotide deletion, \=possible
1			ļ	sequence		nucleotide insertion
						KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
ł				1		KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
		1	}	,	}	DETELHSSEKGLKVEENIQKQSQQTKLSSDDK
				Į		TERKSKHRNERKLSVLGKDGKPVSEYIIKTDE
1		]	ļ	j		NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
1		{				IQKDSLGSKQHGITLQRRSESYSEDKCDMDST
		ł	ļ	ì		NMDSNLKPEEVVHKEKRRTKSLLEEKLVLKS
ł		ļ	ì	ł		KSKTQGKQVKVVETELQEGATKQATTPKPD
ł		ł	i			KEKNTEENDSEKQRKSKVEDKPFEETGVEPV
1	}		1			LETASSSAHSTQKDSSHRAKLPLAKEKYKSD
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1		1	1			ENKSDDKDGKEVDSSHEKARGNSSLMEKKL
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		1	1	}		STSPADHSALPNQSLTVRESEVLKTSDSKEGG
	1	i	ì			EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ
				1		GKVIMPLGSKLTGVIVENENITKEGGLVDMA
1	<b>!</b>		<b> </b>			KKENDLNAEPNLKQTIKATVENGKKDGIAVD
1		j	]	ļ		HVVGLNTEKYAETVKLKHKRSPGKVKDISID
		ļ				VERRNENSEVDTSAGSGSAPSVLHQRNGQTE
	1	İ	1	İ		DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
	f	1	ĺ	1		AGPATITSSETRQSEVALPCTSIEADEGLIGT
	ļ	1	ļ	i		HSRNNPLHVGAEASECTVFAAAEEGGAVVTE
ļ	}	ł	}	}		GFAESETFLTSTKEGESGECAVAESEDRAADL
	1		i	<b> </b>		LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE
	!		}	}		KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG
			1			TEIRAGSISSEEVDGSQGNMMRMGPKKETEG
			ł			TVTCTGAEGRSDNFVICSVTGAGPREERMVT
i		í	!	İ		GAGVVLGDNDAPPGTSASQEGDGSVNDGTE
	İ		1			GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS
	}		i .	{		SESEENGESAMDSTVAKEGTNVPLVAAGPCD
						DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH
1		J	1			ASTCTGLGEESEGVLICESAEGDSQIGTVVEH
		1	1			VEAEAGAAIMNANENNVDSMSGTEKGSKDT
1		1	ļ	·		DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE
[			J '			GPMTSAASDQSDSQLEKVEDTTISTGLVGGS
1		1	(			YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE
1		Ì	1			NEECDGLMATTASGDITNQNSLAGGKNQGK
1		ĺ	(			VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE
		}				ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS
1		1				RSEEKDECAMISTSIGEEFELPISSATTIKCAES
		l				LQPVAAAVEERATGPVLISTADFEGPMPSAPP
		]	1			EAESPLASTSKEEKDECALISTSIAEECEASVS
{ i			[			GVVVESENERAGTVMEEKDGSGIISTSSVEDC
1			Į į		,	EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS
}		}	}			TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA
1						AUSTSTAECMPISASIDRHEENQLTADNPEGN
		}	}			GDLSATEVSKHKVPMPSLIAENNCRCPGPVR
						GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH
1		1				PSAVCAEKEEKHGKECPEIGPFAGRGOKESTL
1		Ì	<b>(</b>			HLINAEEKNVLLNSLQKEDKSPETGTAGGSST
1			1		İ	ASYSAGRGLEGNANSPAHLRGPEQTSGOTAK
]						DSSVSSIRYLAAVNTGAIKADDMPPVQGTVA
1			)		i	EHSFLPAEQQGSEDNLKTSTTKCITGQESKIAP
L	L	L	L	<i>ــــــ</i>	ا ــــــــــــــــــا	PILIO DI UTAGGOSTO INTERIO I INCLIDATO INTE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	į	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
50,,,,,			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
i			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	ĺ	(	1	peptide		/=possible nucleotide deletion, \=possible
i	1	ĺ	1	sequence		nucleotide insertion
	<del>                                     </del>	<del>                                     </del>	<del>                                     </del>	3040000	<del> </del>	SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK
İ		1	1	ļ		WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS
1	j		J	}		SEENVCDIGNEESPLNVLGGLKLKANLKMEA
1		l	1			YVPSEEEKNGEILAPPESLCGGKPSGIAELQRE
	i	ĺ		l		PLLVNESLNVENSGFRTNEEIHSESYNKGEISS
1	[	1		[		GRKDNAEAISGHSVEADPKEVEEEERHMPKR
l	i					KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC
1		1	1	1		PETEPHATKEENSRDLEELPKTSSETNSTTSRV
j	i		1	1		MEEKDEYSSSETTGEKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPFLRPSPARPPPRPPAPFPSPELAGPEPH
1 1302	2032	1"	10.0.	1 32.	0.12	FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG
1		ļ	1			NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE
1	]	1	l .	1	1	DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP
1		į.	1	1		EARETKCYVRSSVGCVEPLTTQAEVTENLDR
	1					KNSQQVFKLLKKK
1303	2653	A -	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV
1303	2033	<b>'</b> '	10171	200	123	LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA
	ł	l	1			RACEICITYI
1304	2654	A	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAONGF
1304	2034	J ^	10104	1 270	1524	YHEAVVLFTQALKLNPQDHRLFGNRSFCHER
	1	1	ł			LGOPAWALADAQVALTLRPGWPRGLFRLGK
		i				ALMGLQRFREAAAVFQETLRGGSQPDAAREL
1	Ī	1		1		RSCLLHLTLQGQRGGICAPPLSPGALQPLPHA
	1		1		İ	ELAPSGLPSLRCPRSTALRSPGLSPLLH
1305	2655	Α-	10194	2	394	TDLLGRRFRVDGAAMAACEGRRSGALGSSQ
1303	2033	^	10174	1 -	374	SDFLTPPVGGAPWAVATTVVMYPPPPPPPHR
]	ļ	1	]	i		DFISVTLSFGESYDNSKSWRRRSCWRKWKQL
ļ	ł	1	i			SRLQRNMILFLLAFLLFCGLLFYINLADHWKG
			1			IRNTCT
1306	2656	A	10195	1	410	IPGSTISLEGPLSKWTNVMKGWQYRWFVLDY
1300	2030	l "	10175	1 *	710	NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI
			1			GIDDEDDSTFTITVDQKTFHFQARDADEREK
1		Ī				WIHALEETILRHTLQLQVRVFTWFPDSSLVGA
	İ		1			FFFWLVSGFFFK
1307	2657	A	10205	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAM
150,	2037	1.	10205	"	500	DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS
		1	1	1	1	SPDQQNYTKSR
1308	2658	A	10214	2	453	ECGGIROPGPPPALASAPAATMNRVGGSPS
1500	2038	1 "	10217	~		AAANYLLCTNCRKVLRKDKRIRVSOPLTRGP
		[		1		SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL
-					1	DNITQVMSLHTQYLESFLRSQFYMLRMDGPL
1		1	1	1	1	PLPYRHYIAIMAAARHQCSYLINM
1309	2659	A	10233	45	421	RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP
1,509	2039	1	10233	33	721	RALESRTFQGSERSRWGPPLESTKENVQCGH
1	1	1	1	1	1	RPAFPNSSWLPFHERLOVONGECPWOVSIOM
		1				SRKHLCGGSILHWWWVLTAAHCFRRTLLDM
1		}		Į	1	AV
1310	2660	A	10241	243	442	AFOLFNAKCESAFLSKRNPLORNWTVLYRRK
1310	2000	1^	10241	275	772	HKKGQSAEIQKKRTRRAFKFQRAITGASLADI
	1	1		1	1	MAK
1311	2661	A-	10261	751	176	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ
1,11,	2001	l ^	10201	/31	170	VTLNSAICVLSTVLIMEFPDLGKHCSEKTCKQ
}		l l		1		LDFLPVKCDACKQDFCKDHFPYAAHKCPFAF
1	1	l	1	l .		QKDVHVPVCPLCNTPIPVKKGQIPDVVVGDHI
[		1		1	1	DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML
}			1	1	1	OMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI
]		1		ļ .		KAG
1312	2662	A	10270	3	669	STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP
1312	4002	^	102/0	1	303	SMTILDKKDGEQAKALFEKVRKFRAHVEDSD
L	1		J	I	<u> </u>	I SIMILIEDINE DE CANADELEY ANTENNE LA EDOD

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LIYKLYVVQTVIKTAKFIFILCYTANFVNAISF EHVCKPKVEHLIGYEVFECTHNMAYMILKL LISYISIICVYGFICLYTLFWLFRIPLKEYSFEKV REESSFSDIPDVKNDFAFLLHMVDQYDQLYS
1313	2663	A	10287	1221	266	KRFGVFLSEVSENKLREISLNHEWTFEKL GAHRVLSPAQGAQPRLRSAASVEVSMVGQR VLLLVAFLLSGVLLSEAAKILTISTLGGSHYLL LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE EKSYQVIRWFSPEDHQKRIKKHFDSYIETALD GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL KNENYDLVFVEAFDFCSFLIAEKLVKPFVAIL PTTFGSLDFGLPSPLSYVPVFPSLLTDHMDFW GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLLKAELWFVNSDCAPDFARPL LPNTVYIGGLMEKPIKPVPQVSEPSAFSLGFT
1314	2664	A	10288	536	1890	NVQLAKFSSTLVFFFSCDADPSALAKYVLAL VKKDKSEKELKALCIDQLDVFLQKETQIFVEK LFDAVNTKSYLPPPEQPSSGSLKVEFFPPQEK DIKKEEITKEEEREKKFSRRLNHSPPQSSSRYR ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD RYNRRGRSRSYSRSRSWSKERLRERDRD RSRTRSRSRTRSRERDLVKPKYDLDRTDPLEN NYTPVSSVPSISSGHYPVPTLSSTITVLAPTHHG NNTTESWSEFHEDQVDHNSYVRPPMPKKRC RDYDEKGFCMRGDMCPFDHGSDPVVVEDVN LPGMQPFPAQPPVVEGPPPPGLPPPPILTPPPV NLRPPVPPPGPLPPSLPPVTGPPPPLPPLQPSG MDAPPNSATSSVPTVVTTGIHHQPPPAPPSLFT ADTYDTDGYNPEAPSITNTSRPMYRHRVHPR AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVSAKLRAAAEAAAERRTRGA GSRGICAGLRSVAPGPEPLKQEEGRREWGSSI GTPSPCGSAQAAAAAAAEATEKIPALRPALL WALLALWLCCATPAHALQCRDGYEPCVNEG MCVTYHNGTGYCKCPEGFLGEYCQHRDPCE KNRCQNGGTCVAQAMLGKATCRCASGFTGE DCQYSTSHPCFVSRPCLNGGTCHMLSRDTYE CTCQVGFTGRNPKCPGGNLNYQFNGIIVVYS GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT LWVMVSGATSTSTSTL
1316	2666	A	10294	118	572	SLSMESNHKSGÖGLSGTQKEAALRALVQRTG YSLVQENGQRKYGGPPPGWDAAPPERGCEIFI GKLPRDLFEDELIPLCEKIGKIYEMRMMMDF NGNNRGYAFVTFSNKVEAKNAIKQLNNYEIR NGRLLGVCASVDNCRLFVGGIPKTKK
1317	2667	A	10301	158	1956	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQ DRPTKSSMRSAAKPWNPAIRAGGHGPDRVRP LPAASSGMKSSKSSTSLAFESRLSRLKRASSE DTLNKPGSTAASGVVRLKKTATAGAISELTES RLRSGTGAFTTTKRTGIPAPREFSVTVSRERSV PRGPSNPRKSVSSPTSSNTPIPTKHLRTPSTKP KQENEGGEKAALESQVRELLAEAKAKDSEIN RLRSELKKYKEKRTLNAEGTDALGPNVDGTS VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG SSSSDVTKASLSPDASDFEHITAETPSRPLSSTS NPFKSSKCSTAGSSPNSVSELSLASLTEKIQKM EENHHSTAEELQATLQELSDQQQMVQELTAE

NO. of   NO. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Decision		, -	,				
		l .	noa				
1318   2668   A   10303   333   879   Corresponding to periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodic periodi periodica periodic periodic periodic periodic periodic periodic				i .			
uence   914   anj to first amino acid residue of peptide residue of peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Pe		, -		1			
amino acid residue of sequence   female   female of sequence   female   female of sequence   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female   female	seq-	uence	•				
residue of   poptide   sequence   Y=Tyrosine, X=Unknown, **Stop codon,   poptide   sequence   sequence   NEKL/DEKTILETSFHOHRERAEQLSQENEKL   NIKL/DEKTILETSFHOHRERAEQLSQENEKL   NIKL/DEKTILETSFHOHRERAEQLSQENEKL   NIKL/DEKTILETSFHOHRERAEQLSQENEKL   NIKL/DEKTILETSFHOHRERAEQLSQENEKL   EMIKRI.KEENEKI.NEFILE.ERINNNMMAKTL   EERWTILEGI.KURGI.KISHLQQ   CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPRENCIALNO, CORPR	uence	j		914	ng to first		
	1				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				l .	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	i	i		peptide	1 -	/=possible nucleotide deletion, \=possible
NEKL/DEKTILETSFHORERAEQU/SQENEKL   MNLOGRYKNEEPT/OGEKIELG/CTGILE   QGRFREKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQQQLTCSLRKVEERNQGL   EMKRI KEENEKLINIQGLTVEERNAMMAKTL   EECRYTLEGIKMENGSLKSHLQG   GPARPAVIVEHYPGADILINSYAGLACVEEP   INDMITTESSLDVAEREIDDODDDILITYAGACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGDETIETIEAAEALLNMDSPOPMI.DEKENTI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGASSIPACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASACH   DGVAKI VASA		1		1		i	
MNILOGEN/KNEEPTTÖGGKIELEÖKCTGIL   CORFEREKLINIQQCQLTCSLRXVEEENQGAL	·	<del>}</del>	<del> </del>	<del></del>	Sequence	<del>                                     </del>	
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NIPSSPEDDMVJAPYTHVSVTLDGIPEVMETQ	i	Į.			1		NDMITESSLDVAEEEIIDDDDDDDITLTVEASCH
1319   2669   A   10322   169   654   MEYRMSGSVAVTRALOGALIGULIDIATALS.	ļ	İ	}	l .	ì		DGDETIETIEAAEALLNMDSPGPMLDEKRINN
1319   2669   A   10322   169   654   MEYRMSGSVAVTRALOGALIGULIDIATALS.			ľ		<u> </u>		NIFSSPEDDMVVAPVTHVSVTLDGIPEVMETO
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1320   2670   A   10323   441   2   XMMQVAVVIGGGQTLGAPLCHGLAAEGYRY   AVVDIQSDKAANVAQEINAEYGESMAYGFG   ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI   ACAAFISDFQLGDFDRSLQVNLVGYPLCARE   FSRLMIRDGIQGRIQINISKSDE   RIRTAGPGSTISSKIDSASAPAARAMPCEYTY   ARLTSDCSRPSLQWYLYRAQSKMRRPRLLLKD   LIKCTLLYGVGRILVLKINYTIEEGDMKNMH   YVDPDHVKRAQKYAQQVLQKESPPKFAKTS   MALFEHRYSVDLLPFVQKAPTDSEA   EFSNGPVVYSALGNEDDELLLGKDIIGTFAAS   ERKMRAHQVLTFLLLFVITSGASENASTSRGG   GLDLPQNVYLCDAIMGVVVEAVAGAGA   LITLLIMILLIGRIPIFKEKEKKSPAVLHFFL   LGTLG	ļ	ĺ	ļ				
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AVVDIQSDKAANVĀĢEIMAEYĢESMAYĢEG   ADATSEQSVLALSRĢVĒLIFGRVDLLVYSĀGI   AKAĀRISDĒQLĀDFŪRSVŪLLVYSĀGI   AKAĀRISDĒQLĀDFŪRSVŪLLVYSĀGI   AKAĀRISDĒQLĀDFŪRSVŪLVGYFLCĀRĒ   FSRLMIRDDĒQGRIIQINSKSDĒ   RIHKTĀGPĀSTĪSSRĪDSAŠĀPĀĀRĀMPCĒYTY   AKLTSDCSRPSLQWYTRĀQSKMRRPRILLKD   LIKKTLLVFFOVRIVILKLNYTTEEDMKNMH   YVDPDHVKRĀQKYĀQĀVLQKESPPKFĀKTS   MALLFĒHRYSVŪLLPFVQKĀPTŪSĒĀ   EFSNGFVVYSĀGLĀBDĪĒLLLGĀDĪGĪFTĀĀS   ERKMRĀHQVLTFLLLFVĪTSGĀSĒNĀSTSRĀG   GLDLPQNVYLLDLAPVĪSGĀSĒNĀSTSRĀG   GLDLPQNVYLLDLAPVĪSVĀSĀGĀG   ALTILLMLĪLLGRLPFIKĒKĒKKSPĀVLHFLFL   LOTLĀ   GSLĀGĀDĒDĒLLLĀGĀDĪGĀPĀVĀSĀGĀGĀLTĪLLMLĪ   LLVRLPFFKĒKĒKKSPĀVLHFLFL   LOTLĀ   VYVSLCDLĀNĪGĪVPĀASTRĀGĀGĀLTĪLLIMLĪ   LLVRLPFFKĒKĒKKSPĀGLĪLPQ   YVSLCDLĀNĪGĪVPĀASTRĀGĀGĀLTĪLLIMLĪ   LLVRLPFFKĒKĒKKSPVGHHFLFLLGTLĀGP   SSLĀGĀGĀLTĪLLIMLĪ   LLVRLPFFKĒKĒKKSPVGHHFLFLLGTLĀGP   NSVTHHĒVKCQĢKPLĀGĪYRKĒBĒKRĀNĀGN   AVRSĀMKSĒĢKIKDĀRĀGPLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGPLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGPLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGPLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGRĀLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGRĀLVPFPNQKSĒĀ   APPPKPPSSCDSTNĀRĀGRĀLVPFPNQKSĒĀ   APPPKRĀGĀGĀGĀLTĪLLĪJĀS   RIKĀĢFSRĀGPVVYPHĢDLĒĒTDĀKKRĒLĪ   YAQDPSTGCYMYYFQVLSKTYCVDĀTRĒTN   RIGRINHSKCOĢKPLĀGBYPHĀTUKL   RGVTATTĢRĀFABVPCVTLĪLĀS   RIKĀGPĀGSTĀGRĀGRPPMTCWL   RGVTATTĢRĀFABVPCVTLATĀGSRĀGRPPMTCWL   RGVTATTĢRĀFABVPCVTLATĀGSRĀGRPPMTCWL   RGVTATTĢRĀFABVPCVTLATĀGSRĀGRPPMTCWL   RGVTATTĢRĀFABVPCVTLATĀGSRĀGRPPMTCWL   LLKĢFĢKDĢFFFSRKĢKĒLDSNPFASL   VYFWEPLNRQVRVĒĢPVKKLPĒĒBĀCYFHS   RRKSSQIGĀVVSHQSSVIPDRĒFYLRKKNĒĒLĒ   QLYQDĢEVPKPKSWGGYVLYPQVMĒFWQĀ   QVINĀLĪDRĪVPRĀGPPTGLPTGBPPLARMFU   LLKĀFĀGĀGĀGRĀGPTPPKTRĀGĒĒ   DWLYĒRLĀP   DWLYĒRLĀP   ARAĀAHGGICRLVRWWRKĀRSVMGJĪĢTSPV   LLASLĢGGLVVILLĪGLAVGSYLVRRSRRPQVT   LLASLĢGGLVVILLĪGLAVGSYLVRRSRRRQVT	L	L	<u> </u>	<u></u>			
ADATSÉGSVLALSRGVDEFGRVDLLVYSAGI   AKAAFISDFQLGDFDRSLQVNLVGYFLCARE   FSRLMIRDGIQGRIQINSKSDE	1320	2670	A	10323	441	2	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV
1321 2671 A 10332 1 453 RHRTAGROGISISRITOSASAP AARAMPCEYTY AKLTSDCSRPSLQWYTRQSKMRPRILLIKD ILKCTILLYFOVRILYHLKINYTTEECDIKMMH YVDPDHVKRAQKYAQQVLQKESPPKFAKTS MALLFEHRYSVOLLPFVQKAPTDSEA  1322 2672 A 10333 25 423 EPSNGPVVYSALGNEDDEILLIGKDIGTFAAS ERKMRAHQVLTFLLLFYTISGASENASTSRGC GLDLPQNYYLCDLDAIWGIVVEAVAGGA LITLLIMILLIGRIPFIKEKEKKSPAVLHFLFL LGTLG  1323 2673 A 10334 52 426 SSLGNEDDEILSLAKDITGMFVASHRKMRAH QVLTFILLFYTTSVASENASTSRGCGGLDLPQ YVSLCDLDAIWGIVVEAVAGGAA LITLLIMILLIGRIPFIKEKEKKSPAVLHFLFL LGTLG  1324 2674 A 10336 1 932 ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEE NSVTHEVKQCKPLAGIYRKREEKNAGN AVRSAMKSEEQKIKDARGPLVPFPNQKSEA AEPPKTPPSSCDSTNAAIAKQALKKPIKGQA PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE LQSEERKIDELIESGKEEGMKIDLIDGKGRG VIATKQFSRGDFVVEYHGDLIEITDAKKREAL YAQDPSTGCYMYYPQLSKTYCVDATRETN RLGRINHSKCGNCQTKLHDIDGYPHLILAS RDIAAGEELLYDYGDRSKASIEAHPWLKH RGVTATEGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDRAFETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSAML LLKGFGKDGFRFTNFESKKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVSHOSSVPDREYJRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRHDRIVPRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRQVT LLASLGVGLVTLLGLAVGSYLVRRSRRRQVT	j	}					AVVDIQSDKAANVAQEINAEYGESMAYGFG
1321   2671   A   10332   1   453   RHRTAGPGSTISSRTDSASAPARAMPCEYTY   AKLTSDCSRFSLQWYTRAQSKMRRPRILLKD   ILKCTLLVFGVRILYILKINYTTEECDMKNMH   YVDPDHVKRAQKYAQQVLQKESPPKFAKTS   MALLFEHRYSVDLLPFVQKAPTDSEA   10333   25   423   EPBNGPVVYSALGNEDDEILLIGKDIGTFAAS   ERKMRAHQVLTFLLLFVITSGASENASTSRGC   GLDLLPQNVYLCDLDAIWGIVVEAVAGAGA   LITLLMLILGRLPFIKEKEKKSPAVLHFIFL   LGTLG	1		1		ļ		ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI
1321   2671   A   10332   1   453   RHRTAGPGSTISSRTDSASAPARAMPCEYTY   AKLTSDCSRFSLQWYTRAQSKMRRPRILLKD   ILKCTLLVFGVRILYILKINYTTEECDMKNMH   YVDPDHVKRAQKYAQQVLQKESPPKFAKTS   MALLFEHRYSVDLLPFVQKAPTDSEA   10333   25   423   EPBNGPVVYSALGNEDDEILLIGKDIGTFAAS   ERKMRAHQVLTFLLLFVITSGASENASTSRGC   GLDLLPQNVYLCDLDAIWGIVVEAVAGAGA   LITLLMLILGRLPFIKEKEKKSPAVLHFIFL   LGTLG		1		ì		Ĺ	AKAAFISDFOLGDFDRSLOVNLVGYFLCARE
1321   2671   A   10332   1   453   RHRTAGPGSTISSRTDSASAPARAMPCEYTY AKLTSDCSRPSLQWYTRAQSKMRRPRLLLKD ILKCTLLVFGVRLYILKLNYTTEECDMKNMH YVDPDHVKRAQKYAQQVLQKESPPKFAKTS MALFERHSYOLLFPFVQKAPTDSEA   10333   25   423   EPSNGPVVYSALGNEDDEILLLGKDIIGTFAAS ERKMRAHQVLITLLFVITSGASENASTSRGC GLDLLPQNVYLCDLDAIWGIVVEAVAGAGA LITLLLMLLLGRLPFIKEKEKKSPAVLHFLFL LGTLG     1323   2673   A   10334   52   426   SSLGNEDDEILSLAKDITGMFVASHRKMRAH QVLTFLLLFVITSVASENASTSRGCGLDLLPQ YVSLCDLDAIWGIVVEAVAGAGA LITLLLFVITSVASENASTSRGCGLDLLPQ YVSLCDLDAIWGIVVEAVAGAGA LITLLFFFKEKEKKSPVGLHFLFLLGTLGF YVSTELLFFFKEKKKSPVGLHFLFLLGTLGF YVSTELLFFFKEKEKKSPVGLHFLFLLGTLGF YVSTELLFFFKEKKKSPVGLHFLFLLGTLGF YVSTELLFFFKEKEKKSPVGLHFLFLLGTLGF YVSTELLFFFKEKEKKSPVGLHFLFLLGTLGF NSVTHHEVGCQKFLAGVTKKTEEKRNAGN AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA AEPPKTPPSSCDSTNAAIAKQALKFJKGKQA PRKKAQGKYCQNKLATDFYVPKRSSKSKAE LQSEEKKTQDRKLTDFYVPKRSSKSKAE LQSEEKKTDGLIESGKEEGMKIDLIDGKGRG VIATKQFSRGDFVVEYHGDLIEITDAKKREAL YAQDPSTIGGYMYYFQVLSKTVCVDATRETN RLGRLINHSKCONCQTKLHDIDGVFHLILIAS RDIAAGEELLYDVGDRSKASIEAHPWLKH RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFFFFTNFESRGGKELDSNPFASL VFYWEPINRQVRVLGPFVKLFFEEAECYFFIS RPKSSQIGAVVSHQSSVPDREYLRKKNEELE QLYQDQEVPKHGLFEEAECYFFIS RPKSSQIGAVVSHQSSVPDREYLRKKNEELE QLYQDQEVPKHGNSGSVPUKLFEEAECYFFIS RPKSSQIGAVVSHQSSVPDREYLRKKNEELE QLYQDQEVPKHGNEGFFFVKLFFEEACCYFFIS RPKSSQIGAVVSHQSSVPDREYLRKKNEELE QLYQDQEVPKHGNEGFFT RPSTRGGELDSPFFASL VFYWEPINRQVRVLGPFT RGCE DWLYERLAP ARAAAHCGICRLVRWRKRRSVWGIQTSFV LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLLGLAVGSYLVRKSRRPQVT LLASLGVGLVTLGLAVGSYLVRKSRRPQVT LLASLGVGLVTL	{	1	1		1	Ī	
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VIATKQFSRGDFVVEYHGDLIEITDAKKREAL YAQDPSTGCYMYYFQYLSKTYCVDATRETN RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEELLYDYGDRSKASIEAHPWLKH RGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	F						
YAQDPSTGCYMYYFQYLSKTYCVDATRETN RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEELLYDYGDRSKASIEAHPWLKH RGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	i .		i	ł	(	1	LQSEEKKRIDELIESGKEEGMKIDLIDGKGRG
YAQDPSTGCYMYYFQYLSKTYCVDATRETN RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEELLYDYGDRSKASIEAHPWLKH RGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1	1	!	l	1		VIATKQFSRGDFVVEYHGDLIEITDAKKREAL
RDIAAGEELLYDYGDRSKASIEAHPWLKH  1325 2675 A 10338 3 870 PGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT		1	1	1			YAQDPSTGCYMYYFQYLSKTYCVDATRETN
RDIAAGEELLYDYGDRSKASIEAHPWLKH  1325 2675 A 10338 3 870 PGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1	1	1	1	<u> </u>		RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS
1325 2675 A 10338 3 870 PGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTROGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	I		1	1	ļ		RDIAAGEELLYDYGDRSKASIEAHPWLKH
RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1325	2675	A	10338	3	870	PGSTISCSELKGTOCRATAGSRGRRPPMTCWI
PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1		1		} ~		
EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT			1	l			
LLKGFGKDGFRFTTNFESRKGKELDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	I	1	i	<b>!</b>			
VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1	1	j	Ĭ	[		
RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT		1	l	l			
QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	I	1	1	l		Į.	
QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1	ļ	l		}		
DWLYERLAP  1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	Į.		<b>!</b>	1			
1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	l .	]	ŀ	1	ļ		QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE
1326 2676 A 10344 2 984 ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT		1	l	1		1	DWLYERLAP
LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT	1326	2676	Α	10344	2	984	
		]	ļ <sup></sup>		_		
	l	1	l		1		LLDPNEKYLLRLLDKTTVSHNTKRFRFALPTA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	İ		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ	1	İ	ĺ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	İ		1	peptide		/=possible nucleotide deletion, \=possible
1	ļ	i	ľ	sequence	l	nucleotide insertion
	<del>                                     </del>	<del></del>		<del>:</del>		HHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSD
l	{	ł	1	i	i	EDQGYVDLVIKVYLKGVHPKFPEGGKMSQY
1	İ		1		]	LDSLKVGDVVEFRGPSGLLTYTGKGHFNIQP
1		1	1	}	į	NKKSPPEPRVAKKLGMLAGGTGITPMLQLIRA
Į.			1			ILKVPEDPTQCFLLFANQTEKDIILREDLEELQ
j		ì	J	ļ	]	ARYPNRFKLWFTLDHPPKDWAYSKGFVTAD
}	ł	ļ	1			MIREHLPAPGDDVLVLLCGPPPMVQLACHPN
1		1	1	ļ		LDKLGYSQKMRFTY
1327	2677	A	10345	1	968	LOSAGEGYTHYLILLESPARPVAAVTQVQRR
1		]	}			RYHRLSDMSMLAERRRKQKWAVDPQNTAW
1		į	1	Ì		SNDDSKFGQRMLEKMGWSKGKGLGAQEQG
1		[	ĺ	[		ATDHIKVQVKNNHLGLGATINNEDNWIAHQ
1			ł	i	]	DDFNQLLAELNTCHGQETTDSSDKKEKKSFS
1	į		i	1		LEEKSKISKNRVHYMKFTKGKDLSSRSKTDL
1	ļ			1		DCIFGKRQSKKTPEGDASPSTPEENETTTTSAF
}	j.		1	,	Ì	TIQEYFAKRMAALKNKPQVPVPGSDISETQVE
	1			l i		RKRGKKRNKEATGKDVESYLQPKAKRHTEG
1			ļ	ļ		KPERAEAQERVAKKKSAPAEEQLRGPCWDQ
					<u></u>	SSKASAQDAGDHVQPA
1328	2678	A	10346	173	439	GSAAMKVKIKCWNGVATWLWVANDENCGI
1	l		1			CRMAFNGCCPDCKVPGDDCPLVWGQCSHCF
				·	ļ	HMHCILKWLHAQQVQQHCPMCRQEWKFKE
1329	2679	A	10351	3	964	QMEPGNDTQISEFLLLGFSQEPGLQPFLFGLFL
		ŀ		l		SMYLVTVLGNLLIILATISDSHLHTPMYFFLSN
[	1	į				LSFADICVTSTTIPKMLMNIQTQNKVTTYIACL
1				ļ	·	MQMYFFILFAGFENFLLSVMAYDRFVAICHP
ĺ		!	ŀ	i		LHYMVIMNPHLCGLLVLASWTMSALYSLLQI
		ŀ				LMVVRLSFCTALEIPHFFCELNQVIQLACSDSF
1	1	ŀ	ļ	I		LNHMVIYFTVALLGGGPLTGILYSYSKIISSIH AISSAQGKYKAFSTCASHLSVVSLFYGAILGV
İ		ļ				YLSSAATRNSHSSATASVMYTVVTPMLNPFI
ł	1	1			ļ	YSLRNKDIKRALGIHLLWGTMKGQFFKKCP
1330	2680	A	10352	34	2573	IPFLKSCCCCLFDFPPPPLDQVQEEECEVERV
1			1030-	,	22.2	TEHGTPKPFRKFDSVAFGESQSEDEQFENDLE
1		1	İ		İ	TDPPNWQQLVSREVLLGLKPCEIKRQEVINEL
	ļ	J	]			FYTERAHVRTLKVLDQVFYQRVSREGILSPSE
		Į.				LRKIFSNLEDILQLHIGLNEQMKAVRKRNETS
			1			VIDQIGEDLLTWFSGPGEEKLKHAAATFCSNQ
t	t .	İ	<b>i</b> :			PFALEMIKSRQKKDSRFQTFVQDAESNPLCRR
	İ	İ				LQLKDIIPTQMQRLTKYPLLLDNIATYTEWPT
1	ł	!				EREKVKKAADHCRQILNYVNQAVKEAENKQ
	}	1				RLEDYQRRLDTSSLKLSEYPNVEELRNLDLTK
	1	!			}	RKMIHEGPLVWKVNRDKTIDLYTLLLEDILV
}						LLQKQDDRLVLRCHSKILASTADSKHTFSPVI
	1	}				KLSTVLVRQVATDNKALFVISMSDNGAQIYE
			1		]	LVAQTVSEKTVWQDLICRMAASVKEQSTKPI
	}				i	PLPQSTPGEGDNDEEDPSKLKEEQHGISVTGL
J						QSPDRDLGLESTLISSKPQSHSLSTSGKSEVRD
						LFVAERQFAKEQHTDGTLKEVGEDYQIAIPDS
J						HLPVSEERWALDALRNLGLLKQLLVQQLGLT
ļ					1	EKSVQEDWQHFPRYRTASQGPQTDSVIQNSE
	!					NIKAYHSGEGHMPFRTGTGDIATCYSPRTSTE
[	[					SFAPRDSVGLAPQDSQASNILVMDHMIMTPE
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE
İ		Ì	]			GDGAVNKEEKDVNLRISGNYLILDGYDPVQE
Į.					ļ <b>,</b>	SSTDEEVASSLTLQPMTGIPAVESTHQQQHSP
} .	!					QNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI
						QSPSSCADSQSQIMEYIHKIEADLEHLKKVEE
L	L		L,	L		SYTILCQRLAGSALTDKHSDKS

ECO ID	CECTO	111-4	CCC.	Dunding	D==1:=4: 1 1	I Amin said semana (Ama)
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	liou.	in in	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine.
uence	Į.		7.44	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	í	i	i	peptide	Sequence	/=possible nucleotide deletion, \=possible
İ	1			sequence		nucleotide insertion
1331	2681	A	10353	1	2100	AVEFAEGALTMAPWPELGDAQPNPDKYLEG
	]	``	10000	] -	]	AAGOOPTAPDKSKETNKTDNTEAPVTKIELLP
	1			1		SYSTATLIDEPTEVDDPWNLPTLQDSGIKWSE
i	!					RDTKGKILCFFQGIGRLILLLGFLYFFVCSLDIL
	l		1	•		SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG
	i			ì	1	VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP
	i		1	ļ	!	IIMGANIGTSITNTIVALMQVGDRSEFRRAFA
1		i	ļ	1		GATVHDFFNWLSVLVLLPVEVATHYLEIITQL
	ļ				•	IVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK
	İ		İ	ĺ		KVISQIAMNDEKAKNKSLVKIWCKTFTNKTQ
1	ľ	Í	(		}	INVTVPSTANCTSPSLCWTDGIQNWTMKNVT
1	l					YKENIAKCQHIFVNFHLPDLAVGTILLILSLLV
1	ļ	l	1		ļ	LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP
1	1	]	1		į	FPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL
			Ļ	•		TPLIGIGVITIERAYPLTLGSNIGTTTTAIL.AAL
1	i	}				ASPGNALRSSLQIALCHFFFNISGILLWYPIPFT
i	İ	ĺ	1		ĺ	RLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP
	i	l	Ì	t		LTVFGLSLAGWRVLVGVGVPVVFIIILVLCLR
	i		ļ			LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW
1	1	]	}		!	DAVVSKFTGCFQMRCCCCCRVCCRACCLLC GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET
		ļ	1	ļ	]	FDNITISREAQGEVPASDSKTECTAL
1332	2682	Ā	10354	30	1377	SOOGSOPHROGPPSLLTAPHSLDLPALPPGPR
1 .55-	2002	1.	10351	}	1.577	GSQGKLRRVLVPMSVKPSWGPGPSEGVTAVP
[	!	ł	}	ĺ	ĺ	TSDLGEIHNWTELLDLFNHTLSECHVELSOST
	(		1			KRVVLFALYLAMFVVGLVENLLVICVNWRG
	ţ		ľ			SGRAGLMNLYILNMAIADLGIVLSLPVWMLE
1	i		į.		1	VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF
ļ	]		Ì		[	LVCLSVDRYVTLTSASPSWQRYQHRVRRAM
1		1	}			CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM
	i		•		ľ	APFETYSTWALAVALSTTILGFLLPFPLITVFN
Ī	į	1	ĺ		į	VLTACRLRQPGQPKSRRHCLLLCAYVAVFV
1	Í	i				MCWLPYHVTLLLLTLHGTHISLHCHLVHLLY
1						FFYDVIDCFSMLHCVINPILYNFLSPHFRGRLL
1	}	1	İ			NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP
						TOPLTPS
1333	2683	A	10358	2	884	AAGAGADGREPASERASRAEPPAVAMGOND
		l		_		LMGTAEDFADQFLRVTKQYLPHVARLCLIST
1		[	[			FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA
1			[ .			SSFVFLNLLGQLTGCVLVLSRNFVQYACFGLF
			}		1	GIIALQTIAYSILWDLKFLMRNLALGGGLLLL
1		}	ł			LAESRSEGKSMFAGVPTMRESSPKQYMQLGG
			}			RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI
						LVAIGFKTKLAALTLVVWLFAINVYFNAFWT
1						IPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL
						GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP
				]		ELPLPHVPGQESAKRRSARRFLIMSELTKELM
1				)		ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS
1			]			ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS
			]			WRDCSQEEQKELLCHTLCDILESACCDHSGS
						YCLVSWLRGKTTEETASISGSPAESSCQVEHS
					İ	SALAVEELGFERFHALIQKRSFRSLPELKDAV
			l		ŀ	LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN
}						VWDGDRECSGMKLLGIHEQAAVGFLTLMEA
						LRYCKVGSYLKISKIPYLDCLASETHLTVFFA
						KDMALVAPEAPSEQARRVFQTYDPEDNGFIP
				İ		DSLLEDVMKALDLVSDPEYINLMKNKLDPEG
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SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	i	USSN	location	corresponding	I-Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		ĺ	İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	ļ	1		peptide	sequence	/=possible nucleotide deletion, \=possible
1	}	ł	1	,	ł	nucleotide insertion
<u> </u>	ļ		ļ	sequence	<b> -</b>	
1	i	l	1			LGIILLGPFLQEFFPDQGSSGPESFTVYHYNGL
1		1	1		1	KQSNYNEKVMYVEGTAVVMGFEDPMLQTD
<u></u>	ļ	l	<b> </b>			DTPIKRCLQTKWPYIELLWTTDRSPSLN
1335	2685	Α	10375	82	2929	TRTKRRLGREKAMASPPRGWGCGELLLPFML
ĺ	1	l				LGTLCEPGSGQIRYSMPEELDKGSFVGNIAKD
	-	1	1			LGLEPQELAERGVRIVSRGRTQLFALNPRSGS
	l	i	1	1		LVTAGRIDREELCAQSPLCVVNFNILVENKM
1	ĺ	ĺ	1	İ	ļ	KIYGVEVEIIDINDNFPRFRDEELKVKVNENA
i		l		ļ		AAGTRLVLPFARDADVGVNSLRSYQLSSNLH
}	J	J	1	]		FSLDVVSGTDGQKYPELVLEQPLDREKETVH
1	1	1				DLLLTALDGGDPVLSGTTHIRVTVLDANDNA
ĺ		ĺ	!	[	<u> </u>	PLFTPSEYSVSVPENIPVGTRLLMLTATDPDE
	1	l			1	GINGKLTYSFRNEEEKISETFOLDSNLGEISTL
		ļ	}	1	)	OSLDYEESRFYLMEVVAODGGALVASAKVV
		l	1		}	VTVQDVNDNAPEVILTSLTSSISEDCLPGTVIA
						LFSVHDGDSGENGEIACSIPRNLPFKLEKSVD
	1		i			NYYHLLTTRDLDREETSDYNITLTVMDHGTP
		ļ	ļ	<u>}</u>	1	PLSTESHIPLKVADVNDNPPNFPQASYSTSVT
	1		ĺ			
	İ	Ì	1			ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE
1	1	ł	i	l	ł	DTFQGAPLSSYVSINSDTGVLYALRSFDYEQL
	}		ļ	ł	1	RDLQLWVTASDSGNPPLSSNVSLSLFVLDQN
l .				]		DNTPEILYPALPTDGSTGVELAPRSAEPGYLV
		l				TKVVAVDKDSGQNAWLSYRLLKASEPGLFA
(	1	ľ		ţ		VGLHTGEVRTARALLDRDALKQSLVVAVED
1	ì	l	i	•		HGQPPLSATFTVTVAVADRIPDILADLGSIKTP
			1		•	IDPEDLDLTLYLVVAVAAVSCVFLAFVIVLLV
1	İ	1	1			LRLRRWHKSRLLQAEGSRLAGVPASHFVGV
ĺ	ĺ	ĺ	1	ľ	ĺ	DGVRAFLQTYSHEVSLTADSRKSHLIFPQPNY
ł	ł	ļ	i		ì	ADTLLSEESCEKSEPLLMSDKVDANKEERRV
		i	1			QQAPPNTDWRFSQAQRPGTSGSQNGDDTGT
1		1				WPNNQFDTEMLQAMILASASEAADGSSTLGG
ĺ		1	ĺ	Ĺ		GAGTMGLSARYGPQFTLQHVLQGELGSDYR
Ī						QNVYIPGSNATLTNAAGKRDGKAPAGGNGN
1	ļ	{	1			KKKSGKKEKK
1336	2686	A	10379	1	557	RPRRRQPSFSCRVLVLEDPPCFRFTNSMNQEK
1330	2080	^	103/3	ļ *	337	LAKLQAQVRIGGKGTARRKKKVVHRTATAD
1			}	1		DKKLQSSLKKLAVNNIAGIEEVNMIKDDGTVI
1			1	1		1 3
1		ł	1	1	Į	HFNNPKVQASLSANTFAITGHAEAKPITEMLP
1	1	1	1	1	1	GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK
122=	0.00	<del> </del>	10555	ļ <u>-</u>	1060	PEDIDEEDDDVPDLVENFDEASKNEAN
1337	2687	A	10380	1	1263	IPGSTISWSPAAARGLSVCRCCRLHPASAMDL
	1	1	1	l	1	FGDLPEPERSPRPAAGKEAQKGPLLFDDLPPA
1		Ì	1	1	ł	SSTDSGSGGPLLFDDLPPASSGDSGSLATSISQ
i		ļ		1	J	MVKTEGKGAKRKTSEEEKNGSEELVEKKVC
1	1	1	1	ļ		KASSVIFGLKGYVAERKGEREEMQDAHVILN
1		[				DITEECRPPSSLITRVSYFAVFDGHGGIRASKF
1	1	1	}			AAQNI.HQNLIRKFPKGDVISVEKTVKRCLLD
J		1	ļ	1	}	TFKHTDEEFLKQASSQKPAWKDGSTATCVLA
i		Į.	1	]		VDNILYIANLGDSRAILCRYNEESQKHAALSL
1		l		1		SKEHNPTQYEERMRIQKAGGNVRDGRVLGV
1	1		l	}		LEVSRSIGDGQYKRCGVTSVPDIRRCQLTPND
1	]	}	)	1	Į	RFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ
!			•	j		TREGKSAADARYEAACNRLANKAVQRGSAD
1		1		1	1	NVTVMVVRIGH
1335	0.00	<u> </u>	10000	ļ	500	<u> </u>
1338	2688	A	10385	3	589	GPSQSMAAGELEGGKPLSGLLNALAQDTFHG
}	]	1	)	!	j	YPGITEELLRSQLYPEVPPEEFRPFLAKMRGIL
İ		1	1	1	]	KSIASADMDFNQLEAFLTAQTKKQGGITSDQ
1		1	]		]	AAVISKFWKSHKTKIRESLMNQSRWNSGLRG
1		1			ì	LSWRVDGKSQSRHSAQIHTPVAIIELELGKYG
1	]	ļ	}	l		QESEFLCLEFDEVKVNQILKTLSEVEESISTLIS
	<del></del>			<del></del>	·	<u></u>

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion QPN
1339	2689	A	10386	50	390	LGAMAKHHPDLIFCRKQAGVAIGRLCEKCDG KCVICDSYVRPCTLVRICDECNYGSYQGRCVI CGGPGVSDAYYCKECTIQEKDRDGCPKIVNL GSSKTDLFYERKKYGFKKR
1340	2690	A	10388	113	3472	SQLRKGASATHSSPSRTDCIAQMMDIYVCLK RPSWMVDNKRMRTASNFQWLLSTFILLYLM NQVNSQKKGAPHDLKCVTNNLQVWNCSWK APSGTGRGTDYEVCIENRSRSCYQLEKTSIKIP ALSHGDYEITINSLHDFGSSTSKFTLNEQNVSL IPDTPEILNLSADFSTSTLYLKWNDRGSVFPHR SNVIWEIKVLRKESMELVKLVTHNTTLNGKD TLHHWSWASDMPLECAIHFVEIRCYIDNLHFS GLEEWSDWSPVKNISWIPDSQTKVFPQDKVIL VGSDITFCCVSQEKVLSALIGHTNCPLIHLDGE NVAIKIRNISVSASSGTNVVFTTEDNIFGTVIF AGYPPDTPQQLNCETHDLKEIICSWNPGRVTA LVGPRATSYTLVESFSGKYVRLKRAEAPTNES YQLLFQMLPNQEIYNFTLNAHNPLGRSQSTIL VNITEKVYPHTPTSFKVKDINSTAVKLSWHLP GNFAKINFLCEIEIKKSNSVQEQRNVTIKGVE NSSYLVALDKLNPYTLYTFRIRCSTETFWKW SKWSNKKQHI.TTFASPSKGPDTWRFWSSDG KNLIIYWKPLPINEANGKILSYNVSCSSDEETQ SLSEIPDPQHKAEIRLDKNDYIISVVAKNSVGS SPPSKIASMEIPNDDLKIEQVVGMGKGILLTW HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV PSNSTETVIESDEFRPGIRYNFFLYGCRNQGY QLLRSMIGYIEELAPIVAPNFTVEDTSADSILV KWEDIPVEELRGFLRGYLFYFGKGERDTSKM RVLESGRSDIKVKNITDISQKTLRIADLQGKTS YHLVLRAYTDGGVGPEKSMYVVTKENSVGL IIAILIPVAVAVIVGVVTSILCYRKREWIKETFY PDIPNPENCKALQFQKSVCEGSSALKTLEMNP CTPNNVEVLETRSAFPKIEDTEIVSPVAERPEN RSDAKPENHVVESYCPPIIEEEIPNPAADETGG TAQVIYIDVQSMYQPQAKPEEQENDPVGGA GYKPQMHLPINSTVEDIAAEEDLDKTAGYPP QANVNTWNLVSPDSPRSIDSNSEIVSFGSPCSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQNKP ND
1341	2691	A	10392	1	5057	MLPPKHLSATKPKKSWAPNLYELDSDLTKEP DVIIGEGPTDSEFFHQRFRNLIYVEFVGPRKTL IKLRNLCLDWLQPETRTKEEIIELLVLEQYLTII PEKLKPWVRAKKPENCEKLVTLLENYKEMY QPEGESLHGVLVVSAGLRCPLGLSASTLLTW SGLDNSLSWAAVGMSCVLWDIELHHDFLGV ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVIISFSGDRDWDRRGRSRDTEPRDRWSITTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMIQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRKAMSVSSLS SLSSPSFTESQPIDFGAMPYVCDECGRSFSVIS EFVEHQIMHTRENLYEYGESFIHSVAVSEVQK

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SEQ ID	SEQID	Mct	SEQ ID NO:	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C-Cysteine, D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod		beginning		
nucl-	peptide	ľ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Į.	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	]	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
i				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ł	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	í	ĺ		peptide	1 '	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del></del>		<del> </del>	Sequence		SOVGGKRFECKDCGETFNKSAALAEHRKIHA
1	ļ	1		•	ł	RGYLVECKNOECEEAFMPSPTFSELOKIYGK
l .	Į.			ĺ		,
j	ļ	ļ	1		ļ	DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
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					ł	KEKMYECKVCGETFLHSSSLKEHQKIHTRGN
[	(		(			PFENKGKVCEETFIPGQSLKRRQKTYNKEKLC
l			İ			DFTDGRDAFMQSSELSEHQKIHSRKNLFEGR
ł					ļ	GYEKSVIHSGPFTESQKSHTITRPLESDEDEKA
}	ļ		ļ		i	FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
	ł	1	ļ	!	!	ASVEAQKSHSVAGPSKPKVMAESTIQSFDAIN
ļ	j	1	1	1		HORVRAGGNTSEGREYSRSVIHSLVASKPPRS
		1	ļ			HNGNELVESNEKGESSIYISDLNDKRQKIPAR
		1		ĺ	l	ENPCEGGSKNRNYEDSVIQSVFRAKPQKSVP
}	l	1	1	1	1	GEGSGEFKKDGEFSVPSSNVREYQKARAKKK
1	-	1	1			YIEHRSNETSVIHSLPFGEQTFRPRGMLYECQ
1	I	1	1	1	ł	ECGECFAHSSDLTEHQKIHDREKPSGSRNYE
	I	1				WSVIRSLAPTDPQTSYAQEQYAKEQARNKCK
	ł	]	1		·	DFRQFFATSEDLNTNQKIYDQEKSHGEESQGE
1	l l			1		NTDGEETHSEETHGQETIEDPVIQGSDMEDPQ
Ī	ľ		ł			KDDPDDKIYECEDCGLGFVDLTDLTDHQKVH
	ł					SRKCLVDSREYTHSVIHTHSISEYQRDYTGEQ
i	ł		Į.		ł	LYECPKCGESFIHSSFLFEHORIHEODOLYSM
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l	1	į .	ŀ	1	ł	KGCDDGFIALLPMKPRRNRAAERNPALAGSA
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ŀ			1		į.	ESFVNPAELADHVTVHKNEPYEYGSSYTHTS
ł	ì	1	ì	1	1	FLTEPLKGAIPFYECKDCGKSFIHSTVLTKHKE
		i				LHLEEEEEDEAAAAAAAAQEVEANVHVPQ
ł		ł	1		}	VVLRIQGLNVEAAEPEVEAAEPEVEAAEPEV
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1	ŀ	1		1		QPNGDADEPDGAGIEDPEERAEEPEGKAEEPE
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1					1	HECTETFTSSTAFSEHLKTHASMIFEPANAFG
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l	Į.			İ	ĺ	ECSGYIERASTSTGGANQADEKYFKCDVCGQ
	ļ <u>.</u>	<u> </u>			<u> </u>	LFNDHLSLARHQNTHTG
1342	2692	A	10393	2	1350	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSA
	1	1		[		ASRRSPAARPPVPAPPALPRGRPGTEGSTSLS
<b>[</b>	į.	1		ĺ		APAVLVVAVAVVVVVVSAVAWAMANYIHV
1	]	]	ļ	1	J	PPGSPEVPKLNVTVQDQEEHRCREGALSLLQ
Ī	ļ	į	1	ĺ	1	HLRPHWDPQEVTLQLFTDGITNKLIGCYVGN
	1			!	1	TMEDVVLVRIYGNKTELLVDRDEEVKSFRVL
1	1	1		Í	[	QAHGCAPQLYCTFNNGLCYEFIQGEALDPKH
1				ĺ		VCNPAIFRLIARQLAKIHAIHAHNGWIPKSNL
Į.	1	1	1	1	1	
j	1	}	)	]	ļ	WLKMGKYFSLIPTGFADEDINKRFLSDIPSSQI
				]	}	LQEEMTWMKEILSNLGSPVVLCHNDLLCKNII
ļ	ļ	J	1	1		YNEKQGDVQFIDYEYSGYNYLAYDIGNHFNE
		ł		1		FAGVSDVDYSLYPDRELQSQWLRAYLEAYK
ł	ì	1		1		EFKGFGTEVTEKEVEILFIQVNQFALASHFFW
[		1		[		GLWALIQAKYSTIEFDFLGYAIVRFNQYFKM
		j	1	ĺ		KPEVTALKVPE
1343	2693	A	10394	102	839	PEAOTSAVLAREKGHLPTMRHEAPMOMASA
		1	1	1		QDARYGQKDSSDQNFDYMFKLLIIGNSSVGK
				ĺ		TSFLFRYADDSFTSAFVSTVGIDFKVKTVFKN
			1	l	]	l
		!		1		EKRIKLQIWDTAGQERYRTITTAYYRGAMGFI
	Į.	i				LMYDITNEESFNAVQDWSTQIKTYSWDNAQ
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1		l	1	1		FFETSAKDNINVKQTFERLVDIICDKMSESLET
	1	1	1			DPAITAAKQNTRLKETPPPPQPNCAC
1344	2694	Λ	10395	2	4136	DRPPWNSRVDDFVTNLIHLSSKGHISPAKDTS
,		1		1	1	LOORTPAEMSPVLHFYVRPSGHEGAASGHTR
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VANPEALKILSAITQPVVVVAIVGLYRTGKSY	1347	2697	A	10402	153	1969	
							VANPEALKILSAITQPVVVVAIVGLYRTGKSY

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	(		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
}	ł	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	i	peptide		/=possible nucleotide deletion, \=possible
			<b> </b>	sequence	<u> </u>	nucleotide insertion
i			•	j		LMNKLAGKNKGFSLGSTVKSHTKGIWMWCV
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1	\					WTLRDFSLDLEADGQPLTPDEYLEYSLKLTQ
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						HRRKLAQLEKLQDEELDPEFVQQVADFCSYI
Ì	ŀ			}		FSNSKTKTLSGGIKVNGPRLESLVLTYINAISR
ł	1	ĺ	1		[	GDLPCMENAVLALAQIENSAAVQKAIAHYD
		1	1			QQMGQKVQLPAETLQELLDLHRVSEREATEV
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		1	1			QEQARVLKERCQGESTQLQNEIQKLQKTLKK
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1348	2698	A	10404	5	892	TQLPAPLSGVLSRLQLGSGAPLLTWVQETAG
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1740	0.00	ļ.,—	10400		1104	THKGKYWGKFYMPKRV
1349	2699	A	10409	59	1184	LRRNCSALGGLFQTIISDMKGSYPVWEDFINK
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1				ļ		AFNLYDLNKDGCITKEEMLDIMKSIYDMMG
1				}		KYTYPALREEAPREHVESFFOKMDRNKDGV
						VTIEEFIESCQKDENIMRSMQLFDNVI
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## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

Pages  $340\ {\rm to}\ 1963$  of this application contain amino acid sequence listings. They can be obtained at the address given below.

Les pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

World Intellectual Property Organization 34, chemin des Colombettes CH-1211 Genève 20